

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 115654

To: Ruixiang Li

Location: REM-4C70 Art Unit: 1646

Wednesday, March 03, 2004

Case Serial Number: 10/060765

From: Beverly Shears Location: Remsen Bldg.

RM 1A54

Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes			
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72 IKRQRRLYCNVG--IGFHLQVLPDGRISGTHBENPYSLLEISTVERGVVSLFGVRSALFV 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 INALVFLGILVGMVVPSPAGTRANNTLLDSRGWGTLLSRSRAGLAGELAGVNWESGYLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
               SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 CORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
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APPLICATION NUMBER: US/09/449,249
FILING DATE: 24-No. 650386-1999
CLASSIFICATION: cUnknown>
PRIOR APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996
ATTORNEY/AGRYI INFORMATION:
NAME: No. 6503886tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.415C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.9%; Score 176.5; DB 4 29.1%; Pred. No. 1.8e-09; tive 27; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIHER INFORMATION: /note= "FGF-6"
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
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                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 198 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46; Conservative
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Best Local Similarity
Matches 46; Conserva
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Job time: 38.4458 secs
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APPLICANT: Baird, J. Andrew
Chandler, Lois Ann
Sosnowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERA
NUMBER OF SEQUENCES: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                    45 --RORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFL 102
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12 LWALVFLGILVGMYVPSPAGTRANNTLLDSRGWGTLLSRSRAGLAGEIAGVNWESGYLVG 71
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CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 CORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
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                                                                                                                                                           Query Match
15.9%; Score 176.5; DB 4;
Best Local Similarity 29.1%; Pred. No. 1.8e-09;
Matches 46; Conservative 27; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 LWVSVLAGLILGACOAHP-----IPDS---SPLLQ-
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kirschner, Marc W. APPLICANT: Kinoshita, No. 6399386iyuki TITLE OF INVENTION: Receptor-Ligand Assay FILE REFERENCE: HU95-01A2.
CURRENT APPLICATION NUMBER: US/09/507,773
CURRENT FILING DATE: 2000-02-18
PRIOR PELING DATE: 1997-06-23
PRIOR PILING DATE: 1997-06-23
PRIOR PILING DATE: 1995-05-15
PRIOR APPLICATION NUMBER: 08/441,629
PRIOR PILING DATE: 1995-05-15
PRIOR PILING DATE: 1995-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/09449249 Patent No. 6503886 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               Sequence 12, Application US/09507773
Patent No. 6399386
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
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TYPE: PRT
CRGANISM: Homo sapien
US-09-507-773-12
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US-09-449-249-15
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                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                         33;
                                                                                                                                                                              15.9%; Score 176.5; DB 3; Length 198; 29.1%; Pred. No. 1.8e-09; tive 27; Mismatches 52; Indels 33
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APPLICANT: MOORE PAUL A.
APPLICANT: GOLEMAN, TIMOTHY A.
APPLICANT: GRUBER, JOACHIM R.
APPLICANT: DILLON, PATRICK J.
APPLICANT: GENTZ, REINER L.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
                                                                                                                                                                                                                                                                  13 LWVSVLAGLLLGACQAHP-----IPDS---SPLLQ-----FGGQV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 CORPDGALYGSLHFDPEACSFRELLLEDGYNVYOSEAH 140
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,082A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION 443.
PRIOR APPLICATION DATA.
APPLICATION NUMBER: PCT/US95/01790
FILING DATE. 14-FEB-1995
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-UW-1995
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,045
FILING DATE: 28-FEB-1997
                                                                                                                ; OTHER INFORMATION: /note= "FGF-6" US-08-718-904-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/09023082A
Patent No. 6077692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUBEN, STEVEN M.
JIMENEZ, PABLO
DUAN, D. ROXANNE
RAMPY, MARK N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAMPY, MARK A.
MENDRICK, DONNA
ZHANG, JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
LENGTH: 198 amino acide
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                     Query Match
Best Local Similarity 29.1%
Matches 46; Conservative
                                                              TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-09-023-082A-14
                                                                                                       FEATURE:
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45 --RORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFL 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 LWALVFLGILVGMVVPSPAGTRANNTLLDSRGWGTLLSRSRAGLAGEIAGVNWESGYLVG 71
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15.9%; Score 176.5; DB 3;
Best Local Similarity 29.1%; Pred. No. 1.8e-09;
Matches 46; Conservative 27; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---IPDS---SUTI---
APPLICATION NUMBER: US 08/862,432
FILING DATE: 23-MAY-1997
FILING DATE: 23-MAY-1997
FILING DATE: 13-AUG-1997
ATTORNEY, AGENT THORMATION:
NAME: STEFFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 36,68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
15.9%; Score 176.5; DB 3
Best Local Similarity 29.1%; Pred. No. 1.8e-09;
Matches 46; Conservative 27; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Kirschner, Marc W.
APPLICANT: Kirschner, Macc W.
APPLICANT: Kirschner, No. 6080718iyuki
APLICANT: Kinschitar, No. 6080718iyuki
FILE REFERENCE: HU95-01A2
CURRENT APPLICATION NUMBER: US/08/776,207A
CURRENT PILING DATE: 1997-06-23
EARLIER APPLICATION NUMBER: 08/41,629
EARLIER APPLICATION NUMBER: 08/41,629
EARLIER FILING DATE: 1995-05-15
EARLIER FILING DATE: 1995-05-15
EARLIER FILING DATE: 1994-07-22
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 198
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-776-207-12
; Sequence 12, Application US/08776207A
; Patent No. 6080718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOPOLOGY: not relevant TOPOLOGY: not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-09-023-082A-14
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US-08-776-207-12
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Patentin Release #1.0, Version #1.30
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CLASSIFICATION: 424
ATTORNEY/AGENT INPORMATION:
NAME: No. 6037329tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.415C1
                                                                                                                                                                       07265/046001
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FILING DATE: 24-SEP-1996
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COMPUTER READABLE FORM:
CMPUTER TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/08718904
Patent No. 6037329
                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INRORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REPRENCE/DOCKET NUMBER: 0726;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                        not relevant
                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: May 12, 1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                     198 amino acids
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                linear
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      SOFTWARE:
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US-08-718-904-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.9%; Score 176.5; DB 2; Length 198; 29.1%; Pred. No. 1.8e-09; tive 27; Mismatches 52; Indels 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-438-439C-20
Sequence 20, Application US/08438439C
Patent No. 5875967
Patent No. 5875967
PAPLICANT: Nathans, Jeremy
APPLICANT: Smallwood, Phillip M.
APPLICANT: Macke, Jennifer P.
TITLE OF INVENTION: FIBEOBROBLAST GROWTH FACTOR HOMOLOGOUS
TITLE OF INVENTION: FACTOR-2 AND METHODS OF USB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----IPDS---SPLLQ-----FGGQV-
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,439C
FLING DATE: May 12, 1995
      ITLE OF INVENTION: FACTOR-2 AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                    ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                          FILING DATE: May 12, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 07:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
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                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 46; Conserva
                            NUMBER OF SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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STRANDEDNESS: no
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GENERAL INFORMATION:
APPLICANT: Baird, J. Andrew
APPLICANT: Chandler, Lois Ann
APPLICANT: Sosnowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                           45 --RQRYLYTDDAQQTEAHLBIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFL 102
                                                                                                                                                                                                                                                                             72 IKRQRRLYCNVG--IGFHLQVLPDGRISGTHEENPYSLLEISTVERGVVSLFGVRSALFV 129
                                                                                                                                                            Gaps
                                                           33;
   Length 198;
                                                                                                                       13 INVSVLAGLILGACOAHP-----IPDS---SPLLO----FGGQV-
                                                        Indels
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/ Match 15.9%; Score 176.5; DB 2 Local Similarity 29.1%; Pred. No. 1.8e-09; les 46; Conservative 27; Mismatches 52
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US-08-867-471-14
                                    US-08-867-471-14
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                                                                                                       --RORYLYIDDAQQTEAHLEIREDGTVGGAADQSPESILIQLKALKPGVIQILGVKTSRFL 102
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                             12 IMALVFLGILVGMVVPSPAGTRANNTLLDSRGWGTLLSRSRAGLAGEIAGVNWESGYLVG 71
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13 IMVSVLAGLLIGACQAHP-----IPDS---SPLLQ----FGGQV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,629
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION 97A:
APPLICATION NUMBER: US 08/279,217
FILING DATE: 22-UUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 AMNSKGRLYATPSFQ-EECKFRETLLPNNYNAYESDLY 166
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                                                                                                                                                                 103 CORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
                                                                                                                                                                                        Query Match 15.9%; Score 176.5; DB 1; Best Local Similarity 29.1%; Pred. No. 1.8e-09; Matches 46; Conservative 27; Mismatches 52;
                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08441629
; Patent No. 5766923
; GENERAL INFORMATION:
    APPLICANT: Kirschner, Marc W.
    APPLICANT: Kirschner, Marc W.
    TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY
    NUMBER OF SEQUENCES:
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Hamilton, Brook, Smith & Reynold STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REPERENCE/DOCKET NUMBER: HU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 661-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
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amino acid
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STATE: Massachusetts
COUNTRY: USA
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US-08-441-629-12
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45 --RORYLYTDDAQOTEAHLEIREDGTVGGAADQSPESILIQLKALKPGVIQILGVKTSRFL 102
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Sequence 14, Application US/08867471

Sequence 14, Application US/08867471

Patent No. 587226

GENERAL INFORMATION:

APPLICANT: Nathans, Jeremy
APPLICANT: Smallwood, Philip M.
APPLICANT: Macke, Jennifer P.
TITLE OF INVENTION: FIRRORROBLAST GROWTH FACTOR HOWOLOGOUS
TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
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Patent No. 5876967
GENERAL INFORMATION:
APPLICANT: Smallwood, Phillip M.
APPLICANT: Machane, Jeremy
APPLICANT: Machane, P.
TITLE OF INVENTION: FIBROBROBLAST GROWTH FACTOR HOMOLOGOUS
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,471
FILING DATE: 02-UN-1997
CLASSIFICATION: DATA:
APPLICATION NUMBER: 08/439,725
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
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                                                                                                                                                                                                                                               ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla
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TELECOMMUNICATION INFORMATION:
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TELEFAX: 617/678-5099
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Best Local Similarity
Matches 46; Conserv
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PRIOR FILING DATE: 1995-06-05
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                                                                                          101 FLCQRPDGALYGSLHFDPRACSFRELLLEDGYNVYQSRAHGLPLHLPGNKSPHRDPAP-- 158
                                                                                                                   95
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APPLICANT: Rampy, Mark A.
APPLICANT: Rampy, Mark A.
APPLICANT: Rampy, Mark A.
APPLICANT: Benefack. Donna
APPLICANT: Louie, Arthur
ITLE OF INVENTION: Therapeutic Uses of Keratinocyte Growth Factor-2;
FILE REFERENCE: 1488.1060002
CURRENT APPLICATION NUMBER: US/09/248,998
CURRENT FILING DATE: 1999-02-12
EARLIER FILING DATE: 30-DEC-1998
EARLIER FILING DATE: 31-FEB-1998
NUMBER: OF SEC ID NOS: 13-FEB-1998
NUMBER: OF SEC ID NOS: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVLQILGVKTSR
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                              40 GGAPRRRKIYC----ATKYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGR
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                                                                                                                                                                             --LPGLPPALPEPPG 179
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15.9%; Score 177.5; DB 4; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41
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APPLICANT: Alderson, Ralph et al.
TITLE OF INVENTION: Fibroblast Growth Factor 11
FILE REFERENCE: PF104 P1
CURRENT APPLICATION NUMBER: US/09/572,406B
CURRENT FILING DATE: 2000-05-16
PRIOR PELICATION NUMBER: 60/135,524
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1099-05-28
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 1998-06-08
PRIOR APPLICATION NUMBER: 09/514,587
PRIOR APPLICATION NUMBER: 09/693,585
PRIOR APPLICATION NUMBER: 09/093,585
PRIOR APPLICATION NUMBER: 08/464,590
                                                                                                                                                                                                                                                                                                                                 Sequence 21, Application US/09248998
Patent No. 6599879
GENERAL INFORMATION:
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Patent No. 6605441
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US-09-248-998-21
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US-09-572-406B-5
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SEQ ID NO 21
LENGTH: 239
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                                                                                                                                                                                                             Gaps
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                                                                                                                                                                 Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08439725A
Patent No. 5633775
GENERAL INFORMATION:
APPLICANT: Smallwood, Philip M.
APPLICANT: Smallwood, Philip M.
APPLICANT: Smallwood, Philip M.
TITLE OF INVENTION: FIBROBROBLAST GROWTH FACTOR HOMOLOGOUS TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSES: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                          Query Match
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
ONEWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.9%; Score 176.5; DB 1; 29.1%; Pred. No. 1.8e-09; tive 27; Mismatches 52;
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CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REPERENCE/POCKET NUMBER: 071
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not relevant
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TELEFAX: 617/678-5099
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Best Local Similarity 29.1
Matches 46; Conservative
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
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                                                                              TYPE: PRT
ORGANISM: Homo mapiens
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DB 4;
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TITLE OF INVENTION: Fibroblast Growth Factor 15
FILE REFERENCE: PF203P1
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CURRENT FILING DATE: 2000-05-04
PRIOR PELING DATE: 1999-05-06
PRIOR FILING DATE: 1999-05-06
PRIOR FILING DATE: 1999-0-25
PRIOR PILING DATE: 1999-0-25
PRIOR PILING DATE: 1999-0-25
PRIOR APPLICATION NUMBER: 09/103,079
PRIOR PILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 09/103,079
PRIOR APPLICATION NUMBER: 09/103,079
PRIOR PILING DATE: 1998-06-23
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CURRENT FILING DATE: 1999-01-13
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PastSEQ for Windows Version 3.0
                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Conklin, Darrell C.
APPLICANT: Raymond, Fenella
APPLICANT: Bukowski, Thomas R.
APPLICANT: Holderman, Susan D.
APPLICANT: Hansen, Birgolt
APPLICANT: Hansen, Birgolt
APPLICANT: Hansen, Birgolt
APPLICANT: GENERAL Paul O.
TITLE OF INVENTION: NOVEL FGF HOMOLOGS
FILE REFRENCE: 96-2001
                                                                              Sequence 35, Application US/09229947 Patent No. 6518236
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; Sequence 5, Application US/09564829
Patent No. 6593112
; GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51; Conservative
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US-09-229-947-35
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Matches 51; Conserv
                                        RESULT 27
US-09-229-947-35
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SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 FLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAP-- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 GGAPRRKKIYC----ATKYHLQLHPSGRVNGSLENSAYSILEITÄVEVGIVAIRGLFSGR
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US-09-390-207-18
Sequence 18, Application US/09390207
Patent No. Patent No. GENERAL INFORMATION:
APPLICANT: Thomason, Arlen
APPLICANT: Liu, Benxian
TITLE OF INVENTION:
FILE REFERENCE: 99-371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
       APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6503886tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.415C1
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.9%; Score 177.5; DB 4; 29.7%; Pred. No. 1.9e-09; itive 23; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                        ); SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-449-249-12
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CURRENT FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PACENTIN VEY. 2.0
                                                                                                                                                                                                                                                                                        LENGTH: 239 amino acids
                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown MOLECULE TYPE: peptide
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; LENGTH: 239
; TYPE: PRT
; ORGANISM: HOMO SADIENB
US-09-390-207-18
                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
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                                                                                                                                                      95
                                                                                                                                 40 GGAPRRRKLYC----ATKYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGR
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                                                       Gaps
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15.9%; Score 177.5; DB 4; Length 239; 29.7%; Pred. No. 1.9e-09; tive 23; Mismatches 57; Indels 41
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us-10-060-765-4.rai

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US-09-425-021-11
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US-09-449-249-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 FLCQRPDGALYGSIHFDPRACSFRELLLEDGYNVYQSRAHGLPLHLPGNKSPHRDPAP-- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 GGQVRQRYLYIDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 GGAPRRKKIYC----ATKYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGR 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 239;
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15.9%; Score 177.5; DB 4; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 15.9%; Score 177.5; DB 3. Best Local Similarity 29.7%; Pred. No. 1.9e-09; Matches 51; Conservative 23; Mismatches 57.
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US-09-368-951-35
Sequence 35, Application US/09368951
Fatent No. 6352971
GENERAL INFORMATION:
APPLICANT: Conklin, Darrell C.
APPLICANT: Conklin, Darrell C.
APPLICANT: Bukowski, Thomas R.
APPLICANT: Bukowski, Thomas R.
APPLICANT: Hansen, Birgit
SEALIER FILING DATE: 1999-10-16
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 35
LENGTH: 239
HANDER OF THE RESERE FOR Windows Version 3.0
                     PILING DATE:
CLASSIPECATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/464,590
FILING DATE: 05-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J. G.
REGISTRATION NUMBER: 30.073
REFERENCE/DOCKET NUMBER: 325800-438
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (201) 994-1700
TELEFAX: (201) 994-1704
                                                                                                                                                                                                                            325800-438
APPLICATION NUMBER: US/09/093,585
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: Bir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-093-585-11
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Chandler, Lois Ann
Sosnowski, Barbara A.

TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THER
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
101 FLCQRPDGALYGSLHFDPEACSFRELLLEBGYNVYQSEAHGLPLHLPGNKSPHRDPAP-- 158
                                     101 FLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAP-- 158
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                                                                                                                   --- LPGLPPALPEPPG 179
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                                                                                                                                                                          152 LWYVSVNGKGRPRRFRTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 LWYVSVNGKGRPRRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 15.9%; Score 177.5; DB 4; Length 3 Best Local Similarity 29.7%; Pred. No. 1.9e-09; Matches 51; Conservative 23; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/449,249
FILING DATE: 24-NO. 6503886-1999
CLASSIFICATION: <unimons.
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Greene, John M.
APPLICANT: Greene, John M.
TITLE OF INVENTION: Fibroblast Growth Factor 15
TITLE OF INVENTION: Fibroblast Growth Factor 15
TITLE OF INVENTION: Fibroblast Growth Factor 15
CURRENT APPLICATION NUMBER: US/09/425,021
CURRENT FILLING DATE: 1999-10-25
EARLIER APPLICATION NUMBER: 09/103,079
EARLIER PILLING DATE: 1998-06-23
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 239
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Patent No. 6503886
GENERAL INFORMATION:
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ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/09425021
Patent No. 6482408
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Baird, J. Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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: 239 amino acids
amino acid
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6 BELLOTTY: ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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US-09-093-585-11
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STEET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MOORE, PAUL A.
APPLICANT: COLEMAN, TIMOTHY A.
APPLICANT: GRUBER, JOACHIM R.
APPLICANT: DILLON, PATRICK J.
APPLICANT: RENTZ, REINER L.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NAME: NO. 6037329temburg Ph.D., Carol REGISTRATION NUMBER: 39,317
REGISTRATION NUMBER: 39,317
RECISTRATION INDER: 760100.415C1
TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 239 amino acide TERNOTH: 239 amino acide STRANDEDMESS: single TOPOLOGY: unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER:
PCT/US95/01790
FILING DATE: 14-FEB-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                              OTHER INFORMATION: /note= "FGF-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/09023082A Patent No. 6077692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JIMENEZ, PABLO
DUAN, D. ROXANNE
RAMPY, MARK A.
MENDRICK, DONNA
ZHANG, JUN
NI, JIAN
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                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                 US-08-718-904-12
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GENERAL INFORMATION:
APPLICANT: Baird, J. Andrew
APPLICANT: Chandler, Lois Ann
APPLICANT: SOBNOWEKI, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAP!
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 -----FLP---
                                                                                                                                                                                                                Sequence 11, Application US/09103079A Patent No. 6013477
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Patent No. 6037329
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington
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Best Local Similarity
Matches 51; Conserv
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ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 GGAPRRRKLYC----ATKYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.9%; Score 177.5; DB 2; Length 239; 29.7%; Pred. No. 1.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 239;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FAPILICATION NUMBER: US/08/207,412B
FILING DATE: 06-MAR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.9%; Score 177.5; DB 2 29.7%; Pred. No. 1.9e-09; iive 23; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Delsher, Theresa A.
APPLICANT: Conklin, Darrell C.
APPLICANT: Raymond, Fenella
APPLICANT: Raymond, Fenella
APPLICANT: Bukowski, Thomas R.
APPLICANT: Bukowski, Thomas R.
APPLICANT: Holderman, Susan D.
APPLICANT: Hansen, Birgit
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL FGF HOMOLOGS
FILE REFERENCE: 96-20
CURRENT APPLICATION NUMBER: US/08/951,822A
CURRENT FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 35
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Mismatches
                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Ferraro, Gregory D
REGISTRATION UNBER: 325800-100
TELECOMMUNICATION INFORMATION:
TELEPAX: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-951-822-35
; Sequence 35, Application US/08951822A
; Patent No. 5989866
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               LENGTH: 239 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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Matches 51; Conserv
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Best Local Similarity
Matches 51; Conserv
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41 GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESILQUKALKPGVIQILGVKTSR 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 YLAMNKKGRLYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGAR---RQPSAER 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 GGAPRRKLYC----ATXYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGR
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                                                                                      --LPGLPPALPEPPG 179
                                                                                                                                            152 LWYVSVNGKGRPRRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPG 203
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                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Greene, John M.
APPLICANT: Rosen, Craig M.
TITLE ROSEN, Craig M.
FILE REFERENCE: PF203D1
CURRENT APPLICATION NUMBER: US/09/103,079A
CURRENT FILING DATE: 1996-06-23
EARLIER APPLICATION NUMBER: 08/462,169
EARLIER FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATCHIN VEY: 2.0
SOFTWARE: PATCHIN VEY: 2.0
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                                                                       101 FLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSP--HRDPAP 158
40 GGAPRRKLYC----ATKYHLQLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGR 95
                                                                                                                                 159 RGP-----ARFLPLPGLPPALPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
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STAFF.

STAFF.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CLERENY APPLICATION DATA:
APPLICATION NUMBER: US/08/464,590A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                        Sequence 11, Application US/08464590A
Patent No. 5763214
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR-11
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.9%; Score 177.5; DB 1
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57
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ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J. G.
REGISTRATION NUMBER: 30,073
REFRENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 994-1700
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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RESULT 16 US-08-462-169B-11 ; Sequence 11, Application US/08462169B

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41 GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQLLGVKTSR 100
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STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Hu, Jing-Shan
ATITLE OF INVENTION: Fibroblast Growth Factor-10
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: John Greene and Craig A. Rosen
ITILE OF INVENTION: Fibroblast Growth Factor-15
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEMARI & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 15.9%; Score 177.5; DB 1 Best Local Similarity 29.7%; Pred. No. 1.9e-09; Matches 51; Conservative 23; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325800-441 (PF203)
                                                                                                         ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD CITY: ROSELAND
                                                                                                                                                                                                                                                    ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 05 JUN 95
CLASSIFICATION: 514
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Patent No. 5817485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J. 62
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 239 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: LINEAR MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                          STATE: NEW JERSEY COUNTRY: USA
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STATE: N.
COUNTRY:
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E: Fish & Richardson P.C.
4225 Executive Square, Suite 1400
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NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/046001
TELECOMMUTCATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
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; LENGTH: 245
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-390-207-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: no
               STREET: 4225 ...
  ADDRESSEE:
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US-09-390-207-28
                                       CITY: La
STATE: Cl
COUNTRY:
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                              GENERAL INFORMATION:
APPLICANT: Nathans, Jeremy
APPLICANT: Smallwood, Philip M.
APPLICANT: Macke, Jennifer P.
TITLE OF INVENTION: FIBROBROBLAST GROWTH FACTOR HOMOLOGOUS
TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Nathans, Jeremy
APPLICANT: Stallwood, Phillip M.
APPLICANT: Macke, Jennifer P.
TITLE OF INVENTION: FIBROBROBIAST GROWTH FACTOR HOMOLOGOUS
TITLE OF INVENTION: FIBROBROBIAST GROWTH FACTOR HOMOLOGOUS
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.1%; Score 179; DB 2; Length 245; 28.8%; Pred. No. 1.4e-09; tive 30; Mismatches 78; Indels 1
                                                                                                                                                                                                                                                                                                                                                 COMPUTER KEALALDE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Nelease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,471
FILING DATE: 02-MV-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 18/439,725
FILING DATE: 12-MAY-1995
ATTORNEY AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38/347
REGISTRATION NUMBER: 38/347
                                                                                                                                                                                                      SSEE: Fish & Richardson P.C.
F: 4225 Executive Square, Suite 1400
La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07265/047001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08438439C Patent No. 5876967
    Sequence 11, Application US/08867471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 07.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617/678-5099
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 51; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: not
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STREET: 42
                            Patent No. 5872
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US-08-438-439C-7
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41 GGOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSR 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 YLAMNKRGRLYASDHYNAE-CEFVERIHELGYNTYASR-----LYRTGSSGPGAQRQPGA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSR 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 RGP-----ARFLPLPGLPPALPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 GGAPRRRKLYC----ATKYHLOLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78; Indels 18; Gaps
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Patent No. 6504530

GRNERAL INFORMATION:
APPLICANT: Thomason, Arlen
APPLICANT: Liu, Benxian

TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
FILE REPERENCE: 99-37

CURRENT FILING DATE: 1999-09-07

NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 245;
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COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: BATEMING SYSTEM: PC-DOS/MG-DOS
SOFTWARE: PATEMILIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,439C
FILING DATE: May 12, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

16.1%; Score 179; DB 2;
Best Local Similarity 28.8%; Pred. No. 1.4e-09;
Matches 51; Conservative 30; Mismatches 78
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40 GGAPRRRKLYC----ATKYHLQLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGR 95
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US-08-439-725A-11
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Sequence 7, Application US/09417721
Patent No. 6451303
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Whitehouse, Martha J.
APPLICANT: Wavanaugh, Michael W.
TITLE OF INVENTION: Anglogenically Effective Unit Dose of FGF and Method of TITLE OF INVENTION: Administering FILE REPERENCE: 1296/12169USO5
CURRENT APPLICATION NUMBER: US/09/417,721
CURRENT FILING DATE: 1999-10-13
PRIOR FILING DATE: 1998-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 GGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 DGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDFENCRFQHQTLE 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 18:1%; Score 201.5; DB 4; Length 134; Similarity 38.3%; Pred. No. 4e-12; 49; Conservative 27; Mismatches 43; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.1%; Score 179; DB 4; Length 240; 28.8%; Pred. No. 1.3e-09; Live 30; Mismatches 78; Indels
                                                                                                                                                                         APPLICANT: DOBERT, S.
APPLICANT: JOBERT, S.
APPLICANT: Glocher, S.
APPLICANT: Glocher, S.
APPLICANT: Glocher, S.
TITLE REPERENCE: GENERT. 054PR.
CURRENT APPLICANTON: WISTS and Encoded Human Proteins.
FILE REFERENCE: GENERT. 054PR.
CURRENT APPLICANTON NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 4031
LENGTH: 134
                                          181 ----LAPOPPDVGSSDPLSMV-GPSQGRSPSY 207
                                                                                                                                             Sequence 4031, Application US/09621976
Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
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Best Local Similarity 28.89
Matches 51; Conservative
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122 NGYDVYHS 129
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                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 DGYNVYQS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: SIGNAL
; LOCATION: -24..-1
US-09-621-976-4031
                                                                                                                                  US-09-621-976-4031
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Matches
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                               101 FLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSP--HRDPAP 158
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                                                                                                                                              40 GGAPRREKIYC----AIKYHLQLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGR
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                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08439725A
Sequence 11, Application US/08439725A
Patent No. 5693775
GENERAL INFORMATION:
APPLICANT: Smallwood, Philip M.
APPLICANT: Smallwood, Philip M.
APPLICANT: Macke, Jennifer P.
TITLE OF INVENTION: FIEROBROBLAST GROWTH FACTOR HOMOLOGOUS TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 16.1%; Score 179; DB 1; Length 245; Best Local Similarity 28.8%; Pred. No. 1.4e-09; Matches 51; Conservative 30; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATM:
APPLICATION NUMBER: US/08/439,725A
FILING DATE: 12-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Fish & Richardson P.C.
4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REPERENCE/DOCKET NUMBER: 07265/047001
TELEPHONE: 619/678-5099
TELEPHONE: 619/678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617/678-5099
INFORMATION FOR SEQ ID NO: 11:
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RESULT 12 US-08-867-471-11

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67 VVDCARGQSAHSLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEEEI 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 SGLWVSVLAGLLLGACQAHPIPDSSPLLQF--GGQVRQRYLYTDDAQ-QTBAHLEIREDG
                                                                                                                                                                                                                                                                                                      Transmembrane Polypeptides and Nucleic
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Best Local Similarity 36.3%; Pred. No. 5.2e-18;
Matches 77; Conservative 27; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Secreted and Transmembrane Intil REPRINGE: 10466-11.

TITLE OF INVENTION: Acids Encoding the Same FILE REPREBREE: 10466-11.

TITLE OF INVENTION: Acids Encoding the Same FILE REPREBREE: 10466-11.

CURRENT APPLICATION NUMBER: US/09/902,775A CURRENT FILING DATE: 2001-07-10.

PRIOR PELICATION NUMBER: PC/1050/04414

PRIOR PELING DATE: 1999-07-26

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-10-15

PRIOR PELING DATE: 1999-11-20

PRIOR PELING DATE: 1999-12-02

PRIOR PELING DATE: 1999-12-07

PRIOR PE
                                                                                                                                                             Roy, Margaret Ann
Srewart, Timothy A.
Tumas, Dania,
Williams, P. Mickey
Wood, William, I.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                        Pan, James
Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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APPLICANT:
                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 265; DB 4; Length 216;
; Pred. No. 5.2e-18;
27; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 ----LAPOPPDVGSSDPLSMV-GPSQGRSPSY 207
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                                                                                   PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 2000-01-05
NUMBER: PCT/US09/30919
PRIOR PLING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
                                                              APPLICATION NUMBER: PCT/US99/20944
           PCT/US99/20594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 59, Application US/09902775A Patent No. 6686451 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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36.3%;
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Filvaroff, Ellen
                                   LING DATE: 1999-09-08
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Best Local Similarity 36.39
Matches 77; Conservative
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Eaton, Dan L.
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US-09-902-775A-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 59
LENGTH: 216
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APPLICANT:
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FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/905,125A

CURRENT PILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER 05 SEQ ID NOS: 423
; SEQ ID NO 59
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-59
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US-09-905-125A-59
; Sequence 59, Application US/09905125A
; Patent No. 6664376
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
TOANT: Botstein, David
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Mather, Jennie P.
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Eaton, Dan L.
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                                                                                                                                                                                     Query Match
Best Local Similarity
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/907,794A

CURRENT FILING DATE: 2001-07-17

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08
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PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
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APPLICATION NUMBER: PCT/US99/30999
FILING DATE: 1999-12-20
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APPLICATION NUMBER: PCT/US99/21090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
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PRIOR APPLICATION NUMBER: PCT/US99/23089
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                                  84
                                                               LEIREDGTVGGAADOSPESKLOLK 84
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Marher, Jennie P.
Pan, James
Pani, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Danielt,
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; Sequence 59, Application US/09907794A
; Patent No. 6635468
                                  61 LEIREDGTVGGAADQSPESLLOLK
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Ashkenazi, Avi
Botstein, David
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Eaton, Dan L.
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127 RPDGYNVYRSEKHRLPVSLSSAKQ-RQLYKNRG---FLPLSHFLPMLPMVPEEPEDLRGH 182
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                                                                                                                                                                                                                                                                                                                                                                    67 VVDCARGOSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMOGLLQYSEEDCAFEEEI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                           128 LEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALP----EPPGI--- 180
                                                                                                                                                  11 SGLWVSVLAGLLLGACQAHPIPDSSPLLQF--GGQVRQRYLYTDDAQ-QTEAHLEIREDG 67
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                                                                                                                                                                                                   14 AGLWLAV-AGRPLA-----FSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRIRADG
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                                                                                  26;
       Length 216;
23.8%; Score 265; DB 4; Length 21. 36.3%; Pred. No. 5.2e-18; tive 27; Mismatches 82; Indels
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NAME/KEY: SIGNAL
LOCATION: -28...1
NAME/KEY: UNSURE
LOCATION: 57
OTHER INFORMATION: Xaa = Ala, Pro
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98.8%;
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Best Local Similarity 98.8
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                     146; Conservative
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Best Local
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Patent No. 6504530

GENERAL INFORMATION:

APPLICANT: Thomason, Arlen

TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides

TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides

FIER REFERENCE: 99-371

CURRENT APPLICATION UMBER: US/09/390,207

CURRENT FILING DATE: 1999-09-07

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 210
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                                                                                                                                                                           Query Match

86.2%; Score 959; DB 4; Length 181;
Best Local Similarity 99.4%; Pred. No. 1.8e-85;
Matches 180; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 SDPLSMVGPSQGRSPSYAS 209
CURRENT FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 181
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Best Local Similarity 78.9
Matches 157; Conservative
                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-09-390-207-5
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35-09-390-207-6
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US-09-390-207-4
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Sequence 6, Application US/09390207

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 NKSPHRDPAPRGPARFLPLPGLPPALPEPPGILAPOPPDVGSSDPLSMVGPSQGRSPSYA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 GVIQILGVXTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPG 148
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GENERAL INFORMATION:
APPLICANT: Thomason, Arlen
APPLICANT: Thomason, Arlen
APPLICANT: Liu, Benxian
TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
FILE REFERENCE: 99-371
CURRENT APPLICATION NUMBER: US/09/390,207
CURRENT FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
LENGTH: 181
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APPLICANT: Dumas Mine Edwards, J.B.
APPLICANT: Dumas Mine Edwards, J.B.
APPLICANT: Johert, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.;
FILE REFERENCE: GENSET. 054 PR.2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO $213
LENGTH: 85
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Pred. No. 9.2e-35;
0; Mismatches 1.
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Pred. No. 1.8e-65;
9; Mismatches 26
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9-09-621-976-5213
; Sequence 5.213, Application US/09621976
; Patent No. 6639063
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Sequence 5, Application US/09390207

Batent No. 6504530

GENERAL INFORMATION:
APPLICANT: Thomason, Arlen
APPLICANT: Liu, Benxian
TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
FILE REFERENCE: 99-3371
CURRENT APPLICATION NUMBER: US/09/390,207
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('GgD2_6')todata2/liaa/5B_COMB.pep:*

('GgD2_6')todata3/liaa/6A_COMB.pep:*

('GgD2_6')todata3/liaa/6E_COMB.pep:*

('GgD2_6')todata3/liaa/PCTUS_COMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-390-207-4
US-09-301-970-6
US-09-907-794A-59
US-09-905-125A-59
US-09-902-775A-59
US-09-902-775A-59
US-09-417-721-7
US-08-439-725A-11
US-08-438-439C-7
US-08-467-471-11
US-08-467-471-11
US-08-464-590A-11
US-08-461-590A-11
US-08-461-169B-11
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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APPLICANT: Thomason, Arlen
APPLICANT: Liu, Benxian
TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
FILE REFERENCE: 99-371
CURRENT APPLICATION NUMBER: US/09/390,207
CURRENT FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 209;
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Pred. No. 1.2e-99;
0; Mismatches 1; Indels
US-09-564-829-5

US-09-248-998-21

US-09-248-998-21

US-08-439-725A-14

US-08-441-629-12

US-08-8471-14

US-08-8438-439C-10

US-08-438-439C-10

US-08-738-904-15

US-09-507-73-12

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                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/09390207; Patent No. 6504530; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 99.4%;
Best Local Similarity 99.5%;
Matches 208; Conservative
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; ORGANISM: Homo sapiens
US-09-390-207-2
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inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal which are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample of is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or useful as molecular weight markers for tissue cyping, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful configuration animals or knock-out animals which are useful configuration animals or knock-out animals which are useful especial for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide. \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$**\$\$\$**

Sequence 208 AA;

1; 1; Gaps Query Match
Best Local Similarity 99.5%; Pred. No. 8.6e-91;
Matches 208; Conservative 0; Mismatches 0; Indels 1;

1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH 60

LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120 61

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CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPLPGLPPALPEPPGI 180 121

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Search completed: March Job time: 128.4 secs

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transmembrane PRO polypeptide.
           01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
     26-AUG-2002; 2002US-00227873
                       (GETH ) GENENTECH INC.
                                                                                                                                                                            Sequence 208 AA;
17-APR-2003
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The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

cuseful for stimulating the proliferation of or gene expression in

periotyce cella. PRO357, PRO222, PRO1272 or PRO4405 polypeptide are useful

cor stimulating the proliferation or differantiation of chondrocyte

cells. PRO357, PRO525, PRO125, PRO1306 or PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TMF)-

cells. PRO337, PRO526, PRO357, PRO1306, PRO1419, PRO1419,

PRO137, PRO526, PRO357, PRO125, PRO1306, PRO1419, PRO1410,

PRO137, PRO526, PRO526, PRO511, PRO1083, PRO1414, PRO1319,

CC PRO1306, PRO1307, PRO1305, PRO1305, PRO1474, PRO1317, PRO1411, PRO1309,

PRO1478, PRO1330, PRO1305, PRO1305, PRO1473, PRO1441, PRO13124,

PRO1478, PRO1330, PRO1305, PRO1305, PRO1474, PRO1317, PRO1414, PRO1318,

CC PRO186, PRO1307, PRO1305, PRO1403, PRO1474, PRO1317, PRO1406,

CC PRO186, PRO1307, PRO1305, PRO1401, PRO1404, PRO1327, PRO1406, PRO1406, PRO6079, PRO6079, PRO1804, PRO1401, PRO1305, PRO1406, PRO1406, PRO6079, PRO6079, PRO1804, PRO1401, PRO1406, PRO1406
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Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                    New PRO polypeptides and nucleic acids encoding the polypeptides, in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; SEQ ID NO 78; 314pp; English.
               Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                                                                                                                                                                    2003-644807/61.
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1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH 60 Gape 1, 98.7%; Score 1098.5; DB 7; Length 208; 99.5%; Pred. No. 8.6e-91; cive 0; Mismatches 0; Indels 1; Conservative Query Match Best Local Similarity Matches 208; Conserv

1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGGVRQRYLYTDDAQQTEAH

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120 CSFRELLLEDGYNVYQSEAHGLPLHPGNKSPHRDFARRFRFRFPLFLFGLPPALPEPFGI 179

180 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 181 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS

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RESULT 40

Ä ADC77779 standard; protein; 208

ADC77779;

(first entry) 01-JAN-2004 Novel human secreted and transmembrane protein PRO10196.

Human, secreted and transmembrane protein, PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; oclon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; release;

Homo sapiens.

gene therapy

US2003088066-A1.

08-MAY-2003

13-AUG-2002; 2002US-00219466

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Goddard A, Godowski PJ; shan JF, Watanabe CK, Wood WI; Gerritsen ME, Goddard Smith V, Stephan JF, Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

WPI; 2003-657980/62.

N-PSDB; ADC77778

One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, or for preparing a medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody, e.g. cancer.

Claim 11; Fig 78; 314pp; English.

The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (1) PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
useful for stimilating the proliferation of or gene expression in
pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
for stimulating the proliferation or differentiation of chondrocyte
cells. PRO357, PRO525, PRO1185, PRO136 or PRO1419 polypeptide
cells. PRO357, PRO525, PRO1185, PRO1366 or PRO1419 polypeptide
cells. PRO3317, PRO5256, PRO357, PRO1366, PRO1419, PRO214,
PRO147, PRO317, PRO5256, PRO357, PRO1306, PRO1419, PRO1419,
PRO147, PRO3137, PRO5256, PRO363, PRO1927, PRO1344, PRO1309,
PRO1478, PRO1184, PRO1126, PRO1196, PRO1192, PRO1244, PRO1319,
PRO1349, PRO1376, PRO1367, PRO1309, PRO1474, PRO13197, PRO1341, PRO1367,
PRO1845, PRO1376, PRO1387, PRO1409, PRO1474, PRO1341, PRO1567,
PRO1849, PRO6079, PRO9846 or PRO10096 polypeptide are useful for
ctimulating the proliferation of normal human dermal fibroblasts cells.
PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for

PRO1274, PRO1412, PRO1340, PRO1338, PRO1760, PRO1567,

Wed Mar

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ADC78025 standard; protein; 208 AA.
                                                                                                                                                                                                                                                                                                                 Claim 11; Fig 78; 308pp; English.
                                                                                                                                                                                                                                  01-JUN-2001; 2001WO-US017B00.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                        29-AUG-2002; 2002US-00232234.
                                                                                                             (first entry)
                                                                                                                                                                                                                                                                  Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                 WPI; 2003-765529/72.
                                                                                                                                                                                                                                                                                       N-PSDB; ADC78024
                                                                                                                                                                                                   US2003096972-A1.
                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                         29-JUN-2001;
09-APR-2002;
                                                                                                                                                                              gene therapy
                                                                                                              01-JAN-2004
                                                                                                                                                                                                             22-MAY-2003.
                                                                                                   ADC78025;
                                121
                                                                              RESULT 38
                                                                                    ADC78025
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contributing the proliferation of normal human dermal fibroblast cells. PRO inhibiting the proliferation of normal human dermal fibroblast cells. PRO collypeptides such as PRO6604, PRO4811, PRO7174, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal which comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of commal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample of in a indicative of the presence of tumour in the mammal. The tumour is lung is indicative of the presence of tumour in the mammal. The tumour or tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful as molecular weight markers, for tissue useful transpendic animals or knock-out animals which are useful cor chromosome and gene mapping or gene therapy. (II) is useful cor chromosome and gene mapping or gene therapy. (II) is useful cor succession of server animals which are useful secreting broads. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, export injuries).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 LEIREDGIVGGAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                               PRO1286, PRO1310, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338, PRO13284, PRO1376, PRO1367, PRO1260, PRO1567, PRO1287, PRO1987, PRO1987, PRO1987, PRO1983, PRO1984, PRO4983, PRO1983, PRO59840, PRO6079, PRO9836 or PRO10096 polypeptide are useful for stimulating the proliferation of normal human dermal fibroblasts cells. PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO188, PRO1194, PRO1272, PRO188, PRO4302, PRO488, PRO4303, PRO5725, PRO7154, or PRO7425, polypeptide are useful for PRO5029, PRO7154, or PRO7425, polypeptide are useful for PRO5029, PRO5025, PRO1194, PRO1955, PRO5029, PRO5029, PRO1194, PRO1955, PRO1964, or PRO7425, polypeptide are useful for PRO5029, PRO50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYTTDDAQQTEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 7; Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.7%; Score 1098.5; DB 7; Length
99.5%; Pred. No. 8.6e-91;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human secreted and transmembrane protein PRO10196.
PRO1244, I
PRO1279,
               PRO1186, PRO1192,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transmembrane PRO polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as molecular weight markers, for treating arthritis and tumor.
                                                                                                                                                                                                                                                                                                                                                                   CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                               119
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Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necroals factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
                                                                                                                      LEIREDGIVGGAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSHFDPEA
                                                                                                                                                                                                                                                                                                                                                                                                                  MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                                                                                        LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
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Smith V, Stephan JF, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human secreted and transmembrane protein PRO10196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 208
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179

US2003073816-A1

120

59

Gaps

1;

cuseful for stimulating the proliferation of or gene expression in useful for stimulating the proliferation of or gene expression in cuseful for stimulating the proliferation of or gene expression in periotyte cells. PR0257, PR0229, PR02120 or PR04405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PR0231, PR0357, PR0155, PR0155, PR0156, PR01419 polypeptide are useful for stimulating the release of tumour necrosis factor [TNF) cape a pr0241, PR0337, PR0526, PR0363, PR0357, PR0725, PR01306, PR01419, PR0214, PR01413, PR0256, PR0186, PR01134, PR0826, PR01805, PR0181, PR0181, PR0181, PR01307, PR013 tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO157, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are sport injuries). This is the a transmembrane PRO polypeptide.

Sequence 208 AA;

61 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPLPGLPPALPEPPGI 180 53 1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH Gaps 1; DB 7; Length 208; Pred. No. 8.6e-91; 0; Mismatches 0; Indels tch
al Similarity 99.7%; Score 1098.5;
al Similarity 99.5%; Pred. No. 8.6e208; Conservative 0; Mismatches LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS Local Similarity 121 181 180 Query Match Matches d g à g ð à

ADC47150 standard; protein; 208 (first entry) 18-DEC-2003 ADC47150; RESULT 37

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Novel human secreted and transmembrane protein PRO10196.

Human, secreted and transmembrane protein, PRO; cytostatic; vulnerary; antiarthritic, pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation;

The invention describes an isolated pro (secreted and trainsmenorarie)

CC polypoptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypoptide are useful for stimulating the proliferation of or gene expression in useful for stimulating the proliferation of or gene expression in constitution the proliferation of construction of chondrocyte for stimulating the proliferation or differentiation of chondrocyte calls. PRO313, PRO357, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tummour necrosis factor (TRF)-calpha from human blood. PRO982, PRO337, PRO523, PRO1306, PRO1419, PRO1419, PRO214, PRO1314, PRO1313, PRO337, PRO523, PRO188, PRO1126, PRO1186, PRO1192, PRO1414, PRO1309, PRO1347, PRO1365, PRO1186, PRO1186, PRO1192, PRO144, PRO1314, PRO1309, PRO1343, PRO1343, PRO1343, PRO1344, PRO1344, PRO1356, PRO1343, PRO1343, PRO1343, PRO1344, PRO1356, PRO1343, PRO1343, PRO1344, PRO1356, PRO9409, PRO New isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO), for use in recombinantly producing a PRO polypeptide, as a hybridization probe, and in gene therapy. Goddard A, Godowski PJ; phan JF, Watanabe CK, Wood WI; tumour; The invention describes an isolated PRO (secreted and transmembrane) dermal fibroblast cell differentiation inhibitor; tumour; lung colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; Gerritsen ME, Goddard Smith V, Stephan JF, Claim 11; Fig 78; 308pp; English. 01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480. 13-AUG-2002; 2002US-00219070. Desnoyers L, (GETH) GENENTECH INC WPI; 2003-801246/75. N-PSDB; ADC47149 JS2003105288-A1. Grimaldi JC, 25-JUL-2000; Homo sapiens gene therapy 05-JUN-2003 Baker KP,

transmembrane PRO polypeptide.

tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO252, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and

Gaps 7; Score 1098.5; DB 7; Length 208; Pred. No. 8.6e-91; 0; Mismatches 0; Indels 1; 98.78; Conservative Query Match Best Local Similarity Matches 208; Conserv

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transmembrane PRO polypeptide
                                                   Sequence 208 AA;
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C polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
polypeptide (I). PRO982, PRO1160, PRO1242 or PRO4182 polypeptide are
cuseful for stimulating the proliferation of on gene expression in
perior to stimulating the proliferation of differentiation of chondrocyte
cells. PRO317, PRO327, PRO125, PRO1306 or PRO419 polypeptide
are useful for stimulating the release of tumour necrosis factor (INP)-
are useful for stimulating the release of tumour necrosis factor (INP)-
cells. PRO3131, PRO356, PRO315, PRO1306, PRO1191, PRO1191,
PRO1317, PRO317, PRO126, PRO1005, PRO1319, PRO1191, PRO1191,
PRO1319, PRO1136, PRO1186, PRO1186, PRO1191, PRO1191, PRO1191,
PRO1381, PRO3130, PRO1186, PRO1186, PRO1191, PRO1191, PRO1141, PRO1312,
PRO1987, PRO1928, PRO1186, PRO1186, PRO1191, PRO1191, PRO1326,
PRO1987, PRO1928, PRO4341, PRO10096, PRO1979, PRO1940, PRO1928,
PRO1987, PRO1928, PRO4341, PRO1001, PRO4333, PRO1944, PRO1932,
PRO1987, PRO5938 or PRO10096 polypeptide are useful for
PRO1987, PRO5938, PRO1988, PRO1988, PRO1988, PRO1988, PRO4932, PRO1988, PRO1988,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New PRO polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wood WI;
                                                                                                                                                           release;
                                                                                    protein; PRO; cytostatic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Godowski PJ;
                                                                                                      antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha; (TMF) alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gerritsen ME, Goddard A, Godowski F
Smith V, Stephan JF, Watanabe CK,
                                      Novel human secreted and transmembrane protein PRO10196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; SEQ ID NO 78; 315pp; English
                                                                                            transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-2002; 2002US-00232231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Desnoyers L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
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                                                                                                 secreted and
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                                                                                                                                                                                                                                                                                                                                                                                            US2003088071-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grimaldi JC,
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                gene therapy
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                                                                                                                                                                                                                                                                60 LEIREDGTVGGAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
                                                                                                                                                                                                                                                                                                                                       180
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Wood WI;
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                                                                                                                                                                        59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNR) alpha release; dermal fibroblast cell proliferation; oclon tumour; lung tumour; cell differentiation inhibitor; tumour; lung tumour; liver tumour; breast tumour; prostate tumour; rectal tumour; prostate tumour; cell differentiation; prostate tumour; rectal tumour; contact tumour; prostate tumour; prostate tumour; cell differentiation; prostate tumour; rectal tumour; contact tumour; prostate tumour; prostate tumour; prostate tumour; prostate tumour; prostate mapping; gene mapping;
                                                                                                                                                                     1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRXLYTDDAQQTEAH
                                                                                                                                                                                                                                                                                                                                       CSFRELLLEDGYNVYQSEAHGLFLHLPGNKSPHRDPAPRGPARFLFLPLPGLFPALPEPPGI
                                                                                                                                                                                                                           61 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
                                                                                                                  1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRXLYTDDAQQTEAH
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                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New PRO polypeptide for use as molecular weight markers for protein electrophoresis purposes and for detecting the presence of tumor in
                                                                 ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard A, Godowski E
ohan JF, Watanabe CK,
              DB 7; Length 208;
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human secreted and transmembrane protein PRO10196.
Score 1098.5; DB 7;
Pred. No. 8.6e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerritsen ME, Goddard
Smith V, Stephan JF,
                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 LAPOPPDVGSSDPLSMVGPSOGRSPSYAS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC47405 standard; protein; 208 AA
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                   Query Match
Best Local Similarity 99.5%;
Matches 208; Conservative
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Grimaldi JC, Gurney AL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
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tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polyamucleotide (II) encoding (I) is useful tor chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO252, PRO1572 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide. is indicative of the presence of tumour in the mammal.

Sequence 208 AA;

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120
                                                                                                                                                                60 LEITEDGIVGGAADQSPESLLQIKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
                                                                                                                                                                                               121 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                                                                                                                                                                                         120 CSFREILLEDGYNVYQSEAHGLPIHLPGNKSPHRDPAPRGPARFLFLPGREPARFIT 179
                                                                   9
                                                                                                59
                                                                                           1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQFKYLYTDDAQQTEAH
                                                                                                                                 61 LEIREDGTVGGAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
                                                                 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                  Gaps
                                  .;
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 DB 7; Length 208;
Score 1098.5; DB 7; Length
Pred. No. 8.6e-91;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                         LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
   Query Match 98.7%;
Best Local Similarity 99.5%;
Matches 208; Conservative
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ADC49027 standard; protein; 208 18-DEC-2003 ADC49027; RESULT 34

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(first entry)

Novel human secreted and transmembrane protein PRO10196.

release; human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF) alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping; gene therapy

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Homo sapiens

US2003088070-AL

08-MAY-2003.

28-AUG-2002; 2002US-00230260

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC

Goddard A, Godowski PJ; ohan JF, Watanabe CK, Wood WI; Gerritsen ME, Goddard Smith V, Stephan JF, Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

WPI; 2003-801155/75 N-PSDB; ADC49026

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The invention describes an isolated PRO (secreted and transmembrane)

CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
cc useful for stimulating the proliferation of or gene expression in
perioryte cells. PRO357, PRO225, PRO1272 or PRO4405 polypeptide are useful
cc stimulating the proliferation of differentiation of chondrocyte
cc are useful for stimulating the release of tumour necrosis factor (TNF)-
are useful for stimulating the release of tumour necrosis factor (TNF)-
cr pro127, PRO337, PRO525, PRO1365, PRO1306, PRO1419, PRO1419, PRO1414,
PRO137, PRO337, PRO525, PRO1805, PRO351, PRO1206, PRO1306,
PRO127, PRO1330, PRO1347, PRO1305, PRO1909, PRO1244, PRO1411, PRO1306,
PRO1286, PRO1330, PRO1347, PRO1305, PRO1409, PRO1244, PRO1411, PRO1413,
PRO1366, PRO1367, PRO1367, PRO1305, PRO1444, PRO1411, PRO1414,
PRO1367, PRO1928, PRO4341, PRO1801, PRO18033, PRO1444, PRO1367,
PRO1867, PRO1928, PRO1367, PRO1801, PRO18043, PRO1444, PRO1316,
CC PRO940, PRO6679, PRO9836 or PRO1809, PRO1444, PRO1316,
PRO181, PRO225, PRO186, PRO1164, PRO1273, PRO1489, PRO4408,
CC PRO940, PRO6798, PRO186, PRO1164, PRO1273, PRO1489, PRO4408,
CC PRO940, PRO6798, PRO186, PRO1164, PRO1273, PRO1489, PRO4408,
CC PRO940, PRO6798, PRO1644, PRO1273, PRO1489, PRO4408,
CC Inhibiting the proliferation of normal human dermal fibroblast cells.
CC Inhibiting the proliferation of normal human dermal fibroblast cells.
CC Involves comparing the presence of tumour, in ammal which
CC Involves comparing the presence of tumour in ammal. The tumour is lung
CC Involves comparing the presence of tumour, prostate tumour, rectal tumour
CC the PRO polypeptides in the test sample as compared to the control sample
CC Involves comparing the presence of tumour, rectal tumour or tumour, breast tumour, prostate tumour, r
        and nucleic acids encoding the polypeptides, useful
                       New PRO polypeptides and nucleic acids encoding the polypeptides, in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                         Claim 11; SEQ ID NO 78; 315pp; English.
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Sequence 208 AA;

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120
                                                                                                                                                                                                 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                                                                59
                                                                                                                                                  1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                        1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                   LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
                                  --
 DB 7; Length 208;
                                  Indels
Score 1098.5; DB 7;
Pred. No. 8.6e-91;
0; Mismatches 0;
                                                                                                                                                                                                                                                                    181 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
     98.7%;
99.5%;
   Query Match
Best Local Similarity 99.5
Matches 208; Conservative
                                                                                                                                          61
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ADC49544 standard; protein; 208 AA. ADC49544; ADC49544 EXXXE

RESULT 35

LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 208

(first entry) 18-DEC-2003

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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polynucleotides encoding them.

The PRO polypeptides and polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TMP)-alpha from human blood, for stimulating the proliferation of or gene chondrocyte cells, for stimulating the proliferation of or gene chordrocyte cells, for stimulating the proliferation of or gene chordrocyte cells, for stimulating the proliferation of or gene chordrocy in operacyte cells or for stimulating the proliferation of or gene normal human dermal fibroblasts. The PRO nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant technology, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents, in gene therapy, in chromosome identification, as chromosome antibodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies, are useful for preparing an edicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies, are useful for preparing and prome and/or cartiage and antibodies, and an anti-PRO second tumours and home and/or cartiage antibage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders (e.g. arthritis, sports injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated PRO polypeptide useful for tissue typing, as molecular weight markers in protein electrophoresis, for treating arthritis, tumor.
                                                                                                                                                                                                                                                                                                                                                                                        Gerritsen ME, Goddard A, Godowski P
Smith V, Stephan JF, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Fig 78; 308pp; English.
                2000WO-US023328.
2000WO-US030873.
2000US-0253646P.
                                                                                                                                                                          28-FEB-2001; 2001WO-US006520.
25-MAY-2001; 2001WO-US017092.
                                                                                                                                                                                                                           2001WO-US017800.
2001WO-US021066.
                                                                                             2000WO-US032678
2000US-00747259
                                                                                                                                                 2000WO-US034956
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C, Gurney AL,
                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Grimaldi JC,
                                                                                                                                                                                                                                 01-JUN-2001;
29-JUN-2001;
                                                                                                                        20-DEC-2000;
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                                                                                                  01-DEC-2000;
                                                                 28-NOV-2000;
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Sequence 208 AA;

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                                    1; Gaps
98.7%; Score 1098.5; DB 7; Length 208; 99.5%; Pred. No. 8.6e-91;
                Pred. No. 8.6e-91;
0; Mismatches 0; Indels
                Best Local Similarity 99.5
Matches 208; Conservative
Query Match
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1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH

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120
                                                                                                                                                                   CSFREILLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGDPPALPEPPGI 179
                                                                                      LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
                                                                                                                                       121 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH 59
                                            LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
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factor alpha release; human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; Wood WI Godowski PJ; Watanabe CK, Novel human secreted and transmembrane protein PRO10196 Goddard A, Gerritsen ME, Goddard Smith V, Stephan JF, ADC49828 standard; protein; 208 AA. 25-JUL-2000; 2000US-0220605P. 01-UUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 200ZUS-00119480. 14-AUG-2002; 2002US-00219075. (first entry) Į,ť GETH) GENENTECH INC. Desnoyers I WPI; 2003-801154/75. US2003088064-A1. Homo sapiens. Grimaldi JC, gene therapy 08-MAY-2003. 18-DEC-2003 ADC49828; Baker RESULT 33 ADC49828 Godowski PJ;

N-PSDB; ADC49827.

ĸ New secreted and transmembrane PRO polypeptide useful for preparing medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody, e.g. cancer.

Claim 11; SEQ ID NO 78; 314pp; English.

LITE ALWEATHON UNDOINED AND INCLORED AND INCOMENTATION OF DEPROPED AND INCOMENTATION OF DEPROPED AND INCOMENTATION OF OF PROBISO DIVIDEDTICE ARE USEFUL for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO1259, PRO1350 or PRO4405 polypeptide are useful for stimulating the proliferation of differentiation of chondrocyte cells. PRO357, PRO725, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrossis factor (TMP)-calpus from human blood. PRO982, PRO357, PRO1305, PRO1306, PRO1419, PRO1419, PRO1419, PRO1419, PRO1414, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1414, PRO1419, PRO1 The invention describes an isolated PRO (secreted and transmembrane)

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2000US-0220607P.
2000US-0220624P.
2000US-0220638P.
2000US-022064P.
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2000US-0222425P.
2000US-0227133P.
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2000US-0219556P.
2000US-0220585P.
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2000US-0212901P.
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                                                                                                                                                                                                                                                                                        98.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PRO polypeptide #39.
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.5
Matches 208; Conservative
                                                                                                                                                                                                                                                Sequence 208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2003096969-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUN-2000;
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                                                                                                                                                                                                            CSFRELLIEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                                                        LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120
                                                                                                                                     LEIREDGIVGGAADOSPESILQIKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
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phan JF, Watanabe CK, Wood WI;
                                   MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, PRO; secreted polypeptide, transmembrane polypeptide, tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, or for preparing a medicament for treating
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Smith V, Stephan JF,
                                                                                                                                                                                                                                                                                 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                                                                                     LAPOPPUVGSSDPLSMVGPSQGRSPSYAS 208
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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Grimaldi JC, Gurney AL,
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may be used in the development and screening of therapeutically useful reagents, in gene therapy, in chromosome identification, as chromosome markers and in generating probes. The PRO polypeptides, or anti-PRO antibodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sporte injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSFRELLIEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 LEIREDGTVGGAADQSPESLLQLKALKÞGVIQILGVKTSRFLCQRPDGALYGSLHFDPBA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDSDEIGFEHSGIMVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1098.5; DB 7; Length
Pred. No. 8.6e-91;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
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The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

useful for stimulating the proliferation of or gene expression in

periotyc cells. PRO357, PRO222, PRO1272 or PRO4405 polypeptide are useful

for stimulating the pro11feration or differentiation of chondrocyce

cells. PRO231, PRO125, PRO1136, PRO1136, PRO1419 polypeptide

cells. PRO231, PRO357, PRO725, PRO1306, PRO1419, PRO214,

pro147, PRO3137, PRO526, PRO1063, PRO531, PRO1061, PRO1141, PRO1304,

PRO147, PRO3137, PRO526, PRO1065, PRO1063, PRO1244, PRO1241,

PRO1330, PRO1330, PRO1367, PRO1065, PRO1073, PRO1244, PRO1340,

PRO1343, PRO1357, PRO1367, PRO1195, PRO1447, PRO13141, PRO1136,

PRO1364, PRO1367, PRO1367, PRO1196, PRO1273, PRO1340, PRO1326,

PRO143, PRO1359, PRO9386 or PRO1069 polypeptide are useful for

PRO940, PRO6729, PRO988, PRO1180, PRO1372, PRO1444, PRO1324,

PRO1341, PRO225, PRO7154, Or PRO1069 polypeptide are useful for

PRO5724, PRO5725, PRO7154, Or PRO7152, PRO1486, PRO4302, PRO4408,

PRO1341, PRO225, PRO7154, Or PRO7154, PRO1714, PRO5778, PRO4408,

PRO5724, PRO5725, PRO7154, Or PRO7425 polypeptide are useful for

CC inhibiting the proilecration of normal human dermal fibroblast cells. PRO

CC inhibiting the presence of tumour in ammal which

are useful for detecting the presence of tumour, rectal tumour or

CC innormal cells of the same cell type, where a higher level of expression of

in a test sample of cells taken from the mammal, and a control sample of

in a test sample of cells taken from the mammal, and a control sample

CC innormal cells of the same cell type, where a higher level of expression of

the PRO polypeptides in the test sample as compared to the control sample

CC innormal cells of the same cell type, where a higher level of expression of

the PRO polypeptides in the test sample as compared (II) encoding (II) is

cuseful for cherapeutic agents. A polymorleotide (II) encoding (II)

CC STORMING USEFUL FORMING USEFUL FORMING USEFUL FORMING U

transmembrane PRO polypeptide.

Sequence 208 AA;

61 LEIREDGTVGGAADOSPESILIOLKALKPGVIQILGVKTSRFLCORPDGALYGSLHFDPEA 120 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPGLPPPFGI 180 59 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH Gaps ; DB 7; Length 208; Indels Pred. No. 8.6e-91; 0; Mismatches 0; Query Match
Best Local Similarity 99.5%; Pred. No. 8.6eMatches 208; Conservative 0; Mismatches 181 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 208 9 121 120 180 원 8 ð 8 d ð g à

human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; Novel human secreted and transmembrane protein PRO10196. ADB72969 standard; protein; 208 AA. (first entry) 04-DEC-2003 ADB72969; ADB72969

chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release, dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping gene therapy

Homo sapiens

JS2003092887-A1.

15-MAY-2003.

L2-AUG-2002; 2002US-00218956.

29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

WPI; 2003-777258/73. N-PSDB; ADB72968

Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as molecular weight markers, for treating arthritis, tumor.

Claim 11; Fig 78; 308pp; English.

The invention describes an isolated PRO (secreted and transmembrane)

CD polypeptide (I). PR0982, PR01160, PR01187 or PR01129 polypeptide are polypeptide for stimulating the proliferation of or gene expression in pericyte cells. PR0357, PR0229, PR01272 or PR04405 polypeptide are useful for stimulating the proliferation of differentiation of chondrocyte cells. PR0357, PR0725, PR01155, PR01196 or PR01419 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PR0357, PR0982, PR0357, PR0725, PR01306 or PR04419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF)-cap br0337, PR0526, PR0363, PR0353, PR01255, PR01306, PR01347, PR0337, PR0356, PR01348, PR01349, PR01369, PR01344, PR01369, PR01349, PR01369, PR01344, PR01369, PR01344, PR01369, PR01344, PR01369, PR01387, PR01305, PR01379, PR01305, PR01379, PR01305, PR01379, PR01306, PR01379, PR0137 tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide

Sequence 208 AA;

Gaps 1; DB 7; Length 208; Indels 98.7%; Score 1098.5; DB 7; 99.5%; Pred. No. 8.6e-91; ive 0; Mismatches 0; Conservative Similarity Matches 208; Query Match Best Local S

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RESULT 29
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Transmembrane polypeptides and polypublecetides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours fe.g. humg tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TMF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene capression in pericyte cells or for stimulating the proliferation of or gene or probes, in chromosome and gene mapping, in generating are useful as hybridisation probes, in chromosome and gene mapping, in generating transgenic animals or knock-out animals which technology, in generating transgenic animals or knock-out animals which can be used in the development and screening of therapy in generating probes. The PRO polypeptides, or anti-PRO antibodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the re-
CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGPPALPEPPGI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated PRO polypeptides, useful for tissue typing, gene therapy, molecular weight markers in protein electrophoresis, and for treating
                                                                                                                                                                                                                     Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.
                             209
                                               LAPOPPDVGSSDPLSMVGPSQGRSPSYAS
                                                                                                                       ADB84699 standard; protein; 208 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Fig 78; 308pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       24-FEB-2000; 2000WO-US005004.
02-WAR-2000; 2000WO-US005841.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                           (first entry)
                                                                                                                                                                                                   Human PRO polypeptide #39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arthritis and tumors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polypeptides designated PRO polypeptides including polypeptides useful for stimulating the proliferation or differentiation of specific cell types, and for diagnosing cancer.
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ohan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNR) alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                 61 LEIREDGTVGGAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
                                                                                                                                                                                                                           1 MDSDETGFEHSGIMVSVLAGILLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                                                   Gaps
differentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. sequence represents a human PRO polypeptide of the invention.
                                                                                                                                                                                   1;
                                                                                                                                         Length 208;
                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human secreted and transmembrane protein PRO10196
                                                                                                                                           DB 7;
                                                                                                                                      Score 1098.5; DB 7;
Pred. No. 8.6e-91;
0; Mismatches 0;
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Smith V, Stephan JF,
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2001WO-US021066.
2002US-00119480.
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                                                                                                                                                98.7%;
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                                                                                                                                                                     Best Local Similarity 99.5
Matches 208; Conservative
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                                                                                                     Sequence 208 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy
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                                                                                                                                                    Query Match
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Human, PRO; secreted polypeptide, transmembrane polypeptide; tumour; cancer; lung; colon, breast; prostate; rectum, liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.

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ADB87117 standard; protein; 208 AA
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                                                                                                                                                                                                                            Human PRO polypeptide #39
                                                                                                                            Sequence 208 AA;
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The invention describes an isolated PRO (secreted and transmembrane)

CC polypeptide (1). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
polypeptide (1). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
cells. PRO317, PRO229, PRO1272 or PRO4405 polypeptide are useful
cor stimulating the proliferation of differentiation of chondrocyte
cells. PRO321, PRO325, PRO1155, PRO1306 or PRO419 polypeptide
are useful for stimulating the release of tumour necrosis factor (TNF)-
are useful for stimulating the release of tumour necrosis factor (TNF)-
cre alpha from human blood. PRO982, PRO337, PRO1725, PRO1306, PRO1192,
PRO1347, PRO326, PRO1265, PRO1055, PRO8937, PRO1726, PRO1190, PRO1141,
PRO1347, PRO3130, PRO1186, PRO1192, PRO1197, PRO1141, PRO11316,
PRO1184, PRO1136, PRO1186, PRO1195, PRO1197, PRO1141, PRO13136,
PRO1940, PRO6079, PRO9836 or PRO10056 polypeptide are useful for
cre stimulating the proliferation of normal human dermal fibroblasts cells.
PRO5123, PRO5725, PRO7184, PRO1187, PRO1484, PRO432,
PRO1940, PRO6079, PRO9836 or PRO10056 polypeptide are useful for
cre useful for detecting the presence of tumour are useful for
cre useful for detecting the presence of tumour in animal which
cre useful for detecting the presence of tumour in the named. The tumour is lung
cre useful for detecting the presence of tumour rectal tumour or
cre useful for detecting in the test sample as compared to the control sample of
cre normal cells of the same cell type, where a higher level of expression of
the PRO polypeptides in the test sample as compared to the control sample
cre the PRO polypeptides in the test sample as compared to the ordering are
cre the PRO polypeptides in the test sample as compared to the control sample of
cre the PRO polypeptides in the test sample as compared to the ordering capenic and gene mapping or gene therapeutic agents. A polymorleotide (II) is useful
cre the proposed and gene mapping or gene therapy. (II) is useful
cre section or tumour. Present control sample of
cre suseful for transing bone an
Claim 11; Fig 78; 308pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transmembrane PRO polypeptide.
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Wood WI;

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, W

Baker KP, Desnoyers L, Grimaldi JC, Gurney AL, (GETH) GENENTECH INC.

WPI; 2003-657981/62.

N-PSDB; ADB87116

01-JUN-2001; 2001MO-US017800. 29-JUN-2001; 2001MO-US021066. 09-APR-2002; 2002US-00119480.

13-AUG-2002; 2002US-00219479.

US2003088067-A1 Homo sapiens.

08-MAY-2003.

120 60 LEIREDGTVGGAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPBA 119 180 179 9 59 61 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPRA 120 CSFREILLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGUFPALFBFGT 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH 1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH 121 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI Gaps 1; DB 7; Length 208; Score 1098.5; DB 7; Length Pred. No. 8.6e-91; 0; Mismatches 0; Indels LAPOPPOVGSSDPLSMVGPSOGRSPSYAS 208 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 98.7%; Query Match Best Local Similarity 99.5 Matches 208; Conservative

The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polypuclectides encoding them.

The PRO polypeptides and polymuclectides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prestate tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TMP) alpha from human blood, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene comman in periotyte cells or for stimulating the proliferation of normal human dermal fibroblasts. The PRO mucleic acide are useful as hybridisation probes, in chromosome and gene mapping, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents, in generating probes. The PRO polypeptides by recombinant reagents, in generating probes. The PRO polypeptides or anti-PRO antibodies, are useful for preparing a medicament for treating a metical prodes, and in the development and screening of therapeutically useful as markers and in generating probes. The PRO polypeptides or anti-PRO antibodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies and in the development and servents and shows and for cartilates. Ϊ, antibodies, such as periorte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention. 60 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120 59 or as 1 MDSDETGFEHSGLWYSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH Gaps One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, o hybridization probes in chromosome and gene mapping. ٦: Score 1098.5; DB 7; Length 208; Pred. No. 8.6e-91; 0; Mismatches 0; Indels 1; claim 11; Fig 78; 314pp; English. 98.78; Matches 208; Conservative Similarity Sequence 208 AA; Н 61 121 Query Match Best Local ਨੋ 셤 à g ð

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Gaps

1,

DB 7; Length 208;

9 59 119 180

us-10-060-765-4.rag

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condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducting the redifferentiation of chondrocytes. PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.
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Pred. No. 8.6e-91;
0; Mismatches 0; Indels
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01-JUN-2001; 2001WO-US017800.
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                                                                                                                                                                                                                                                                                                                                          98.7%;
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                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 99.5
nes 208; Conservative
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                                                                                                                                                                                                                                                                          Sequence 208 AA;
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Grimaldi JC,
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09-APR-2002;
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                          180
                                                                                                                                                                                        useful
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Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New PRO polypeptides and nucleic acids encoding the polypeptides, usefue.g. in gene therapy, disease diagnosis, chromosome identification and
                                                                                                                                              CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon, breast; prostate; rectum; liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.
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Smith V, Stephan JF, Watanabe CK,
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB84945;
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gene therapy, as
treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               release;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, secreted and transmembrane protein, PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release (TMF) alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; tumour; lung tumour;
Gerritsen ME, Goddard A, Godowski P
Smith V, Stephan JF, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated PRO polypeptide useful for tissue typing, molecular weight markers in protein electrophoresis, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human secreted and transmembrane protein PRO10196.
                                                                                              181 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                              180 LAPQPEDVGSSDPLSMVGPSQGRSPSYAS
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us-10-060-765-4.rag

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are useful for stimulating the release of tumour necrosis factor (TNF)-
alpha from human blood. PRO982, PRO357, PRO136, PRO1419, PRO214,
PRO247, PRO337, PRO526, PRO353, PRO5131, PRO1401, PRO1419, PRO214,
PRO1478, PRO1134, PRO9126, PRO1105, PRO1071, PRO1411, PRO11309,
PRO1487, PRO130, PRO136, PRO1305, PRO1305, PRO1071, PRO1411, PRO13139,
PRO1286, PRO1330, PRO1347, PRO1305, PRO1379, PRO1274, PRO1340, PRO1338,
PRO1387, PRO1376, PRO1387, PRO1409, PRO1474, PRO1979, PRO1344, PRO4322,
PRO1887, PRO1928, PRO4341, PRO1409, PRO1474, PRO1979, PRO1444, PRO4322,
PRO1987, PRO529, PRO9836 or PRO10096 polypeptide are useful for
pRO181, PRO5229, PRO788, PRO1194, PRO1373, PRO3488, PRO4408,
PRO181, PRO5225, PRO7154, or PRO1425 polypeptide are useful for
inhibiting the proliferation of normal human dermal fibroblast cells.
CC inhibiting the proliferation of normal human dermal fibroblast cells.
CC inhibiting the proliferation of normal human dermal which
involves comparing the level of expression of the above PRO polypeptides
involves comparing the level of expression of the above PRO polypeptides
CC in a test sample of cells taken from the mammal, and a control sample of
CC the PRO polypeptides in the test sample as compared to the control sample
CC the PRO polypeptides in the test sample as compared to the control sample
CC the PRO polypeptides in the test sample as compared to the control sample
CC the PRO polypeptides in the test sample expression of the mammal.
CC the PRO polypeptides in the test sample expression of the mammal with the tumour is a lung
CC the PRO polypeptides in the test sample expression of the control sample
CC the PRO polypeptides in the test sample expression of the control sample
CC the PRO polypeptides in the test sample expression of the control sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful for generating transgenic animals or knock-out animals which are useful is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ransmembrane PRO polypeptide
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Sequence 208 AA;

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120
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                                                                                                           1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                     LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
                                                                                                                                                                                                                               121 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI
                                                                           1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                       1; Gaps
98.7%; Score 1098.5; DB 7; Length 208; 99.5%; Pred. No. 8.6e-91; ive 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                           LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                                                                                                               LAPOPPOVGSSDPLSMVGPSQGRSPSYAS
                                           208; Conservative
 Query Match
Best Local Similarity
Matches 208; Conserv
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Novel human secreted and transmembrane protein PRO10196 ADB78297 standard; protein; 208 (first entry) 04-DEC-2003 ADB78297; RESULT 24

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Human, secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; tumour necroais factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; clond fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping; gene therapy

The invention describes an isolated kWO (Secreted and Ladismenorally polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in the stimulating the proliferation of or gene expression in the proliferation of defect of chandrocyte cells. PRO357, PRO225, PRO1152 or PRO4405 polypeptide are useful contained the proliferation of defect of chandrocyte calls. PRO31, PRO357, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TMF)-calpha from human blood. PRO982, PRO1357, PRO1305, PRO1419, PRO1419, PRO1317, PRO1307, PRO1419, PRO1419, PRO1134, PRO1862, PRO1008, PRO1009, PRO1407, PRO1419, PRO1134, PRO1367, PRO1136, PRO1136, PRO1136, PRO1136, PRO1136, PRO1136, PRO1136, PRO1136, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1378, PRO1376, PRO1378, PRO1376, PRO1378, PRO1378 for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (1) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful Wood WI; New isolated PRO polypeptide useful for tissue typing, gene therapy, a molecular weight markers in protein electrophoresis, and for treating the invention describes an isolated PRO (secreted and transmembrane) Godowski PJ; Goddard A, Gouc,...
TE Watanabe CK, Gerritsen ME, Goddard Smith V, Stephan JF, Claim 11; Fig 78; 308pp; English transmembrane PRO polypeptide. 01-JUN-2001; 2001MO-US017800. 29-JUN-2001; 2001MO-US021066. 09-APR-2002; 2002US-00119480. 13-AUG-2002; 2002US-00219478. Desnoyers L, (GETH) GENENTECH INC. WPI; 2003-765495/72. N-PSDB; ADB78296. US2003092889-A1 Homo sapiens. Baker KP, De Grimaldi JC, 15-MAY-2003

Sequence 208 AA;

ή. 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYIDDAQQTEAH 60 1; Gaps 98.7%; Score 1098.5; DB 7; Length 208; 99.5%; Pred. No. 8.6e-91; ive 0; Mismatches 0; Indels 1; al Similarity 99.5 208; Conservative Query Match Best Local 9 Matches

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antiarthritic, pericyte cell proliferation;
pericyte cell differentiation; chondrocyte cell proliferation;
chondrocyte cell differentiation; tumour necrosis factor alpha release;
(TNF)-alpha release; dermal fibroblast cell proliferation;
dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
colon tumour; breast tumour; prostate tumour; rectal tumour;
liver tumour; tissue typing; chromosome mapping; gene mapping;
gene therapy.

Homo sapiens.

US2003088068-A1.

08-MAY-2003,

13-AUG-2002; 2002US-00219481

01-JUN-2001; 2001MO-US017800. 29-JUN-2001; 2001MO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ; Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

WPI; 2003-657982/62. N-PSDB; ADB80673. One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.

Claim 11; Fig 78; 305pp; English.

The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I) PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

polypeptide (I) PRO982, PRO1160, PRO1187 or PRO4192 polypeptide are

cusful for stimulating the proliferation of or gene expression in

periorte cells. PRO357, PRO212, PRO1155, PRO1180, PRO1419 polypeptide

cells. PRO31, PRO357, PRO715, PRO1150, PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TMF)
cells. PRO31, PRO357, PRO715, PRO1160, PRO1419, PRO1414,

PRO317, PRO137, PRO518, PRO1181, PRO1181, PRO1181, PRO1181,

PRO147, PRO3130, PRO3136, PRO1186, PRO1192, PRO1197, PRO1141, PRO1181,

PRO1478, PRO1181, PRO1186, PRO1186, PRO1192, PRO1197, PRO1141, PRO1181,

PRO1867, PRO1328, PRO4187, PRO1186, PRO1197, PRO1141, PRO1181,

PRO1867, PRO1328, PRO4184, PRO1186, PRO1197, PRO1141, PRO1181,

PRO1867, PRO1328, PRO4188, PRO1186, PRO1187, PRO1181, PRO1181,

PRO1867, PRO1328, PRO4188, PRO1186, PRO1187, PRO1181, PRO1181,

PRO1867, PRO1328, PRO7186, PRO1186, PRO1187, PRO1181, PRO1181,

PRO1867, PRO1328, PRO7186, PRO1186, PRO1197, PRO1181, PRO1181,

PRO1867, PRO1186, PRO1186, PRO1186, PRO1187, PRO1181, PRO1186,

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PRO1867, PRO1186, PRO1186, PRO1186, PRO1187, PRO1181, PRO1186,

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PRO1867, PRO1186, PRO1186, PRO1186, PRO1187, PRO1186,

PRO1867, PRO1186, PRO1186, PRO1186, PRO1186, PRO1186, PRO1186,

PRO1868, PRO1186, PRO1186,

Sequence 208 AA;

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                                                                                                                                                           60 LEIREDGTVGGAADQSPESILQIKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
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Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human, secreted and transmembrane protein, PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   release;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumour;
                                                                                             1 MDSDETGFEHSGLMVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                                                                                  61 LEIREDGTVGGAADQSPESILIQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
                                                                                                                                                                                              CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI
                                                               1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRVLYTDDAQQTEAH
                                Gaps
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                                1;
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Score 1098.5; DB 7; Length 208; Pred. No. 8.6e-91;
                                Indels
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                               0
               Pred. No. 8.6e
0; Mismatches
                                                                                                                                                                                                                                                                 181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
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                                                                                                                                                                                                                                                                                                                                                                                   ADB73215 standard; protein; 208
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29-JUN-2001; 2001WO-US021066.
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 98.7%;
99.5%;
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                 Best Local Similarity 99.5
Matches 208; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
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     Query Match
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Claim 11; Fig 78; 315pp; English

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invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is the amino acid sequence of a human PRO protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEIREDGTVGGAADOSPESILQIKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120
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Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; prostate tumour; lissue typing; chromosome mapping; gene mapping;
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                                                                                                                                                                                                                                                                                     Score 1098.5; DB 7; Length 208;
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0; Mismatches 0;
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                                                                                                                                                                                                                                                                                     98.7%;
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29-JUN-2001; 2001WO-US021066.
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                                                                                                                                                                                                                                                                                                                        Best Local Similarity ... Matches 208; Conservative
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N-PSDB; ADBB3567.
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                              Sequence 208 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                   88888888
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The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I) PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

polypeptide (I) PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

certain a prosest, PRO1262, PRO1272 or PRO4465 polypeptide are useful

certain a prosest, PRO357, PRO1272 or PRO4465 polypeptide are useful

cells. PRO357, PRO725, PRO1156, PRO1160, PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TNF)-

are useful for stimulating the release of tumour necrosis factor (TNF)-

are useful for stimulating PRO91065, PRO315, PRO124, PRO136,

PRO417, PRO3137, PRO526, PRO3105, PRO1095, PRO10192, PRO1136,

PRO125, PRO1181, PRO136, PRO1186, PRO1192, PRO1197, PRO1141, PRO1131,

PRO126, PRO1181, PRO126, PRO1186, PRO1192, PRO1197, PRO1147, PRO1131,

PRO125, PRO1181, PRO1367, PRO1186, PRO1192, PRO1244, PRO1314,

PRO1926, PRO1181, PRO1367, PRO1186, PRO1192, PRO1194, PRO1192,

PRO1940, PRO6079, PRO6079, PRO18601, PRO4313, PRO144, PRO1312,

PRO1941, PRO223, PRO7184, PRO1184, PRO1197, PRO1194, PRO132,

PRO1941, PRO223, PRO7184, Or PRO1096, polypeptide are useful for

contail cate that a presence of tumour in a mammal which are useful for

contail cate of the presence of tumour in a mammal which are useful for the same call type, where a higher level of expression of

contail calls of the same call type, where a higher level of expression of

the PRO POPPEPTIAGE in the test sample as compared to the control sample

cummal calls of the same call type, where a higher level of expression of

the PRO polypeptides in the test sample as compared to the control sample

cumour, colon tumour, breast tumour, prostate tumour, retal tumour is lung

tumour, colon tumour, breast tumour, prostate tumour, retal tumour or

liver tumour. (I) is useful as molecular weight markers, for tissue

creening useful seaence of tumour and semetable. The mammal card or cartoridated and

creating useful seaence and and cartoridated (II) encoding (II) are sereining useful expression o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
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Pred. No. 8.6e-91;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human secreted and transmembrane protein PRO10196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS
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Best Local Similarity 99.5
Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 208 AA;
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Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;

61 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA

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mortality; morbidity; fibroblast growth factor 21; FGF-21; antiinflammatory; respiratory; antibacterial; immunosuppressive; vasotropic; haemostatic; nephrotropic; glucose level regulator; glucose uptake stimulator; insulin sensitivity enhancer; systemic inflammatory response syndrome; respiratory distress; acute lung injury; acute respiratory distress syndrome; multiple organ dysfunction syndrome; sepsis; multiple organ dysfunction syndrome; sepsis; chronic obstructive pulmonary disease; emphysema; chronic bronchitis; pancreatitis; ischaemia; multiple trauma; tissue injury; haemorrhagic shock; immune-mediated organ injury; shock; renal failure.
                                                             Human fibroblast growth factor 21 SEQ ID NO:1.
ADA37038 standard; protein; 208 AA.
                                                                                                                                                                                                                                                                         08-JAN-2003; 2003WO-US000010.
                                                                                                                                                                                                                                                                                             15-JAN-2002; 2002US-0348890P
                                                                                                                                                                                                                                                                                                                                         Kharitonenkov A;
                                           (first entry)
                                                                                                                                                                                                                                                                                                                   (ELIL ) LILLY & CO ELI
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 208 AA;
                                                                                                                                                                                                                            #O2003059270-A2
                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                    24-JUL-2003.
                                           20-NOV-2003
                                                                                                                                                                                                                                                                                                                                         Heuer JG,
                      ADA37038;
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The present invention describes a method for the reduction of mortality and morbidity in critically ill patients, which involves the administration of fibroblast growth factor 21 (FGF-21) (1). (1) has antiinflammatory, respiratory, antibacterial, immunosuppressive, vascropic, heamostatic and nephrotopic activities, and can be used as a correction of regulator, a glucose uptake stimulator, and an insulin glucose level regulator, and some insulin gensitivity enhancer. (1) can be used in the manufacture of a medicament for the reduction of morbidity and mortality in critically ill patients suffering from systemic inflammatory response syndrome (SIRS), respiratory distress, acute lung injury, acute respiratory distress syndrome, multiple organ dysfunction syndrome, sepsis and chronic proncive pulmonary disease (e.g. emphysems and chronic broncities pulmonary disease (e.g. emphysems and chronic broncibles pancreatitis, ischaemia, multiple trauma and tissue injury, haemorrhagic shock, immune-mediated organ injury, shock and renal callure. FGF-12 regulates glucose levels in response to sepsis; reduces morbidity and mortality that occurs in critically ill patients; and stimulates glucose uptake and enhances insulin sensitivity. The present sequence represents the human FGF-21 amino acid sequence, which is given in the exemplification of the present invention.
Use of fibroblast growth factor 21 for reduction of mortality and morbidity in patients suffering from e.g. systemic inflammatory response syndrome and acute respiratory distress syndrome.
                                                                                                                                                                                                                                                               Disclosure; Page 15-16; 22pp; English.
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This invention relates to one hundred and twenty two novel nucleic acids encoding human PRO membrane bound proteins or receptors. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate printenance. The information is offern transmitted by secreted printenance. The information is offern transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor liquand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the
                                                                                                                                                                                                                                                    One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Fig 78; 315pp; English.
Grimaldi JC, Gurney
                                                                                                         2003-522018/49
                                                                                                         WPI; 2003-522018
N-PSDB; ABT43920
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Gaps

1;

98.7%; Score 1098.5; DB 7; Length 208; 99.5%; Pred. No. 8.6e-91; ive 0; Mismatches 0; Indels 1;

Conservative

208;

Matches

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60 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
                      180
                                  Godowski PJ;
~* Wood WI;
                     CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPLPGLPPALPEPPGI
                                                                                                                                                                                     Human membrane bound receptor/protein PRO10196 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerritsen ME, Goddard A, Godowski P
Smith V, Stephan JF, Watanabe CK,
                                                                                                                                                                                                       Human, PRO, membrane bound protein, membrane bound receptor, cell proliferation, cell migration; cell differentiation; mitogenic factor; survival factor; oytotoxic factor; differentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour.
                                                           LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                               180 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 208
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                                                                                                                                ABJ72096 standard; protein; 208
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2000WO-US005841.
2001WO-US017800.
2001WO-US021066.
                                                                                                                                                                                                                                                                                                                             29-AUG-2002; 2002US-00232224.
                                                                                                                                                                                                                                                                                                                                                 99US-0146222P
                                                                                                                                                                                                                                                                                                                                                                                               09-APR-2002; 2002US-00119480
                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                        US2003065147-A1.
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02-MAR-2000;
01-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                28-JUL-1999;
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                                                                                                                                                                      16-OCT-2003
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                                                                                                                                                   ABJ72096;
                         121
                                                                                                              RESULT 20
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60 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel isolated PRO protein encoding nucleic acid. The nucleic acid of the invention may be useful for preparing PRO polypeptides and anti-TRO antibodies for detecting the presence of a useful in a mammal. Furthermore, the molecules of the invention may be useful for stimulating proliferation or gene expression in pericyte cells, the release of tumour necrosis factor (TNF)-alpha from human blood, the proliferation or differentiation of chordrocyte cells and for inhibiting the proliferation of normal human dermal fibroblast cells. Finally, the molecules may be utilised during gene therapy. The current sequence is that of the human PRO protein of the invention
                                                                                                                                                                                                                                                                                                     A, Godowski PJ;
Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 CSFRELLLEDGYNVYQSEAHGLPLHPGNKSPHRDPAFRGPARFLPLFGLPPALPBFPGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI
PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte; tumour necrosis factor; proliferation; differentiation; gene therapy; dermal fibroblast.
                                                                                                                                                                                                                                                                                                                                                                                                     New PRO protein encoding nucleic acid, useful for preparing PRO polypeptides and anti-PRO antibodies for detecting the presence tumor in a mammal.
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Pred. No. 8.6e-91;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted/transmembrane polypeptide PRO 10196.
                                                                                                                                                                                                                                                                                                        Goddard A,
                                                                                                                                                                                                                                                                                                        Gerritsen ME, Goddard P
Smith V, Stephan JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Fig 78; 324pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.7%;
                                                                                                                                                                       26-AUG-2002; 2002US-00227884.
                                                                                                                                                                                                       2001WO-US017800.
                                                                                                                                                                                                                      29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                        Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                         2003-503301/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-503301.
N-PSDB; ABT44547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 208 AA;
                                                                                                        US2003027988-A1.
                                                                           Homo sapiens
                                                                                                                                                                                                          01-JUN-2001;
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                                                                                                                                         06-FEB-2003
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The invention relates to an isolated mucleic acid encoding a PRO polypeptide. Nucleic acids that encode PRO can be used to generate either transgenic animals or knock-out animals useful in developing and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy for replacing defective gene, in chromosome identification, as chromosome markers, or in generating probes to isolate in lull length PRO cDNA. The PRO polypeptides are useful for chondrocyte stimulation, TNF-alpha stimulation, human dermal fibroblasts stimulation and for detecting the presence of tumour in an mammal. The PRO polypeptides are useful is an electrophoresis and the isolated nucleic acids may be used for protein electrophoresis and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides are useful in diagnostic assays for protein electrophoresis and the infinity purification of PRO from recombinant cell culture or patural sources. The present sequence represents the amino acid sequence of a human secreted/transmembrane PRO polypeptide
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                                                                                                                                                                                                                                                                                                                                                     Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, or in generating probes.
             gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.7%; Score 1098.5; DB 6; Length 208; 99.5%; Pred. No. 8.6e-91; ive 0; Mismatches 0; Indels 1;
           Human, chondrocyte stimulation, TNF-alpha stimulation, gene
human dermal fibroblast stimulation, tumour, tissue typing,
affinity purification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 19; Fig 78; 315pp; English
                                                                                                                                                                                                          28-AUG-2002; 2002US-00230338.
                                                                                                                                                                                                                                                              29-JUN-2001; 2001MO-US021066
09-APR-2002; 2002US-00119480
                                                                                                                                                                                                                                                01-JUN-2001; 2001WO-US017800
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Best Local Similarity 99.5
Matches 208; Conservative
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                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
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Grimaldi JC, Gurney
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 208 AA;
                                                                                                                               US2003044934-A1
                                                                                             Homo sapiens
                                                                                                                                                                    06-MAR-2003
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RESULT 19 ADA37038 19

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                                                                                                                                                                                                                                                                          The present sequence represents human fibroblast growth factor 21 (FGP-21). FGF-21 is located to chromosome 19, more specifically to 19q13.1-qter. The present invention describes a method for treating a mammal exhibiting type 2 diabetes or type 1 diabetes, or treating a mammal comprising FGF-21 which has at least 95% amino acid sequence identity to the 20% amino acid sequence given in ABP96156. Also described: (1) inducing an increase in glucose uptake in adipocyte cells by administering FGF-21 to induce an increase in glucose uptake; and (2) administering FGF-21 to induce an increase in glucose uptake; and (2) administering a medicament for treating type 1 diabetes, type 2 diabetes or obesity in a mammal using FGF-21 has antidiabetic and anorectic activities. The method is useful for treating a mammal exhibiting type 2 or 1 diabetes or for treating a mammal exhibiting type 2 or 1 diabetes or for treating a mammal for obesity. The method is preferably useful for treating thumans exhibiting type 1 or type 2 diabetes, and for treating domestic animals for obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                  Treating a mammal exhibiting Type 2 diabetes or Type 1 diabetes or obesity, by administering composition comprising fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LEIREDGTVGGAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte; differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
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                                                                                                                                  Shiyanova TL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.7%; Score 1098.5; DB 6; Length llarity 99.5%; Pred. No. 8.6e-91; Conservative 0; Mismatches 0; Indels
                                                                                                                                   Kharitonenkov A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABJ72266 standard; protein; 208 AA
                                                                                                                                                                                                                                                        Claim 3; Fig 1; 32pp; English
                                        22-JUL-2002; 2002WO-US021290
                                                                 2001US-0308702P
2002US-0347991P
                                                                                                                                  Glasebrook AL, Hammond LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                              2003-248106/24.
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                                                                                                                                                                         N-PSDB; ABZ79797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 208 AA;
                                                                   30-JUL-2001;
10-JAN-2002;
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Best Local Simi
Matches 208;
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                13-FEB-2003.
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The invention relates to a novel isolated nucleic acid encoding a fully defined PRO polypeptide. The molecules of the invention may be useful for stimulating proliferation or gene expression in pericyte cells or the release of TMF-alpha from human blood. Other possible uses include the stimulation or inhibition of chondrocyte proliferation or differentiation, the stimulation of human dernal fibroblast cell proliferation and the detection of the presence of a tunnur within a mammal. Furthermore, the nucleic acid may be useful for the manufacture of a medicament for diagnosing or treating a tumour within a mammal or to measuring or detecting the expression of an associated gene, as well as during gene therapy. The current sequence is that of the human PRO protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding for a PRO protein, useful for the manufacture of a medicament for diagnosing or treating tumors or for measuring or detecting expression of an associated gene.
                                                                                                                                                                                                                                                                                                                                                                                  Goddard A, Godowski PJ;
ohan JF, Watanabe CK, Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                     Gerritsen ME, Goddard Smith V, Stephan JF,
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                                                                                                                                                                                                               01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                          28-AUG-2002; 2002US-00230414
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Best Local Similarity 99.5%;
Matches 208; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        Desnoyers L,
C, Gurney AL,
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                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 208 AA;
                                                    US2003050448-A1
                                                                                                                                                                                                                                                                                                                                                                                                                        Grimaldi JC,
Homo sapiens
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                                                                                                         13-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                           Baker KP,
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ID ABJ7
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ndureottue sequences. The rate purpoperates or bioteractors are detected as pharmaceuticals, diagnostics, blosensors or bioteractors. These are particularly useful for detecting tumnour fee.g. lung tumnour, colon tumnour, becast tumnour, prostate tumnour, rectal tumnour, or liver tumnour) in a mammal, for slimulating the release of TNF-alpha from human blood, for stimulating proliferation or differentiation of chondrocyte cells, for stimulating proliferation. The PRO mucleic acid or normal human dermal fibroblast proliferation. The PRO mucleic acid or polypeptide is also useful for treating tumnours or various bone and/or artilage disorders (e.g. sports injunies or arthritis), or wounds. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
122 PRO (secreted and transmembrane) polypeptides whose sequences are fully defined in the specification; or (b) any of 122 nucleotide sequences having e.g. 4814, 2504 or 1759 bp fully defined in the specification; or the full length coding sequence of any these 122 nucleotide sequences. The PRO polypeptides or polynucleotides are useful
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Sequence 208 AA;

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LEIREDGIVGGAADQSPESILQIKALKPGVIQILGVKTSRFICQRPDGALYGSLHFDPRA 120
                                                                                                                                        LEIREDGIVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
                                                                                                                                                                                121 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
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                                                                                     1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                          1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                              Gaps
                            ;
 6; Length 208;
                              0; Indels
Score 1098.5; DB (Pred. No. 8.6e-91;
                              0; Mismatches
                                                                                                                                                                                                                                                                   LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 208
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98.7%;
99.5%;
                              Conservative
              Local Similarity
ses 208; Conserv
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 Query Match
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ABU82086 standard; protein; 208 AA 25-JUN-2003 ABUB2086; RESULT 14 ABU82086

(first entry)

Novel human secreted and transmembrane protein PRO10196.

Human; secreted and transmembrane protein; PRO; cardiant; cytostatic; antiangiogenic; hypotensive; vulnenry; antiarteriosclerotic; gene therapy; cardiovascular disorder; endothelial disorder; angiogenic disorder; cardiac hypertroph; trauma; cancer; age-related macular degeneration; atherosclerosis; hypertension; atterial restenosis; rhemaroid arthritis; angina; mycardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.

Homo sapiens

US2003088063-A1

08-MAY-2003

12-AUG-2002; 2002US-00219003

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60 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
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for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH 59
                                                                                                                                                                                                                                                                                                                                                                                   The invention describes one hundred and eighty seven nucleic acids encoding novel human secreted and transmembrane (PRO) polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, agerelated macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
                                                                                                                                    Godowski PJ;
wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDSDETGFEHSGLWVSVIAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
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                                                                                                                                                                                                                                                                    One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                                                                                                                    Gerritsen ME, Goddard A, Godowski P
Smith V, Stephan JF, Watanabe CK,
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al Similarity 99.5%; Pred. No. 8.6e-91;
208; Conservative 0; Mismatches 0; Indels
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            25-JUL-2000; 2000US-0220664P.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                      Desnoyers L,
                                                                                                               (GETH ) GENENTECH INC.
                                                                                                                                                                                                              WPI; 2003-393229/37.
N-PSDB; ACA68535.
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                                                                                                                                                        Baker KP,
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ABP96156 standard; protein; 208 AA (first entry) 12-MAY-2003 ABP96156; ABP96156 ID ABP9

Human; fibroblast growth factor 21; FGF-21; chromosome 19; 19q13.1-qter; diabetes; obesity; antidiabetic; anorectic; type 2 diabetes; type 1 diabetes. Human fibroblast growth factor 21 protein SEQ ID NO:2.

Homo sapiens.

WO2003011213-A2

directly from the

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Homo sapiens
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Matches
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                                                                                                                                                                180
                                                                                                                                         60 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
                                                                                                                                                                                                                                                                                                                                                                          Human, PRO polypeptide; secreted and transmembrane protein; anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goddard A, Godowski PJ;
phan JF, Watanabe CK, Wood WI;
                                                                                                                                                                             CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPG1
                                                                          1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                              MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                     LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPRA
                                                                                                                                                                CSFRELLLEDGYNVYOSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPLPGLPPALPEPPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating
                                                      Сарв
                                                      1;
                                 Length 208;
                                                     Indels
                                 DB 5;
                                Score 1098.5; DB 5;
Pred. No. 8.6e-91;
0; Mismatches 0;
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Smith V, Stephan JF,
                                                                                                                                                                                                           LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
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01-QUN-2001; 2001UO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                98.7%;
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                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                      Human PRO polypeptide #39
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
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                                            Local Similarity
es 208; Conserv
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            Sequence 208 AA;
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                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPLPGLPPALPEPPGI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted and transmembrane protein; PRO; cytostatic; antiarthritic; osteopathic; gene therapy; INF-Agonist-Alpha; chondrocyte stimulator; fibroblast modulator; pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour; oolon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; bone disorder; cartilage disorder; sports injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                  1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
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                                                                                                                                                                                                                                                                                         1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
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                                                                                                                                                          Length 208;
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data for this patent was obtained in electronic format USPTO web site at segdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                             DB 6;
                                                                                                                                                             98.7%; Score 1098.5; DB 6; 99.5%; Pred. No. 8.6e-91; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABO33743 standard; protein; 208
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29-JUN-2001; 2001MO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                              Local Similarity
nes 208; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arthritis; wound
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                                                                                                    Sequence 208 AA;
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Protein
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The present invention relates to new extracellular messenger polypeptides and polymucleotides encoding them. XMES is useful in the diagnosis, treatment and prevention of neurological laceful in the diagnosis, stroke, or Alzheimer's disease), autoimmune/inflammatory disorders (e.g. acquired immune deficiency syndrome, AIDS, Addison's disease, or allergies), developmental disorders (e.g. renal tubular acidosis, anaemia or Cushing's syndrome, and cell growing tractions, and aneurysm or vascular malformation), and cell proliferative disorders (e.g. cancer), and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of extracellular messengers. XMES may also be used in the treatment of viral, bacterial, fungal, parasitic, protozoal and helminthic infections, trauma, disorders associated with hypopitultarism, hypothyroidism or genadal steroid hormones, and man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alzheimer's disease; autoimmune disorder; renal tubular acidosis; stroke; acquired immune deficiency syndrome; AIDS; Addison's disease; cytostatic; developmental disorder; anaemia; Cushing's syndrome; endocrine disorder; vascular malformation, cell profiferative disorder; gene therapy; cancer; heuroprotective; trauma; hypopituitarism; hypothyroidism; antihelminthic; hyperthyroidism; gonadal steroid hormone; pancreatic disorder; nootropic; diabetes mellitus; immunosuppressive, anti-inflammatory; antibacterial; antiviral; antifungal; protozoal; allergy.
                           120 CSFREILIEDGYNVYQSEAHGLPLHIPGNKSPHRDFADRGFARFLFLFGLPFALPEPFGI 179
121 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   extracellular messenger; neurological disorder; epilepsy; XMES-3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pancreatic disorders such as type I or type II diabetes mellitus. TXMES may be used for somatic or germline gene therapy. The present sequence is human XMES-3 protein
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Lu Y, Baughn MR, Duggan BM, Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human extracellular messenger (XMES)-3 protein.
                                                                                                          209
                                                                                                                                     180 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 208
                                                                                                       LAPOPPDVGSSDPLSMVGPSQGRSPSYAS
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                                                                                                                                                                                                                                                                                      AAE17601 standard; protein; 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-2000; 2000US-0210233P.
23-JUN-2000; 2000US-0213465P.
14-NOV-2000; 2000US-0249019P.
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                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                 22-APR-2002
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                                                                                                                                                                                                                                        RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated human polypeptide (1) for zFGF11 (a fibroblast growth factor), and the encoding polymucleotide (II). (I) and (II) are used in methods of the invention stimulating proliferation of mesenchymal cells, detecting the presence of zFGF11 in a biological sample, detecting the presence of FGFRIIC in a biological sample and stimulating proliferation of osteoblastic lineage cells. The polypeptides, nucleic acid and/or antibodies of the invention may be used in treatment of despenaration, anyotrophic lateral sclerosis, cerebrovascular stroke, neuropathy associated with diabetes mellitus, neural cell development or despenaration, anyotrophic lateral sclerosis, cerebrovascular stroke, neuropathy associated with lack of maintenance of neuronal development. Molecules of the nervous system or lack of neuronal development. Molecules of the invention may also be useful for improving cardiac function and for promoting wound healing of the epidermis. The present sequence represents the amino acid sequence of
                                                                                                                             Human; fibroblast growth factor; FGF; zFGF11; mesenchymal cell; FGFRIIIC; osteoblastic lineage cell; diabetes mellitus; neuropathy; neural cell development, amyotrophic lateral scherosis; cerebrovascular stroke; neuronal differentiation; congenital disorder; nervous system disorder; cardiac function; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                            28. .208 _____/note= "Mature fibroblast growth factor homologue, zFGFI1. This sequence is specifically claimed in claim 4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polypeptide for zFGFI1 (fibroblast growth factor) useful in treatment of disorders associated with diabetes mellitus, neural cell development or degeneration, amyotrophic lateral sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
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                                                                                  Human fibroblast growth factor (FGF) homologue, zFGF11.
                                                                                                                                                                                                                                                                                                                                                                              1. .27
/label= Signal_sequence
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Fig 1; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JAN-2001; 2001US-00755695
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                                         05-NOV-2002 (first entry)
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Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cerebrovascular stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen Z;
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N-PSDB; ABK91310.
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Azimzai Y; S, Hafalia A;

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mellitus, neural cell development or degeneration, amyotrophic lateral sclarosis, cerebrovascular stroke, neuropathy associated with lack of maintenance of neuronal differentiation and congenital disorders of the nervous system or lack of neuronal development, promoting angiogenesis and wound healing, for revascularisation in eye, complications related to poor circulation such as diabetic food ulcers improving cardiac function, modulating surfactant production in the lung epithelium, to reduce damage to the tissue caused by ischaemia or ischaemia-reperfusion events, particularly in the heart or brain and for inducing skeletal muscle neogenesis and/or hyperplasia, kidney regeneration and/or for treating of systemic and pulmonary hypertension. Antagonists of 2FGF11 are useful for inhibiting disorders associated with kidney epithelium such as glomerulonephritis
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                                                                                                                                                                                                                                                                                                                                                                                                             CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
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                                                                                                                                                                                                                                                                                                                                                  1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTBAH 59
                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                    Score 1098.5; DB 4; Dems...
Pred. No. 8.68-91;
Transcheg 0; Indels
                                                                                                                                                                                                                                                                                             0; Mismatches
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2000US-0220585P.
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2000WO-US023522.
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                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                              Local Similarity
les 208; Conserv
                                                                                                                                                                                                                                    Sequence 208 AA;
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25-UUL-2000;
25-UUL-2000;
25-UUL-2000;
25-UUL-2000;
25-UUL-2000;
26-UUL-2000;
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01-AUG-2000;
22-AUG-2000;
23-AUG-2000;
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                                                                                                                                                                                                                                                                 Query Match
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One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumors such as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or liver tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO protein sequences of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to one hundred and twenty two nucleic acids encodeding PRO polypeptides. The sequences of the 122 PRO polymucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for nucleic acids, polypeptides. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in pericyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating or inhibiting the proliferation of normal human dermal fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have
                                                                                                                                                                                                                                                                                     Wood WI;
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                                                                                                                                                                                                                                                                  Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Fig 78; 359pp; English.
                                                                                                                     2001WO-US006666.
2001US-00816744.
2001US-00854208.
2001US-00854280.
2001WO-US017092.
                 2000WO-US030873.
2000US-0253646P.
                                                 2000WO-US032678
2000US-00747259
                                                                                     2000WO-US034956
2001WO-US006520
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Best Local Similarity 99.5'
Matches 208; Conservative
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N-PSDB; ABK33574.
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                                                                  20-DEC-2000;
20-DEC-2000;
28-FEB-2001;
                                                                                                                       01-MAR-2001;
22-MAR-2001;
10-MAY-2001;
10-MAY-2001;
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                 10-NOV-2000;
28-NOV-2000;
01-DEC-2000;
24-AUG-2000;
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                                                                                                                                                                                                                                                                        Baker KP,
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ABG32358;

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Human; fibroblast growth factor; FGF; zFGF11; chromosome 19; restenosis; proliferation, mesenchymal cell; osteoblastic lineage cell; osteoblassis; chromosomal disorder; chondroarcom; atherosclerosis; obesity; fracture, bone formation; diabetes mellitus; neural cell development; angiogenesis; amyotrophic lateral sclerosis; cerebrovascular stroke; neuropathy; ulcer; congenital disorder; wound healing cardiac function; glomerulonephritis; surfactant production; anorectic; ischaemia; neogenesis; hyperplasia;
CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             zFGF11 protein. zFGF11 gene is located on chromosome 19 zFGF11 is useful for stimulating proliferation of mesenchymal cells, osteoblastic lineage cells. zFGF11 is useful for identifying chromosomal disorders associated with abnormal expression of zFGF11 protein. zFGF11 is also useful for stimulation, inhibition or proliferation of myocytes, smooth muscle cells, adipocytes, chondrocytes, neural tube-derived stem cells, neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel rEGF11 polypeptide and polymucleotide, a member of fibroblast growth factor family, for stimulating proliferation of mesenchymal, osteoblastic lineage cells and treating diabetes, obesity, osteoporosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is human fibroblast growth factor (FGF) homologue,
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derived cells and endothelial cells and inhibiting chondrosarcomas,
atherosclerosis, restenosis and obesity. Stimulation of osteoblasts
results in bone formation useful for treating bone defects, fractures,
osteoporosis and other deficiencies in bone structure and formation.
zFGFI1 is useful for treating disorders associated with diabetes
                                                                                                                                                                                                                                                                                 Human fibroblast growth factor (FGF) homologue, zFGF11 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Human_mature_zFGF11_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Heparin binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                 hypertension; cytostatic; vasotropic; therapy
                                                                                            181 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                   LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal peptide
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                                                                                                                                                                                    AAE05078 standard; protein; 208
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/note= "1
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/label=
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N-PSDB; AAD09151.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel sbgFGF-19a polypeptide, a member of fibroblast growth factor family and polynucleotides encoding them useful for diagnosing, treating stroke, psoriasis, cancer, atherosclerosis, rheumatoid arthritis and cirrhosis.
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                                                                                                                                                                                                                                                                                                                                      Human; sbgFGF-19a; fibroblast growth factor; stroke; cancer; psoriasis; traumatic brain injury; cerebral ischemia; atherosclerosis; rhenmatic draftritis; cirrhosis; sarroidosis; wound repair; idiopathic pulmonary fibrosis; tumour development; vaccine developmental disorder; skeletal disorder; acrocephaly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a human shgFGF-19a polypeptide. The polypeptide is a member of fibroblast growth factor family of polypeptides. The polymucleotides and polypeptides are useful in the treatment of diseases such as stroke, traumatic brain injury, cerebral ischemia, cancer, atherosclerosis, rheumatoid arthritis, cirrhosis, psoriasis, sarcoidosis, idiopathic pulmonary fibrosis, tumour developmental disorders, skeletal disorders, wound repair, and acrocephaly. They are also useful as vaccines for inducing an immunological response in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEIREDGTVGGAADQSPESLLQLXALXPGVIQILGVXTSRFLCQRPDGALYGSLHFDPEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mcqueney MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                       Amino acid sequence of a human sbgFGF-19a polypeptide.
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Pred. No. 1.8e-91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                         209
                                                                                                              LAPQPPDVGSSDPLSMVGPSQGRSPSYAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM CORP.
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The present sequence is that of human JAFFA, a novel member of the fibroblast growth factor family. Analysis of rare sequences in the Milennium datebase led to the identification of an expressed sequence tag from a buman prostate tumour library which coded for a novel hypothetical signal peptide. Further analysis led to the identification of JAFFA, The invention provides JAFFA polypeptides, polymolecides and anti-JAFFA antibodies. It also provides antisense nucleic acid molecules, recombinant expression vectors, host cells and transgenic animals. JAFFA proteins may be useful for developing novel diagnostic and therapeutic proteins may be useful for developing novel diagnostic and therapeutic agents for JAFFA-associated disorders such as cancers and other disorders which demonstrate ABO(H) blood group disorders and for controlling cellular proliferative and/or differentiative disorders. The JAFFA call in may be used to treat and/or diagnose a variety of immune disorders such as autoimmune disease and multiple sclerosis. The proteins may also be used to screen for naturally occurring JAFFA substrates, to screen for drugs or compounds which modulate JAFFA antibodies, which can be used to detect and isolate JAFFA proteins, regulate the bioavailability of JAFFA proteins and modulate JAFFA activity.
                                                                                                                                                                                                                    Isolated JAFFA nucleic acid molecules which encode novel fibroblast growth factor family members (JAFFA) are useful for developing novel diagnostic and therapeutic agents for JAFFA-associated disorders such as
                                                                                                                                                                                                                                                                                                                                                      Claim 2; Fig 1; 137pp; English.
99US-00444165
                                               (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                       WPI; 2001-355881/37.
N-PSDB; AAF90326, AAF90327.
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                                                                                                    Khodadoust MM;
22-NOV-1999;
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0 120 61 LEIREDGTVGGAADQSPESILQIKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120 9 9 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGGVRQRYLYTDDAQQFEAH LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPRA CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI Gaps 0; 99.4%; Score 1106; DB 4; Length 209; 99.5%; Pred. No. 1.8e-91; ive 0; Mismatches 1; Indels (LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS Local Similarity 99.5 es 208; Conservative 181 181 Query Match 19 121 Matches g qq ð В à 셤 Š

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Fibroblast Growth Factor; FGF; treatment; cirrhosis; mucositis; diabetes;
                                                                                                                                                                                                                inflammatory bowel disease, Crohn's disease, obesity, tubular necrosis, renal tubule damage, gastrointestinal abnormality, wasting syndrome; neurodegenerative disease, haematopoietic cell reconstitution, cachexia,
                                                                                                                                                      Human Fibroblast Growth Factor-like (FGF-like) polypeptide.
                                 AAU00957 standard; protein; 209 AA
                                                                                                                 (first entry)
                                                                                                               24-MAY-2001
                                                                          AAU00957;
RESULT
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The sequence represents a fibroblast growth factor-like (FGF-like)

polypeptide. FGF-like protein and its associated nucleic acid play a role
in modulating body growth, maturation or life-span. They are also useful
for treating, preventing or ameliotating disorders such as cirrhosis,
inflammatory bowel disease, mucositis, Crohn's disease, diabetes,
obseity, gastrointestinal abnormalities, neurodegenerative diseases,
damage to renal tubules as a result of acute tubular necrosis,
haematopoietic cell reconstitution following chemotherapy, wasting
syndromes (e.g., cancer associated cacheria), damage to che corneal
cpithelium, lens or retinal tissue, multiple sclerosis, myopathies, short
steture, delayed maturation, excessive growth (e.g. acromegaly),
cremature maturation, alopecia, abnormalities of androgen target organs,
bronchopulmonary dysplasia, acute respiratory distress syndrome,
cof the eye or other tissues, atherosclerosis, hypercholesterolemia,
cof the eye or other tissues, atherosclerosis, hypercholesterolemia,
carchiac function, immune system dysfunction, cancer, Parkinson's disease,
senile dementia, Alzheimer's disease, and decreased cognitive function ö androgen target organ abnormality, respiratory distress syndrome, stroke, cancer, atherosclerosis, hypercholesterolaemia, osteoporosis; baldness, osteoathritis; muscle atrophy, sarcopenia; wrinkles, increased fatigue, decreased stamina, decreased cardiac function; immune system dysfunction; parkinson's disease, Alzheimer's disease, decreased cognitive function; chemotherapy; corneal epithelium damage; retinal tissue damage; myopathy multiple sclerosis; short stature; delayed maturation; excessive growth; acromegaly; premature maturation; alopecia; bronchopulmonary dysplasia; 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH Novel isolated fibroblast growth factor-like polypeptide useful for treating, preventing or ameliorating cirrhosis, inflammatory bowel disease, mucositis, Crohn's disease, diabetes, obesity, stroke and 0 99.4%; Score 1106; DB 4; Length 209; 99.5%; Pred. No. 1.8e-91; Indels "Mature human FGF-like protein" 0; Mismatches "Signal peptide" Location/Qualifiers Claim 13; Fig 2; 138pp; English. 07-SEP-1999; 99US-00391861. 23-AUG-2000; 2000US-00644052. 05-SEP-2000; 2000WO-US024373 .209 Matches 208; Conservative /note= senile dementia; human. . 28 /note= WPI; 2001-226743/23. Local Similarity (AMGE-) AMGEN INC. N-PSDB; AAS00779 Sequence 209 AA; WO200118172-A2 Thomason AR, osteoporosis Homo sapiens 15-MAR-2001 61 Query Match Peptide Protein d ò d ò

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The invention relates to fibroblast growth factor (FGF)-like polypeptides and nucleic acid molecules encoding such polypeptides. Sequences of the invention are useful for treating, preventing or ameliorating a medical condition. They are useful for treating dermal wounds, epidermolysis, bullosa, male pattern alopecia, gastric ulcer, duodenal ulcer, erosive condition. They are useful for treating dermal wounds, epidermolysis, bullosa, male pattern alopecia, gastric ulcer, duodenal ulcer, erosive consorpatilis, oseophageia reflux disease, inflammatory bowel disease, con a gastritis, oseophageia reflux disease, inflammatory bowel control to to insured gut to train the pattern applysema, pulmonary inflammation, pulmonary fibrosis, chepatic cirrhosis, toxic insults to the liver, fulminant liver failure, viral hepatitis, mucositis, multiple sclerosis and other cremochopulmonary dysplasia, acute respiratory distress syndrome or other conchopulmonary dysplasia, acute respiratory distress syndrome or chercond propresentation of neuronal cells, promoting constant lines, tumours of the eye or the other tissues and organs. CFG FGF-like polypeptides are useful stimulating andiogenesis, promoting or wound healing, modulating differentiation of neuronal cells, adipocytes and skeletal muscle cells, preventing or ameliorate skin aging, convenenting hair loss, stimulating encound and differentiation of neuronal cells, and bone marrow cells and maintaining organs before transplantation and for supporting cultures of primary cells and tissues. Sequences of the invention are also used in gene therapy and as vaccines.
CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPLPGLPPALPEPPGI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fibroblast growth factor; FGF-like protein; wound healing; bullosa; epidermolysis; erosive gastritis; inflammatory bowel disease; ulcer; oesophagitis; Crohn's disease; hyaline membrane disease; emphysema; pulmonary fibrosis; hepatic cirrhosis; liver failure; angiogenesis; multiple sclerosis; neurodegenerative disease; lung abnormality; viral hepatitis; respiratory distress syndrome; tumour; skin aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel fibroblast growth factor-like polypeptide useful for treating, ameliorating and/or preventing dermal wounds, gastric ulcer, Crohn's disease and pulmonary inflammation.
                                                                                                                                                   LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                Human FGF-21 protein.
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                                                                                                                                                                                        CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPLPGLPPALPEPPGI 180
                                                                                                                                                                                                    The present sequence is human FGF-21 protein which is a member of the FGF family
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/note= "protein kinase C predicted phosphorylation site"
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                                                       Score 1113; DB 5;
Pred. No. 4.3e-92;
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/note= "N-myristoylation"
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/label= Mature_protein
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    /label= Signal_peptide

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                                                        100.0%;
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98. .100
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Best Local Similarity
Matches 209; Conserv
                                   Sequence 209 AA;
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standard; protein; 209
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                                                                                                                                                                                                                                                                                                                              Human FGF-related protein.
        Query Match
Best Local Similarity 100.
Matches 209; Conservative
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N-PSDB; ABK52425.
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les 209; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21). For proteins regulate growth and differentiation of a variety of cell types. FGF-21 nucleic acids and polypeptides are useful for treating diseases and disorders characterised by inadequate numbers of hepatic cells, preferably cirrhosis of the liver. They may also be used in the treatment of infertility, impotence, and testicular cancer, as well as leukemia, lymphoma, autoimmune disease, or proliferative disorders of the
                                                                                                                               120
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                                                                                                                                                    LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120
                                                                                                                                                                           CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid molecule useful for treating disease, e.g. infertility,
                                                                                                                                                                                                                                                                                                                                                                                Fibroblast growth factor-21; FGF-21; cell growth; cell differentiation; hepatic cell; cirrhosis; infertility; impotence; testicular cancer; leukemia; lymphoma; autoimmune disease; thymus proliferative disorder.
                                                                                                                                                                                      1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                        MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
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                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of human fibroblast growth factor-21 (FGF-21).
the FGF family
                                                               0,
                                           Length 209;
                                                               Indels
some members of
                                        Score 1113; DB 4;
Pred. No. 4.3e-92;
Mismatches 0;
                                                                                                                                                                                                                     LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
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 amino acid sequences of
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11-MAY-2000; 2000US-0203633P.
                                                                                                                                                                                                                                                                                               AAB68417 standard; protein;
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                                                                Conservative
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N-PSDB; AAF85329.
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                                                     Similarity
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                      Sequence 209
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                                                                                                                                                                                                                                                                                                                                                                     61 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120
                                                                                                                                                                                                                                                                          LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein and a partial peptide of the protein useful for treating
njuries, burns, thrombosis, arteriosclerosis, hepatopathy, pancreopathy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09
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                                                                                                                                                       MDSDETGFEHSGLWVSVLAGLILGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
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hepatopathy; FGF-related protein.
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100.0%; Pred. No. 4.3e-92;
live 0; Mismatches 0;
100.0%; Score 1113; DB 4; 100.0%; Pred. No. 4.3e-92;
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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2004
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OM protein - protein search, using sw model

Run on:

March 2, 2004, 15:50:07 ; Search time 125.4 Seconds
(without alignments)
470.913 Million cell updates/sec

US-10-060-765-4 1113

1 MDSDETGFEHSGLWVSVLAG......SSDPLSMVGPSQGRSPSYAS 209 Perfect score:

BLOSUM62 Scoring table: Sequence:

1586107 segs, 282547505 residues Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:* 1: geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* Database

geneseqp2003as:* geneseqp2003bs:* geneseqp2002s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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lptí	267	117	289	326	351	957	951	378	530	358	501	177	743	980	156	997	394	289	038	960	268	674	215	297	945
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ADB78051	ADB87117	ADB84699	ADB83814	ADB72969	ADC36807	ADC21797	ADC49828	ADC49027	ADC49544	ADC47405	ADC47150	ADC78025	ADD06260	ADC77779	ADD50742	ADD50988	ADD50469	ADD50223	ADD51234
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ALIGNMENTS

Fibroblast growth factor; FGF; FGF-like polypeptide; mitogenic; fat deposition; vulnerary; antiulcer; dermatological; anoretic; antidiabetic; antiinflammatory; cytostatic; hepatic; virucide; neuroprotectant; pulmonary; gene therapy; vaccine; human. Human fibroblast growth factor (FGF)-21. AAG65667 standard; protein; 209 AA. (first entry) 07-JAN-2002 AAG65667; RESULT 1 AAG65667

Homo gapiens.

WO200172957-A2.

04-OCT-2001.

31-MAR-2000; 2000US-00540118. 02-APR-2001; 2001WO-IB000664.

(ITOH/) ITOH N.

Itoh N;

WPI; 2001-611623/70.

New human nucleic acid encoding fibroblast growth factor-like peptide, useful for treatment and diagnosis of e.g. wounds and inflammatory bowel disease.

Disclosure, Fig 3; 172pp; English.

The invention provides human nucleic acids encoding fibroblast growth factor (FGF)-like peptide. The FGF-like polypeptides can be expressed by entandard recombinant methodology and are mitogenic for a wide range of cells, inducing differentiation and prolliferation, and inhibiting deposition of fat. The FGF-like polypeptides, polynuclectides and range of diseases and conditions, e.g. wounds, ulcers, skin aging, obesity, diabetes, alopecia, inflammatory bowel disease, emphysema, viral heaptilis, multiple sclerosis, respiratory distress syndrome, tumors of the eye, etc., also for maintaining organs before transplant and supporting culture of primary cells and tissues. Sequences AAG65647-67

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Sequenc.
Sequence 1b,
Sequence 17, App.
Sequence 20, Appl
Sequence 2, Appli
"quence 2, Appli
"ce 2, Appli
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Sequence 4, Appli
Sequence 14225, A
Sequence 4355, Ap
Sequence 28, Appl
Sequence 28391, A
Sequence 7, Appli
Sequence 7, Appli
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396, App
14221, A
10731, A
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Sequence 5, Appli
Sequence 2, Appli
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Sequence 2086, Ap
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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S-07-603-133B-17
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Perfect score:
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Sequence 5499, Ap		Sequence 29728, A	Sequence 6926, Ap	Sequence 3, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 21514, A	Sequence 12, Appl	Sequence 3716, Ap	Sequence 288, App	Sequence 4500, Ap	Seguence 4626, Ap	Sequence 4652, Ap	Sequence 8159, Ap	Seguence 3429, Ap	Seguence 13575, A
US-09-543-681A-5499	US-09-352-990-28	US-09-252-991A-29728	US-09-543-681A-6926	US-08-785-048-3	US-08-996-799-3	US-08-785-048-2	US-08-996-799-2	US-09-252-991A-21514	US-07-603-133B-12	US-09-134-001C-3716	US-09-198-452A-288	US-09-134-001C-4500	US-09-328-352-4626	US-09-134-000C-4652	US-09-543-681A-8159	US-09-134-001C-3429	US-09-489-039A-13575
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37	37	37	37	3.7	37	37	37	37	37	37	36.5	36	36	36	36	36	36
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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US-09-390-207-5
Sequence 5, Application US/09390207
Patent No. 6504530
GENERAL INFORMATION:
APPLICANT: Thomason, Arlen
APPLICANT: Liu, Benxian
TITHE OF INVENTION Fibroblast Growth Factor-Like Polypeptides
FILE REFERENCE: 99-371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 86; DB 4; Length 85; 100.0%; Pred. No. 1.4e-07; ative 0; Mismatches 0; Indels
       Sequence 5213, Application US/09621976
; Sequence 5213, Application US/09621976
; Patent No. 663963
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REPERENCE: GENSET: 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/390,207
CURRENT FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SIGNAL
LOCATION: -28..-1
NAME/KEY: UNSURE
LOCATION: 57
OTHER INFORMATION: Xaa = Ala, Pro
NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Xaa = Leu, Val
US-09-621-976-5213
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Best Local Similarity 100.
Matches 16; Conservative
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US-09-621-976-5213
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Query Match
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US-09-390-207-6
US-09-390-207-6
; Sequence 6, Application US/09390207
; Parent No. 6504530.
; GENERAL INFORMATION:
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REPERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6.2
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APPLICANT: Thomason, Arlen
APPLICANT: Liu, Benxian
TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
FILE REFERENCE: 99-371
CURRENT APPLICATION NUMBER: US/09/390,207
CURRENT FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 209
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                                                                                                                       Length 181;
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Pred. No. 3.1e-07;
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                                                                                                                     100.0%; Somilarity 100.0%; Processor to the conservative 0;
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Best Local Similarity 100.0%;
Matches 16; Conservative 0
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Best Local Similarity 87.5%;
Matches 14; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 181
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CORGANISM: Homo sapiens
US-09-390-207-2
                                                   TYPE: PRT
CORGANISM: Homo sapiens
US-09-390-207-5
                                                                                                      Query Match
Best Local Similarity
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17 RORYLYTDDDDDTEAH 32

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RESULT 5

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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
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| Sequence 4, Application US/09390207 | Sequence 4. Application US/09390207 | Patent NO. 6504530 | GENERAL INFORMATION: APPLICANT: Thomason, Arlen | APPLICANT: Thomason, Arlen | TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides | FILE REFERENCE: 99-371 | CURRENT APPLICATION NUMBER: US/09/390,207 | CURRENT FILING DATE: 1999-09-07 | NUMBER OF SEQ ID NOS: 41 | SOFTWARE: PatentIn Ver. 2.0 | SEQ ID NO 4 | LEASTH: 210 | LEAST
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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US-09-489-039A-14225
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STATE: Massachusetts
COUNTRY: USA
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COMPUTER READABLE FORM:
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CORGANISM: Mus musculus
US-09-390-207-4
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Matches 10; Conserve
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US-09-107-532A-4355
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Sequence 28391, Application US/09252991A

Sequence 28319, Application US/09252991A

Patent No. 655195

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 28391

LENGTH: 152
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Sequence 10181, Application US/09489039A

Patent NO. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

FILE REFERENCE: 2709-2004001

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 10181

LENGTH: 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                      731 RÓQFRYADDPEÓBE 744
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1 RORYLYTDDAQQTE 14
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129 WRDDAPQTESH 139
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Matches 7; Conserv
                                                                                                RESULT 9
US-09-252-991A-28391
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US-09-489-039A-10181
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US-09-147-236-7
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Gaps

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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
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APPLICANT: O'TOOLE, Paul W.
APPLICANT: O'TOOLE, Paul W.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTYON: Polynucleotides, materials incorporating
TITLE OF INVENTYON: 2000-004/00/634,238
CURRENT FILLING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 396
LENGTH: 164
                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 4; Length 136;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
  APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
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Pred. No. 40;
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Mismatches
                                                                  CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 4224
LENGTH: 136
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COCATION: (1)...(164)
COTHER INFORMATION: Xaa = Any Amino Acid
US-09-634-238-396
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Havukkala, Ilkka J.
Bloksberg, Leonard, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Lactobacillus rhamnosus
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Dekker, James
Christensson, Anna C.
                                                                                                                                                                                                                                                                                                                                                                    44.28;
53.88;
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23 FLYTDEAMRVRFH 35
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Best Local Similarity 53.8
Matches 7; Conservative
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                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                      ; NAME/KEY: SIGNAL
; LOCATION: -41..-1
US-09-621-976-4224
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                        FEATURE:
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APPLICANT: TONOUCHI, Nacto
APPLICANT: TONOUCHI, Takayasu
APPLICANT: TSUCHIDA, Takayasu
APPLICANT: TAHARA, Nackiuminin
APPLICANT: TAHARA, Takahisa
TITLE OF INVENTION: NOVEL GENE, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE
TITLE OF INVENTION: NOVER, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE
TITLE OF INVENTION NOVER: US/09/522,474
CURRENT APPLICATION NUMBER: US/09/147,236
PRIOR PILLING DATE: 1999-04-08
PRIOR FILLING DATE: 1999-01-099
PRIOR FILLING DATE: 1997-10-09
APPLICANT: TAHARA, Naoki
APPLICANT: TAHARA, Naoki
APPLICANT: TAKABISA
TITLE OF INVENTION: NOVEL GENE, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE
FILE REFERENCE: 6537-011-0PCT
CURRENT APPLICATION NUMBER: US/09/147,236A
CURRENT FILING DATE: 1999-04-08
EARLIER APPLICATION NUMBER: PCT/JP97/03633
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATCHIN VET. 2.1
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70.0%; Pred. No. 1.4e+02;
tive 1; Mismatches 2; Indels
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Patent No. 6639063
GENERAL INPORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09522474
Patent No. 6573076
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                       ORGANISM: Acetobacter xylinum
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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US-09-621-976-4224
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LENGTH: 735
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                                                                                                                                                                                                                                                                               TYPE: PRT
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Gaps
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APPLICANT: Redmond, Mark J.
APPLICANT: Ijaz, Mohammed K.
APPLICANT: Parker, Michael D.
TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISBASE
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 747;
  Length 557;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 2006-1888
ZIP: 2006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/089,397A
FILING DATE: 07-UL-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.2%; Score 38; DB 3; I 42.9%; Pred. No. 2.1e+02; ative 3; Mismatches 5;
44.2%; Score 38; DB 4; 1
ilarity 60.0%; Pred. No. 1.5e+02;
Conservative 3; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 29311-20003.03
TELECOMMUNICATION INFORMATION:
TELERPORE: (202) 887-1500
TELERPOX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                 APPLICANT: FRENCHICK, PATRICK J.
APPLICANT: FRENCHICK, PATRICK J.
APPLICANT: POTTER, ANDREW A.
APPLICANT: JAZ, MOHAWAD K.
APPLICANT: GILCHRIST, JAMES E.
APPLICANT: REDMOND, MARK J.
TITLE OF INVENTION: ROTAVIRUS VACCINES
NUMBER OF SEQUENCES: 24
CORRESPONDERSEE: 2000 Pennsylvania Avenue, NW
                                                                                                                                                                                                                                                 Sequence 16, Application US/08089397A
Patent No. 6086880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/07603133B Patent No. 5298244
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amino acid
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Matches 6; Conservative
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MOLECULE TYPE: protein
                                                                                                                                        522 robrekrkah 531
                                                                                             7 TDDAQQTEAH 16
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       Query Match
Best Local Similarity
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US-07-603-133B-17
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                                               Matches
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Sequence 5669, Application US/09134001C

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BUILDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION UNDER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-10-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 5569
LENGTH: 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gary Breton et. al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS CREEKENCE: 2709.2004001
CURRENT PERION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1999-01-29
RIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 10731
LENGTH: 526
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         TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.2%; Score 38; DB 4; Length 526; 54.5%; Pred. No. 1.40+02; tive 2; Mismatches 3; Indel8
                                                                                                                                                                                                                                                                                                     Score 38; DB 4; Length 285;
Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                     CURRENT APPLICATION NUMBER: US/09/489, 039A CURRENT FILING DATE: 2000-01-27 PRIOR FILING DATE: 1999-01-29 NUMBER: OS EQ ID NOS: 14342 SEQ ID NOS: 14221 LENGTH: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10731, Application US/09489039A Patent No. 6610836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Klebsiella pneumoniae
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204 YVYSDNAQHVAMH 216
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Matches 6; Conservative
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Matches 6; Conserv
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US-09-489-039A-10731
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Gaps

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44.2%; Score 38; DB 1; Length 776; 42.9%; Pred. No. 2.2e+02; iive 3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY. USA
ZIP: Z0006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
COMPUTER: USPECIATION DATA:
APPLICATION NUMBER: US/08/089,397A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: SABARA, MARTA I.J.
APPLICANT: FRENCHICK, PATRICK J.
APPLICANT: POTTER, ANDREW A.
APPLICANT: IJAZ, MOHAMMAD K.
APPLICANT: GILCHERST, JAMES B.
APPLICANT: REDMOND, MARK J.
TITLE OF INVENTION: ROTAVIRUS VACCINES
NUMBER OF SEQUENCES: 24
REFERENCE/DOCKET NUMBER: 9313-0004.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/08089397A Patent No. 6086880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REPERENCE/DOCKET NUMBER: 29311
TELECOMMUNICATION INFORMATION:
TELEFARM: (202) 887-050
TELEFARM: (202) 887-0763
INFORMATION FOR SEQ ID NO: 15:
                TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250
TELEFAX: (415) 327-2951
                                                                                                                                                                                                                                                                                                                                                                                                   302 QYTYTRDGEEVTAH 315
                                       TELEPHONE: (415) 327-725
TELEFAX: (415) 327-2951
TELEKX: 706141
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 776 amino acids
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AMINO ACID
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 42.5-
These 6; Conservative
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Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                        TOPOLOGY: linear;
MOLECULE TYPE: protein
US-07-603-133B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-089-397A-15
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US-08-089-397A-15
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Redmond, Mark J.
APPLICANT: Redmond, Mark J.
APPLICANT: Ijaz, Mohammed K.
APPLICANT: Ijaz, Mohammed K.
APPLICANT: Parker, Michael D.
TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
SIREET: 545 Middlefield Road, Suite 200
CITY: Manlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 1; Length //o, Pred. No. 2.2e+02;
                                                                                                                   COUNTRY:

ZIP: 94025
COMPUTER READBLE FORM:
MUDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/603,133B
FILING DATE: 1991025
CLASSIFICATION: 1424
ATTORNEY/AGENT TRFORMATION:
NAME: RODINS, RODERTAIN:
REFERENCE/DOCKET NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9313-0004.00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 17:
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CURRENT APPLICATION DATA:
PIPLICATION NUMBER: US/07/603,133B
FILING DATE: 19901025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                              ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-603-133B-20; Sequence 20, Application US/07603133B; Patent No. 5298244
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RODING, RODERE L.
REGISTRATION NUMBER: 33,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS LENGTH: 776 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: protein
    NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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COUNTRY:
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OF THE MYSTERY SWINE DISEASE,
                 APPLICANT: Moorman, Robertus J
APPLICANT: Moorman, Chohanna J
APPLICANT: Mellenberg, Johanna J
TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
TITLE OF INVENTION: VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
STREET: 525 South 300 East
STREET: 525 South 300 East
STREET: Utah
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meulenberg, Johanna J
TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISI
VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.2%; Score 38; DB 3; Length 2396; 54.5%; Pred. No. 7.2e+02; Live 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/157,005
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91201398.4
FILING DATE: 06-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92200781.0
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL92/00096
FILING DATE: 05-JUN-1992
ATTONNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                             ZIP: 84111
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: WINDOWS95
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wensvoort, Gert
Terpstra, Catharinus
Pol, Johannes M
Moorman, Robertus J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09565864
Patent No. 6455245
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 532-1922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Turner, Allen C. REGISTRATION NUMBER: 33041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (801) 531-9168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2396 amino acids
Pol, Johannes M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||:: |: |
2278 YTDDSRYTQDH 2288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-747-863-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 YTDDAQQTEAH 16
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Best Local Similarity
Matches 6; Conserv
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TELEFAX: (8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 24
US-09-565-864-2
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                                                                                                                                                                                                     APPLICANT: Wensvort, Gert
APPLICANT: Terpstra, Catharinus
APPLICANT: Terpstra, Catharinus
APPLICANT: Pol, Johannes M
APPLICANT: Moorman, Robertus J
APPLICANT: Moulenberg, Johanna J
TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
TITLE OF INVENTION: VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
TITLE OF INVENTION: VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
CORRESPONDENCES: 9
CORRESPONDENCES: ADDRESSE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STRIE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 7.2e+02;
3; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,005
FILLING DATE: 26-NOV-1993
CLASSIFICATION: 424
PRICR APPLICATION DATA:
APPLICATION NUMBER: EP 91201398.4
FILING DATE: 06-JUN-1991
PRICR APPLICATION DATA:
APPLICATION NUMBER: EP 92200781.0
FILING DATE: 18-MAR-1992
PRICR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL92/00096
FILING DATE: 05-JUN-1992
APPLICATION NUMBER: PCT/NL92/00096
FILING DATE: 05-JUN-1992
APPLICATION NUMBER: PCT/NL92/00096
FILING DATE: 105-JUN-1992
NUME: MORAN: THOMBER: PCT/NL92/00096
FILING DATE: 105-JUN-1992
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Patent No. 6197310
GENERAL INFORMATION:
APPLICANT: Wensvoort, Gert
APPLICANT: Terpstra, Catharinus
                                                                                                                                Sequence 2, Application US/08157005
Patent No. 5620691
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: MOLALL, ALTERNATION NUMBER: 16,579
REGISTRATION NUMBER: 4481
TELEPCOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELERX: (212) 315-1931
TELEX: 422523 COOP UI
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2396 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.2%;
            302 QYTYTRDGEEVTAH 315
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2278 YTDDSRYTQDH 2288
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Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-157-005-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 YTDDAQQTEAH 16
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Sequence 3993, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BUILDER BENERAL US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3993
LENGTH: 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CAID
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2086
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APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
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Indels
9
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53.3%; Pred. No. 1.2e+02;
iive 3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 4;
Pred. No. 1.2e+02;
1; Mismatches 5
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5499, Application US/09543681A
Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2086, Application US/09540236; Patent No. 6673910
  ä
                                                                                 294 ROGNIYTGDTONTNSN 309
                                             1 RORYLYTDDAQQTEAH 16
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Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RORYLYTDDAQQTEA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RORYLYTDDAQOTE 14
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Best Local Similarity 53.3
Matches 8; Conservative
  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT; ORGANISM: M.catarrhalis
US-09-540-236-2086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 28
US-09-543-681A-5499
                                                                                                                                                                           US-09-134-001C-3993
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    Matches
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US-09-252-991A-31483

is Sequence 31483, Application US/09252991A

is Sequence 31483, Application US/09252991A

patent No. 6551795

igeneral information:
    APPLICANT: Marc J. Rubenfield et al.
    APPLICANT: Marc J. Rubenfield et al.
    APPLICANTON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
    TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

    CURRENT PAPLICATION NUMBER: US 60/074,788

    PRIOR FILING DATE: 1999-02-18

    PRIOR FILING DATE: 1998-07-27

    NUMBER OF SEQ ID NOS: 33142
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Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/157,005
FILING DATE: CURNOWN
APPLICATION NUMBER: EP 91201398.4
FILING DATE: 06-JUN-1991
APPLICATION NUMBER: EP 92200781.0
FILING DATE: 18-MAR-1992
APPLICATION NUMBER: PCT/NL92/00096
FILING DATE: 05-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/565,864
FILING DATE: 05-May-2000
CLASSIFICATION: <Unknown>
                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Moran, Thomas F
REGISTRATION NUMBER: 16,579
REFERENCE/DOCKET NUMBER: 44819
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEPHONE: (212) 315-1931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Intear
; MOLECULE TYPE: procein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-565-864-2
         STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2396 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 422523 COOP UI INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.0%;
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54.5%;
                                                                                          ZIP: 10112
COMPUTER READABLE FORM:
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2278 YTDDSRYTQDH 2288
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                                                 STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 YTDDAQQTEAH 16
                             New York
                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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LENGTH: 310
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APPLICANT: GARY BRETON:
APPLICANT: GARY BRETON
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL.
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 4; Length 497;
Pred. No. 2e+02;
4; Mismatches 3; Indels
                           Length 400;
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Requence No. 5763246

GENERAL INFORMATION:
APPLICANT: Hodgson, John
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5763246el tRNA SynthetaBe
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCES: ADDRESSER: SmithKiine Beecham Corporation
STREET: 709 Swedeland Road
                        Score 37; DB 4; Le:
Pred. No. 1.6e+02;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,048
FILING DATE: 17-JAN 1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P31355-3
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6926, Application US/09543681A Patent No. 6605709
                                                                                                                                                                                                                         295 EQYLYRRAADDGQHACQPRTEAH 317
                                                                                                                                                           2 QRYLY---TDDAQ-----QTEAH 16
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FILING DATE: 19-JAN-1996
APPLICATION NUMBER: 9615845.6
FILING DATE: 27-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38,891
                           Query Match
Best Local Similarity 43.5%;
Matches 10; Conservative
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Best Local Similarity 46.2%;
Matches 6; Conservative
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REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: PA
COUNTRY: USA
ZIP: 19406-0339
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||: || ::|:
260 QRYIVTDSIKETK 272
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APPLICATION NUMBER: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-543-681A-6926
                                                                                                                                                                                                                                                                                                                                                            US-09-543-681A-6926
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US-09-252-991A-29728
US-09-252-991A-29728
US-09-252-991A-29728
Sequence 29728, Application US/09252991A
Fatent No. 6551795
Fatent No. 6551795
FARENAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29728
LENGTH APPLICATION
LE
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match
43.0%; Score 37; DB 4; Length 338;
Best Local Similarity 43.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29 Application US/09352990
Sequence 20 Application US/09352990
Sequence 20 Application US/09352990
GENERAL INFORMATION:
APPLICANT: Famodu, Layo O.
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetase
FILE REFERENCE: BB-1191
CURRENT APPLICATION NUMBER: US/09/352,990
CURRENT APPLICATION NUMBER: 60/092,866
EARLIER RAPLICATION NUMBER: 60/092,866
SARLIER RAPLICATION NUMBER: 60/092,866
SARLIER RILING DATE: July 15, 1998
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Microsoft Office 97
LENGTH: 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.0%; Score 37; DB 3; I 46.7%; Pred. No. 1.5e+02; tive 3; Mismatches 5;
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 200-04-05
PRIOR PELING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
LENGTH: 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 REVYLYTDSRKDKPYH 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272 ORGLWFDDPERPECH 286
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                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RORYLYTDDAQQTEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Synechocystis sp
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Matches 7; Conservative
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Gaps ;

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Mismatches

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Matches
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                                                                                                                                                                                                                                                      43.0%; Score 37; DB 1; Length 547; 60.0%; Pred. No. 2.2e+02; tive 3; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08996799
Patent No. 5965416
GENERAL INFORMATION:
APPLICANT: Hodgson, John
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5965416el tRNA Synthetase
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 1940 6-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskerte
COMPUTER: IBM Comparible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,799
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P31355-3
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/785,048
FILING DATE: 17-JAN-1997
APPLICATION NUMBER: 9601099.6
FILING DATE: 19-JAN-1996
APPLICATION NUMBER: 9615845.6
FILING DATE: 27-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31355-3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 547 amino acids
TYPE: amino acid
                                                                          INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 547 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 610-270-44
TELEFAX: 610-270-5090
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                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide
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512 TDDIEKTKAH 521
                                                                                                                                                                                                                                                                                                                                         7 TDDAQQTEAH 16
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43.0%; 60.0%;

Query Match Best Local Similarity

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                                                                                                                                                  Sequence 2, Application US/08785048
Patent No. 576246
GENERAL INFORMATION:
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5763246el tRNA Synthetase
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Smithfline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hodgson, John
APPLICANT: Hodgson, John
APPLICANT: Lawlor, Elizabeth
TITLE OF INTENTION: No. 5965416el tRNA Synthetase
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,048
FILING DATE: 17-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 9601099.6
FILING DATE: 19-JAN-1996
APPLICATION NUMBER: 961845.6
FILING DATE: 27-JUL-1996
APPLICATION NUMBER: 9615845.6
FILING DATE: 27-JUL-1996
APPLICATION NUMBER: 9615845.6
APPLICATION NUMBER: 9815845.6
APTORNEY, AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08996799; Patent No. 5965416; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: POTELECOMMUNICATION INFORMATION TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 553 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||| ::|:|
518 TDDIEKTKAH 527
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512 TDDIEKTKAH 521
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7 TDDAQQTEAH 16
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                                                                                                                                                                                                                                                                                                                                                                                                           STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-785-048-2
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                                                                                                                                    US-08-785-048-2
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPBUTICS FILLE REFERENCE: GTC-007 CURRENT APPLICATION WUMBER: 18/90/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Redmond, Mark J.
APPLICANT: Ijaz, Mohammed K.
APPLICANT: Parker, Michael D.
TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/603,133B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
43.0%; Score 37; DB 1; Le
Best Local Similarity 42.9%; Pred. No. 3.2e+02;
Matches 6; Conservative 3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: Morrison & Foerster
STREFT: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/055,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3716, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                 Sequence 12, Application US/07603133B Patent No. 5298244 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RODINE, RODERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9313-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250
TELEFAX: (415) 327-2951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 775 amino acids
                                                                       | |:|: ||
254 RHRHLHADDFADRPAH 269
                              1 RORYLYTDDAQQTEAH 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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US-09-134-001C-3716
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## SEQUENCE 215174, Application US/09252991A
## SEQUENCE 215174, Application US/09252991A
## SEQUENCE 215174, Application US/09252991A
## SEQUENCE 215175
## SECUENCE 115175
## SE
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43.0%; Score 37; DB 4; Length 635;
Best Local Similarity 43.8%; Pred. No. 2.6e+02;
Matches 7; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 2; Length 553; pred. No. 2.2e+02; 1; Indels
                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FRSESEG TO Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,799
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P31355-3
                                                                                                                                                                                                                                                                                                                                                                                                                        PILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/785,048
FILING DATE: 17-JAN-1997
APPLICATION NUMBER: 9601099.6
FILING DATE: 19-JAN-1996
APPLICATION NUMBER: 961089.6
FILING DATE: 27-JUL-1996
APPLICATION NUMBER: 9615845.6
FILING DATE: 37-JUL-1996
APPLICATION NUMBER: 9615845.7
FILING DATE: 37-JUL-1996
APPLICATION NUMBER: 98185.7
TELECOMNINICATION INFORMATION:
TELECOMNINICATION INFORMATION:
TELECOMNINICATION INFORMATION:
TELEFAN: 610-270-4478
TELEFAN: 610-270-5090
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                                                                                                                                                            ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIDE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 553 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 43.0
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide US-08-996-799-2
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518 TDDIEKTKAH 527
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US-09-252-991A-21514
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                                                                                                         STATE: PA
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| Sequence 4500, Application US/09134001C
| Patent No. 6380370
| GENERAL INFORMATION:
| APPLICANT: Lynn Doucette-Stamm et al Amino ACID SEQUENCES RELATING TO STAPHYLOCOCCUS;
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| FILE REFERENCE: GTC-007
| CURRENT FILING DATE: 1998-08-13
| PRIOR APPLICATION NUMBER: US 60/064,964
| PRIOR APPLICATION NUMBER: US 60/065,779
| PRIOR FILING DATE: 1997-08-14
| NUMBER OF SEQ ID NOS: 5674
| LENGTH: 82
| LENGTH: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 288, Application US/09198452A;
Parent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering of INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
TITLE REPERENCE: 9710-003-98452A
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
SEQ ID NOS: 6849
LENGTH: 789
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                                                                                                                                                                                        43.0%; Score 37; DB 4; Length 1335; 43.8%; Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
41.9%; Score 36; DB 4; Length 82;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4500
                                                                                                 ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               629 RYLYSDEEKEEALAQEETH 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 RYLYTDDAQ----QTEAH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                       107 KOOSLSTDDANONOTN 122
                                                                                                                                                                                                                                                                                         1 RORYLYTDDAQQTEAH 16
  PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3116
LENGTH: 1335
                                                                                                                                                                                          Query Match
Best Local Similarity 43.88
Matches 7; Conservative
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Best Local Similarity
Matches 8; Conserv
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US-09-198-452A-288
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Search completed: March 2, 2004, 16:09:01
Job time : 3.86667 secs
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Q8axal brachydanio
Q8x515 rattus norv
Q9yd8 encorhynchu
Q9yd8 nocorhynchu
Q9y31 notophthalm
Q9931 notophthalm
Q96219 mus musculu
Q96728 mus musculu
Q8r517 rattus norv
Q8r577 mattus norv
Q8bst0 mus musculu
Q9bst0 mus musculu
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Ogdano gallus gall
Ogvigl rattus norv
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                                                                  March 2, 2004, 15:51:42; Search time 87.0833 Seconds (without alignments) 757.244 Million cell updates/sec
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1113
1 MDSDETGFEHSGLWVSVLAG......SSDPLSMVGPSQGRSPSYAS 209
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                    1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                               OM protein - protein search, using sw model
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08C7A8
08R5L7
08BST0
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QBR5L5
Q9YGDB
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Q8C399
Q9YH31
Q9ESL9
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Q9DDN0
Q8VI81
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_mhc:*
sp_organelle:*
                                                                                                                                                                                                                                                     Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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sp_rodent:*
sp_virus:*
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Match Length DB
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803.5
206.5
206.5
176.5
171
171.5
171
170.5
168
168
167.5
168
167.5
161
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161
161
161
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                                                                                                                     Title:
Perfect score:
                                                                                                                                                                   Scoring table:
                                                                                                                                              Sequence:
                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
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Q9est9 rattus norv Q9dfc9 brachydanio Q9iai6 gallus gall Q7zzn4 qallus qall		QBvcy9 mus musculu Q9erg5 mus musculu Q86yn7 homo sapien Q9iai5 gallus gall Q8nfi9 homo sapien Q95k97 macaca fasc	Q9erw3 rattus norv Q9iai3 gallus gall Q9es18 mus musculu Q9e559 homo sapien Q80454 meleagris g Q42407 gallus gall Q911b9 ovis aries	08917 095147 0722K 09627 09677
Q9EST9 Q9DFC9 Q9IA16 Q7ZZN4	Q8NF90 Q9W6A2 Q95L12 Q9FVY1 Q8R4X0 Q89096	Q8VCY9 Q9ERQ5 Q86YN7 Q91A15 Q8NF19	Q9ERW3 Q9IAI3 Q9ESLB Q96E59 Q804S4 Q42407	Q9V179 Q9SL47 Q7ZZK5 Q9ERN5 Q9OY71 ALIGNMENTS
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4444 4444 4		13.6 13.6 13.6 13.5 13.5 13.5		4.0000 0.0000 0.0000 0.0000 0.0000
159.5 159.5 159	157.5 155.5 155.5 153	152.5 151.5 151 151 151 150	148.5 147.5 147.5 144.5 144.5 143.5	141.5 1338 1336 1335 1332
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61 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRXLYTDDAQQTEAH
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                        99.4%; Score 1106; DB 4; Length 209; 99.5%; Pred. No. 8.2e-94; tive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                    Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC018404; AAH18404.1; -.
GO; GO:0008083; Frowth factor activity; IEA.
InterPro; IPR008996; Cytok ILI_like.
InterPro; IPR002348; ILI_HBGF.
                                                                                                                                                                                                                                                                                            InterPro; irrov.

Pfam; PP00167; FGF; 1.

PRINTS; PR00262; ILLHBGF.

ProDom; PD000831; ILL HBGF; 1.

SMART; SN00442; FGF; 1.

SMART; SN00442; FGF; 1.
                                                                    Last sequence update)
Last annotation update)
                                                        Created)
                           PRT;
                                                       01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2003 (TrEMBLrel. 25, Fibroblast growth factor 21. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.5
Matches 208; Conservative
                             PRELIMINARY;
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                          NCBI TaxID=9606;
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                                          QBN683;
                             Q8N683
RESULT 1
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SEQUENCE FROM N.A.
MEDLINE-20564778; PubMed=11110663;
Ladher R.K., Anakwe K.U., Gurney A.L., Schoenwolf G.C.,
Francis-West P.H.,
"Identification of Synergistic Signals Initiating Inner
                                                                                                                                                                                                        Development.";
Science 290:1965-1968 (2000).
EMBL; AR315355; AAG39478.1; -.
EMSP; P09038; IBFG.
GO; GO:0008083; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok IL1_like.
InterPro; IPR00248; IL1_HBGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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hes 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=10116;
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RRAKA KRAKA 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 GYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGLLAPQPPDVGS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLWVSVLAGL-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI _TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Futus norvegicus FGF21.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB078901; BAB84299.1; --
GO; GO:0008083; F:growth factor activity; IEA.
InterPro; IPR008996; Cyrok II.1_like.
InterPro; IPR008996; II.1_HBGF.
PEAM; PF00167; FGF; 1.
PRINTS; PR00167; FGF; 1.
PRINTS; PR00181; III.HBGF; 1.
SYART; SM00442; FGF; 1.
SEQUENCE 208 AA; 22857 MW; D232445902CDB8EA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 72.2%; Score 803.5; Dest Local Similarity 78.9%; Pred. No. 5.6e-Matches 157; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 AA
                                                                                                                                                                                                                                                         LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                      181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
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Best Local Similarity
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[1]
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Q9DDN0
LD Q9DDN0
DT 01-M
DT 01-M
DT 01-C
DB Fibx
DB Fibx
CG SERAR
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CC Arch
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                                                                                                                                                                                                                                                                                                                                                                                                            18 LAGLLLGACQAH--PIPD-SSPLLQFG-GQ-VRQRYLYTDDAQQ--TEAHLEIREDGTVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.6%; Score 206.5; DB 11; Length 218; 30.7%; Pred. No. 5.2e-11; tive 37; Mismatches 92; Indels 11;
                                                                                                                                                                                 DB 13; Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 GYNVYQSEAHGLPLHLPGNKSPH----RDPAPRGPARFLPLPGLPPA----
                                                                                                                                                                                 19.5%; Score 216.5; DB 13; Length 30.9%; Pred. No. 6.6e-12; tive 33; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Rattus", norvegicus FGF15.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB078900; BAB84298.1; -.
GO; GO:0008083; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok III_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 AA; 25207 MW; ED898684B5307C58 CRC64;
Pfam; PF00167; FGF; 1.
PRINTS; PR00262; ILIHBGF.
ProDom; PD000831; ILI HBGF; 1.
SMART; SM00442; FGF; I.
PROSITE; PS00247; HBGF FGF; 1.
SRQUENCE 227 AA; 24568 MW; 875D76FBFD09F8E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NAR-2002 (TrEMBLrel. 20, Created)
01-NAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 AFEPE----VYSSPLETDSMDPFGITSKLSPVKSPSF 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 --LPEPPGILAPQPPDVGSSDPLSMVGP-SQGRSPSY 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Pfam; PROD167; FGF; 1.
PRINTS; PROD262; ILLHBGF.
ProDom; PDO00831; ILL HBGF; 1.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 SDYLL---GIKRVRRLYCNVG--IGFHLQVLPDGRINGVHNENQYSLIEISAVERGVVSL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 LGVKTSRFLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYOSEAH-GLPLHLPGN--- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 GYNVYQSEAHGLPLHLPGNKS-PHRDPAPRGPARFLPL--PGLPPALPEPPGILAPQPPD 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 SSPLLOFGGOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQI 93
70
             71 GAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPRACSFRELLLED
                                                                    13 LWVSVLAGLILGACOAHPIPDSSPLLQFG-GQV-RQRYLYTDDAQQTEAHLEIREDGTVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                     Ralliere C., Rescan P.-Y.;
Ralliere C., Rescan P.-Y.;
Ralliere C., Rescan P.-Y.;
Ralliere C., Rescan P.-Y.;
Ralliere C., Rescan of a fgf6 gene in zebrafish.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
REBL; AF516334; AA015997.1; -.
ROS; GO:0008083; F:growth factor activity; IEA.
RINEEPRO; IPR001064; Crystallin.
R InterPro; IPR002996; Crystallin.
R InterPro; IPR002996; Cryck ILL]—like.
R Prints; PR00167; FGF; 1.
R PRINTS; PR00262; ILLHBGF.
R ProDom; P0000891; ILLHBGF; 1.
SMART; SMO0442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match
Local Similarity 28.4%; Score 176.5; DB 13; Length
Local Similarity 28.4%; Pred. No. 2.8e-08;
hes 56; Conservative 26; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00225, CRYSTALLIN BETAGANMA; 1.
PROSITE; PS00247; HBGF FGF; 1.
SEQUENCE 205 AA; 23244 MW; 2BDBID93D6533696 CRC64;
                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 EHSGLW---VSVLAGLLLGACQAHPIPD------
                                                                                                                                                                                                                                                  205 AA
                                                                                                                                                                        195 SDSMDPFRMVEDVDHLVKSPSF 216
                                                                                                                                                          188 VGSSDPLSMVGPSQG--RSPSY 207
                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 KRGHRASPAMTVTHFLP 203
                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
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Q8R5L5
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208 AA.

PRT;

PRELIMINARY;

QBR5L5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rescan P.Y.;
"Identification of a fibroblast growth factor 6 (FGF6) in a non-
mammalian vertebrate: Continuous expression of FGF6 accompanies muscle
                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Bukaryota; Metazoda; Chordeta; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 208;
                                                                                                                                                                                                                                      "Rattus norvegicus FGF6 mRNA.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB079674; BABB4704.1;
GO; GO:0008083; F:growth factor activity; IEA.
InterPro; IPR001064; Crystallin.
InterPro; IPR001964; Cryck IL1_like.
InterPro; IPR00348; IL1_HBGF.
PRINTS; FR00262; IL1HBGF.
ProDom; PD00081; IL1 HBGF; 1.
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
PROSITE; PS00247; HBGF FGF; 1.
SEQUENCE 208 AA; 22789 MW; 4BEEA0301BB78986 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 LCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 6-related protein.
                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 15.4%; Score 171.5; DB 1
1 Similarity 36.4%; Pred. No. 8.2e-08;
36; Conservative 21; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO, GO:0008083; F:growth factor activity; IEA.
InterPro; IPR001064; Crystallin.
InterPro; IPR008996; Cytok III_like.
PIEAFPC; IPR002348; III_HBGF.
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EMBL, Y16850; CAA76422.1; -.
HSSP, P31371; 1G82.
    Created)
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MEDLINE=99096461; PubMed=9878802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS, PR00262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
                                                              Fibroblast growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                    Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eiber hyperplasia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                          NCBI TaxID=10116;
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NCBI_TaxID=8316;
                                                                                     NCBI_TaxID=10090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 FLCQRPDGALYGSLHFDPEACSFREILLEDGYNVYQSEAHGLPLHLPGNKSP--HRDPAP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 YLAMNIKEGRLYASEHYNAE-CEFVERIHELGYNTYASR-----LYRTGPGGRRQPGA 149
                                                                                                                                                                                                                                                                                                  78 LGIKRVRRLYCNAG--IGFHLQVLPDGRINGVHNENQYSLIEISTVERGVVSLYGVRSEL 135
                                                                                                                                                                                                                                                                      44 ---VRORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSR 100
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                                                                                                                                                                                43
                                                                                                                                                                                                          40 GGAPRRRKLYC----ATKYHLQLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGR
                                                                                                                                                                                10 HSGIWVSVLAGLLLGACQAHPIPD------SSPLLQFGGQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                   Query Match
15.4%; Score 171; DB 13; Length 206;
Best Local Similarity 26.9%; Pred. No. 9e-08;
Matches 43; Conservative 28; Mismatches 57; Indels 32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.4%; Score 171; DB 11; Length 245; 35.0%; Pred. No. 1.1e-07; tive 20; Mismatches 48; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Rattus norvegicus FGF3 mRNA.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB079262; BAB84564.1; -.
GO; GO:0008083; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok III_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERMIT PRODUCT; FGF; 1.
PRINTS; PRODUCS; ILLHBGF.
PRODOM; PROMO442; FGF; 1.
SMART; SMO0442; FGF; 1.
SEGUENCE 245 AA; 27150 MW; C9305D307E7D0648 CRC64;
  PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
PROSITE; PS00247; HBGF_FGF; 1.
SEQUENCE 206 AA; 23375 MW; BB883328F17EB6E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   101 FLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYOSEAH 140
                                                                                                                                                                                                                                                                                                                                                                                                              136 FVAMNSRGRLYGTTVFHDE-CKFRESMLPNNYNAYESSVY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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(TrEMBLrel. 23, L
(TrEMBLrel. 25, L
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les 43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 RGP 161
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01-MAR-2003 (
01-OCT-2003 (
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Q8C399;
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Q8C399
ID Q8C3;
AC Q8C3;
DT 01-M;
DT 01-M;
DT 01-M;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Head;

XT MELNIR=22534683; PubMed=12466851;

XT The FANTOM Consortium,

the RIKEN Genome Exploration Research Group Phase I & II Team;

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

Nature 420:553-573(2002).

K GO, 770 full-length cDNAs.";

Nature 420:553-573(2002).

R GO, GO:0008093; F:growth factor activity; IEA.

R GO, GO:0008093; F:growth factor activity; IEA.

RICEPPC: IPR001064; CYStallin.

R INTEPPC: IPR001064; CYStallin.

R INTEPPC: IPR001996; CYtok ILL like.

R INTEPPC: IPR001996; LILHBGF.

R PROMIT: PR00167; FGF; 1.

R PROMORSAIT ILL HBGF: 1.

R SWART: SM00442; FGF; 1.

R PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 GOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESILIQLKALKPGVIQILGVKTSRF 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 GIKRQRRLYCNVG--IGFHLQVPPDGRISGTHEENPYSLLEISTVERGVVSLFGVKSALF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No....., 1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative fibroblast growth factor-4.
Putative fibroblast growth factor-4.
Bukaryota, Metazoa, Chordata; Craniata, Vertebrata; Buteleostomi; Amphibia; Batrachia; Caudata; Salamandridae;
Notophthalmus.
Fibroblast growth factor 6 (Fragment).
Was musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.3%; Score 170.5; DB 11; Length 195; 36.4%; Pred. No. 9:3e-08; ive 21; Mismatches 39; Indels 3;
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U76998; AAC98812.1; -.
HSSP; P09038; 1BFF.
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PRINTS; PR00262; IL1HBGF.
PRODOM; PD000831; IL1 HBGF; 1.
SWART; SW00442; FGF; I.
PROSITE; PS00225; CRYSTALIN BETAGAWMA; 1.
SROSITE; PS 00247; HBGF FGF; I.
SEQUENCE 196 AA; 22033 MW; AC4688CD989C6EAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 195 AA; 21318 MW; BA8A90EF368994FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 LCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0008083; F:growth factor activity; IEA InterPro; IPR001064; Crystallin. InterPro; IPR008996; Cytok ILL like. InterPro; IPR002348; ILL HBGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36; Conservative
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Best Local Similarity
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                                              5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 IQILGVKTSRFLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 PDSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGA-ADQSPESLLQLKALKPGV 90
                                                                                                                                                                                    60 ------HIBIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQR 105
                                                                                                                                 15 VLIGLISGLARCIPMPSPGNGTLEWSWET----LYSQSLARLAGGQRTDAHRYGEYLLGI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Gaps
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                              36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
15.1%; Score 168; DB 11; Length 212;
Best Local Similarity 33.5%; Pred. No. 1.8e-07;
Matches 54; Conservative 19; Mismatches 62; Indels 26
Query Match 15.1%; Score 168; DB 13; Length 196; Best Local Similarity 28.9%; Pred. No. 1.6e-07; Matches 44; Conservative 27; Mismatches 45; Indels 36
                                                                                            ----AQOTEA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Itch N.;
"Mus musculus mRNA for FGF-20(FGF20).";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB049218; BAB16406.1; --
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ProDom; PD000831; ILL HBGF; 1.
SWART; SM00442; RGF; 1.
SPROSTIE; PS00247; HBGF FGF; 1.
SEQUENCE 212 AA; 23659 FW; 174DBCE8915B69EF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 GRRYFVALINKDGTPRDGARSKRRQKFTHFLPRPVDPERVPE 202
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 20.
                                                                                            17 VLAGLILGACQAHPIPD-SSPLLQFGGQVRQRYLYTDD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1891346; Fgf20.
GO; GO:0008083; F:growth factor activity; IEA.
InterPro; IFR008996; Cytok_III_like.
InterPro; IFR002348; III_HBGF.
Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                    106 PDGALYGSLHFDPEACSFRELLLEDGYNVYQS 137
                                                                                                                                                                                                                                                                                                          131 SKGRLFGSKYFSDE-CKFKEMLLPNNYNAYES 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 AA.
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01-DBC-2001 (TrEMBLrel. 19,
01-DBC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
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60 HLEIREDGTVGGAADQSPESILIQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPE 119
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STRAIN=C57BL/6J; TISSUE=Heart;
STRAIN=22324683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK052233; BAC34892.1; -.
EMBL; AK052233; EAC4892.1; -.
MCD; MCS:10813346; Fg120.
MCD; G0:0008083; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok ILI_like.
                                                                                                                                                                      MEDIJUNE-21439472; PubMed-11555861;
Christensen R.N., Weinstein M., Tassava R.A.;
"Fibroblast growth factors in regenerating limbs of Ambystoma: Cloning
and semi-quantitative RT-PCR expression studies.";
J. Exp. Zool. 290:529-540(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Ambystoma mexicanum (Axolot1).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Ambystomatidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 ACSFRELLLEDGYNVYQSEAH-GLPLHLPGN----KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
15.0%; Score 167.5; DB 13; Length
Best Local Similarity 35.1%; Pred. No. 9.9e-08;
Matches 39; Conservative 23; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00167; FGF; 1.
PRINTS; PR00262; IL1HBGF.
ProDom; PD000831; IL1 HBGF; 1.
SMART; SM00442; FGF; I.
PROSITE; PR00247; HBGF FGF; 1.
SEQUENCE 211 AA; 23614 MW; 6CF4714BD4F6CDFE CRC64;
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Last annotation update)
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01-WAR-2003 (TrEMBLrel. 23, Last sequ
01-OCT-2003 (TrEMBLrel. 25, Last anno
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                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                          NCBI_TaxID=8296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 NVYQS-----EAHGLPLH----LPGNKSPHRDPAPRGPARFLPLPGLPPALPEPP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 VIYSSMLYRQQBSGRAWFLGLNKEGQVMKGNRVKKTKPA---AHFLPKP-LEVAMYREP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 DDSINSTLFNLIPVGLRVVAIQGVKIGLYIAMNGEGYLXPSELFTPE-CKFKESVFENYY 154
                                                                                                                                                                                                                                                 108 VSİRGVDSGLYLGMNDKGELYGSEKLTSE-CIFREQFEENWYNTYSSNIYKHGDTGRRYF 166
                                                                                                                                     91 IQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH-----GLPLH 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 GACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQ------QTEAHLEIREDGTVGGAA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 GLCNGNLVDIFSKVRIFG--LKKKRLRRQDPQLKGIVTRLYCRQGYYLQMHPDGALDGTK 95
                                                                                                      90
                                                                                                   32 PDSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGA-ADQSPESLLQLKALKPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80; Indels 38; Gaps
                                                 24; Gaps
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  14.8%; Score 165; DB 11; Length 211; 34.4%; Pred. No. 3.3e-07; ive 16; Mismatches 65; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEE-2002) to the EMBL/GenBank/DDBJ databases
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ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
PROSITE; PS0047; HBGF FGF; 1.
SEQUENCE 247 AA, 27720 MW; 427C3C760894996E CRC64;
                                                                                                                                                                                                                                                                                                        146 LPGNKSPHRDPAPRGPAR-----FLPLPGLPPALPE 176
                                                                                                                                                                                                                                                                                                                                                     167 VALNK----DGTPRDGARSKRHQKFTHFLPRPVDPERVPE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tron N.;
"Rattus norvegicus FGF14 mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23,
23,
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
Fibroblast growth factorl4.
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                                                         55; Conservative
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hes 62; Conserv
     Query Match
Best Local Similarity
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01-MAR-2003
01-MAR-2003
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SEQUENCE FROM N.A.

STRAIN=CFORL/6J; TISSUE=Pituitary;
MEDLINE=22354683; PubMed=12466851;
The FARTOM Consortium,
The FARTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 NVYQS-----EAHGLPLH-----LPGNKSPHRDPAPRGPARFLPLPGLPPALPEPP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 VIYSSMLYRQQESGRAWFLGINKEGQVMKGNRVKKTKPA----AHFLPKP-LEVAMYREP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : : | : | : | : | 38 GLCNGNIVDIFSKVRIFG-LKKRRIRRQDPQLKGIVTRLXCRQGYYLQMHPDGALDGTK 95
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MEDLINE=21439472; PubMed=11555861;
MEDLINE=21439472; PubMed=11555861;
MEDLINE=21439472; PubMed=11555861;
MEDLINE=21439472; PubMed=11555861;
"Fibroblast growth factors in regenerating limbs of Ambystoma: Cloning and semi-quantitative RT-PCR expression studies.";
J. Exp. Zool. 290:529-540(2001).
EMBL; AF360988; AAL16961.1;
EMBL; AF360988; AAL16961.1;
O. GO:0008083; Figrowth factor activity; IEA.
InterPro; IPR001064; Crystallin.
InterPro; IPR008996; Cytok III_like.
InterPro; IPR008996; Cytok III_like.
InterPro; IPR008396; Cytok III_like.
InterPro; IPR008396; Cytok III_like.
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Amphibia, Batrachia, Caudata, Salamandroidea, Ambystomatidae,
                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Last annotation update)
Last annotation update)
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Best Local Similarity 29.8%; Pred. No. 9.4e-07;
Matches 62; Conservative 28; Mismatches 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 GACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQ-
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01-DEC-2001 (TrEMBLrel. 19, Created)
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01-OCT-2003 (TrEMBLrel. 25, 1
Fibroblast growth factor 14.
Mus musculus (Mouse).
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SEQUENCE FROM N.A.
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                RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 VSİRGVDSGLYLGMNGKGELYGSEKLISE-CIFREQFEENWYNTYSSNIYKHGDIGRRYF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 PGSVELAHIHGILRRRQLYC----RTGFHLQILPDGSVQGTRQDHSLFGILBFISVAVGL 107
                                                                                                                                                                                                                                                                               60 HLEIREDGTVGGAADQSPESLIQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPE 119
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                                                                                                                                                                                                                                                                                                                               71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "FGE-20," a novel neurotrophic factor, preferentially expressed in the substantia nigra pars compacta of rat brain.";
Blochem, Biochem, Biochem, 277:355-360(2000).
BMB.; AB020021; BAB13763.1; -.
PIR; JC7511; JC7511.
HSSP; P31371; JG82.
GO; GO:0008083; F:growth factor activity; IEA.
InterPro; IPR008986; Cycok_ILL_like.
                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohmachi S., Watanabe Y., Mikami T., Kusu N., Ibi T., Akaike A.,
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                                                                                                                                                                                       ch 14.4%; Score 160; DB 13; Length 111; 1 Similarity 37.4%; Pred. No. 4.2e-07; 34; Conservative 21; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFINTS; PR00262; ILLHBGF.
PRINTS; PR00262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; I.
PROSITE; PS00247; HBGF FGF; 1.
SRQUENCE 212 AA; 23537 MW; 4F858BEFE772B977 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 LPGNKSPHRDPAPRGPAR-----FLPLPGLPPALPE 176
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 AA.
    Prodom; PD000091; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
PROSITE; PS00247; HBGF_FGF; 1.
NON TER 11 111
SEQÜENCE 111 AA; 12607 MW; 4A3A52ED3901
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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MEDLINE=20490008; PubMed=11032730;
MEDLINE=20490008; PubMed=11032730;
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PRINTS; PR00262; ILLHBGF
                                                                                                                                                                                                                     Local Similarity
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SEQUENCE FROM N.A.
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FGF-20.
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47 ----RYLYTDDAQQTBAHLEIRBDGTVGGAADQSPBSLLQLKALKPGVIQILGVKTSRFL 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 IKRLRRLYCNVG--IGFHLQVLPGGKITGVHNENRYSLLEISBVERGVVTLFGVRSGLFV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
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5 SALLPILVIGLMTSSVRCAPLPGGHSGPVERRWETLYSRSLARIPGEKRDISRDSDYLTG
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Gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes;
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                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE_2043337; PubMed=10976049;

A Grandel H., Draper B.W., Schulte-Merker S.;

T "dackel acts in the ectoderm of the zebrafish pectoral fin bud maintain ABR signaling.";

Devabopment 12:4169-4178(2000).

R EMBL; AR283555; AAG13950.1; -.

R AFSP; P31371; 1G82.

R AFINT; CBB-GRERE 001006-1; fgf4.

R OG; GO:0008083; F:growth factor activity; IEA.

R OG; GO:0008083; F:growth factor activity; IEA.

InterPro; IPR008996; Cytok III_like.

InterPro; IPR008996; Cytok III_like.

R Pfan; PF00167; FGF; II.

R PRINTS; PR00262; III.HBGF.

R PRODOM; P0000831; III. HBGF. 1.

R PRADOM; P0000831; III. HBGF; 1.

R PRADOM; P0000841; HGF; 1.

R PROSITE; PS00044; HGF; II.

R PROSITE; PS00044; HGF; II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 SGLWVSVLAGLLLGACQAHPIPD------SSPLLQFGGQVRQ--
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor homologous factor 4 isoform 1A
                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 4.
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191 AA
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 HRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 26.3%
Matches 51; Conservative
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   PRELIMINARY;
                                                                                                                                                                                                                                                                                                              Cyprinidae; Danio.
NCBL TaxID=7955;
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61 SSPAASLGSQGSGLEQSSFQWSPSGRRTGSLYCRVGIGFHLQIYPDGKVNGSHEANMLSV 120
                                                                                                                                                                                   81 LQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPRACSFRELLLEDGYNVYQSEAH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 ----GLPLHLPGNKSPHRDPAPRG-----PARFLP-----LPGLP----PAL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 RTEKTGREWYVALNK---RGKAKRGCSPRVKPQHISTHFLPRFKQSEQPELSFTVTVPEK 236
                                                                                              37 LGQAEAGGLPRGPAVTDLDHLKGILRRRQLYC----RTGFHLEIFPNGTIQGTRQDHSRF 92
                                                                     23 LGACQAHPIPDS---SPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGA-ADQSPE
                                                                                                                                                       79 SLLOLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yang J.C.;
"Identification of fibroblast growth factor-5 as an overexpressed
autigen in wultiple human adenocarcinomas.";
Cancer Res. 61:5511-5516(2001)
                                                                                                                                                                                                                                               139 AH-----GLPLHLPGNKSPHRDPAPRGPAR------FLPLPGLPPALPE 176
                                                                                                                                                                                                                                                                                      152 LYKHVDIGRRYYVALNK----DGIPREGIRIKRHOKFIHFLPRPVDPEKVPE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-21347229; PubMed=11454700;
Hanada K.-I., Perry-Lalley D.M., Ohnmacht G.A., Bettinotti M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanada K.-I., Yang J.C.; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases. Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases. EMBL; ABSJ8149; ARNO4097.1.; -

GO; GO:00080081; F:growth factor activity; IEA. InterPro; IPR008996; Cytok ILI_like. InterPro; IPR003948; ILI_HBGF. Pfam; PF00167; FGF; I. PRINTS; PR00262; ILIHBGF. ProDom; PD000831; ILI_HBGF; I. SMART; SM00442; FGF; I. SMART; SM00442; FGF; I. SRQUENCE 268 AA; 29550 MM; 28B7268B2678IBCF CRC64;
    Pred. No. 1.6e-06;
; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
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27.6%; Pred. No. 2.2e-06;
tive 28; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                     268
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    ilarity 32.0%; Pro
Conservative 21;
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    Similarity
55; Conserv
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    Best Local
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 DDSSNSTLENLIPVGLRVVAIQGVKTGLYIALNNEGFLYTSELFTPE-CKFKESVFENYY 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 NVYQS------EAHGLPLH----LPGNKSPHRDPAPRGPARFLPLPGLPPALPEPP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 VIYSSMLYRQQESGRAWFLGLNXEGQVMKGNRVKKTKPA----AHFLPKP-LEVAMYREP 198
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MEDLINE=20112823; PubMed=10644718; Mathans J.; Mathans J.; Mano-Sanjuan I., Smallwood P.M., Nathans J.; Mathans J.; Isoform Diversity among Fibroblast Growth Factor Homologous Factors Is Generated by Alternative Promoter Usage and Differential Splicing...; J. Biol. Chem. 275:2589-2597 (2000). EMBL: AF199605; AAF31392.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yoshioka H., Ishimaru Y., Sugiyama N., Tsunekawa N., Noce T.,
Kaashara M., Morohashi K.;
"Mesonephric FGF9 is the initiation signal for Gonadal Organogenesis
in chick.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38;
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                                                                                                                                                                                                                                                                                                                                                                                                                     14.3%; Score 159; DB 13; Length 237; 29.3%; Pred. No. 1.4e-06; ive 30; Mismatches 79; IndelB 3
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InterPro; IPR008996; Cytck IL1_like.
InterPro; IPR008996; Cytck IL1_like.
InterPro; IRR002349; IL1_HBGF.
PRINTS; PR00262; IL1HBGF.
PRODOM; P0000831; IL1_HBGF.
SMART; SM00442; FGF; I.
SMART; SM00247; HGF; TGF; 1.
SROSITE; PS00247; HGF FGF; 1.
SROSITE; PS00247; HGF FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                              237 AA; 26816 MW; F13076736548BB22 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                        GO; GO:000803; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok ILL like.
PinterPro; IPR00348; ILL HBGF.
PRINTS; PR00262; ILLHBGF.
PRINTS; PR00262; ILLHBGF.
PRODER: SM00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 GACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQ--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
Les 61; Conserv
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SEQUENCE
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Paradis V., Silversides D.W.;
Paradis V., Silversides D.W.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY033825; AAK61609.2; --
GO; GO:008083; Figrowth factor activity; IEA.
InterPro; IPR008996; Cytok ILI_like.
InterPro; IPR002348; ILI_HBGF.
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae, Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                          SEQUENCE FROM N.A.
               NCBI TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 DSSYTLENLIPVGLRVVALQGVQTKLYLAMNSEGYLYTSEHFTPE-CKFKESIFENYYVT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95
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                                                                                                                                                      Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
MEDLINE=20112823; PubMed=10644718;
MUNDZ-Sanjuan I., Smallwood P.M., Nathans J.;
Munoz-Sanjuan It, Smallwood P.M., Nathans J.;
Isoform Diversity among Fibroblast Growth Ractor Homologous Factors
Is Generated by Alternative Promoter Usage and Differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDILIRE-99065510; PubMed=9847253;
MEDILIRE-99065510; Nimband B.K., Fallon J.F., Nathans J.;
MENDRESSION of chicken fibroblast growth factor homologous factor (FMF)-1 and of differentially spliced isoforms of FMF-2 during development and involvement of FMF-2 in chicken limb development."; pevelopment 126:409-421(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 13 isoform 1S (Fibroblast growth factor homologous factor 2 isoform 1T+1S').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.0%; Score 155.5; DB 13; Length 29.4%; Pred. No. 3e-06; Live 26; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00262; III.HBGF.
ProDom; PD000831; II.1 HBGF; 1.
SMART; SM00442; FGF; 1.
PROSITE; PS0024; HBGF FGF; 1.
SEQUENCE 245 AA; 27605 MW; DAODAFEDBALB8F28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q95L12;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO, GO:0008083; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok III like.
InterPro; IPR002348; IU1 HBGF.
Pfam; PF00167; FGF; 1.
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                                    245 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                   Splicing.";
J. Biol. Chem. 275:2589-2597(2000)
BMBL; AF108755; AAD21576.1; -.
EMBL; AF199611; AAF31398.1; -.
HSSP; P31371; 1G82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53; Conservative
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                                    PRELIMINARY;
                                                                                                                                  FGF13 OR FHF-2.
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q95L12
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                                      Q9W6A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 23
Q95L12
           RESULT 22
                         29W6A2
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91 IQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH-----GLPLH 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                            49 PAVTDLDHLKGILKRRQLXC----RTGFHLEIFPNGTIQGTRKDHSRFGILEFISIAVGL 104
                                                                                                                                                                                                                                                                                                                                                                          32 PDSSPLLQFGGQVRQRYLYTDDAQQTEAHLBIREDGTVGGA-ADQSPESILQLKALKPGV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-99373151; PubMed=10441498;

MEDLINE-99373151; PubMed=10441498;

R Koga C., Adati N., Nakata K., Mikoshiba K., Furubata Y., Sato S.,

R Koga C., Adati N., Nakata T., Shiokawa K., Yokoyama K.K.;

The H., Sakaki Y., Kurokawa T., Shiokawa K., Yokoyama K.K.;

The Third Sakaki Y., Kurokawa T., Shiokawa K., Yokoyama K.K.;

The H., Sakaki Y., Kurokawa T., Shiokawa K., Yokoyama K.K.;

The H., Sakaki Y., Kurokawa T., Shiokawa K., Yokoyama K.K.;

The H., Sakaki Y., Rurokawa T., Shiokawa K., Yokoyama K.K.;

The Theorem Biophys. Res. Commun. 261:756-765(1999).

R PIR., JG7082.

R PIR., JG7082.

R InterPro; IPR0018996; Cytok III. like.

R InterPro; IPR0018996; LI. HBGF.

R PEAM: PPR00167; FGF; 1...
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                                                                                                                                                                                                                                                                                                                24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28;
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                                                                                                                                                                                                                                   Length 208;
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SEQUENCE 208 AA; 23438 MW; 268881D36E757D4D CRC64;
PERMIT PRO0167; FGF; 1. —
PRINTS; PR00262; ILLHBGF.
PRODOM; PD000831; ILLHBGF; 1.
SMART; SM00442; FGF; 1.
PROSTIE; PS00247; HBGF FGF; 1.
SEQUENCE 208 AA; 23454 MW; 05FD0E2048CCC5E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 LPGNKSPHRDPAPRGPAR-----FLPLPGLPPALPE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 VALNK----DGTPREGTRIKRHOKFTHFLPRPVDPDKVPE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.7%; Score 153; DB 13;
ilarity 31.5%; Pred. No. 4.1e-06;
Conservative 22; Mismatches 65;
                                                                                                                                                                                                                                      / Match 13.9%; Score 155; DB 6; Local Similarity 32.5%; Pred. No. 2.7e-06; nes 52; Conservative 19; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 AA
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PRELIMINARY;
CBI_TaxID=10090, 10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P31371; 1G82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8VCY9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 27
Q8VCY9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 EACSFRELLLEDGYNVYQS-----EAHGLPLH-----LPGNKSPHRDPAPRGPARF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160
                                                                                                           84 KALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLP 143
                                                                                                                                                        98 ISVAIGLVSIRGVDTGLYLGMNDKGELFGSEKLTSE-CIFREQFEENWYNTYSSN---- 151
                                               QAHPIPDSSP--LLQFGGQVRQRYLYTDDAQQTBAHLBIREDGTVGGA-ADQSPESLLQL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 HLEIREDGTVGGAADQSPES-LLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 YLOMHPDGALDGTKDDSTNSTLFNLIPVGLRVVALQGVKTGLYIAMNGEGYLYPSELFTP
                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 21, Last sequence update)
Fibroblast growth factor-like factor-4D (Fragment).
Rattus norvegicus (Rat).
Eukarupca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                  144 IHLPGNK-----SPHRDPAPRGPAR-----FLPLPGLPPALPE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Liu C., Dib-Hajj S.D., Waxman S.G.;

Liu C., Dib-Hajj S.D., Waxman S.G.;

Fibrolast growth factor homologous factor-4D.";

Submitted (FEB-2001) to the EMBL/Genbank/DDBJ databases.

EMBL; AF348523; AAL83904 1; -.

EMBL; AF348523; AAL83904 1; -.

EMBL; Figrowth factor activity; IEA.

InterPro; IPR00836; Cytok III_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 LPLPGLPPALPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 AA; 23346 MW; 046C18019C63EBA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 13.7%; Score 153; DB 11;
1 Similarity 32.7%; Pred. No. 4.2e-06;
53; Conservative 21; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam, PF00167; FGF; 1.—
PRINTS, PRO0262; IIJHBGF.
ProDom; PD00083; ILL HBGF; 1.
SMART; SMO442; FGF; 1.
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NON TER 1
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                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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Matches
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089096
089096
AC 08909
DT 01-NO
DT 01-NO
DT FFIbro
GN FFIbro
GN Mus m
OS Rattu
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119 EACSFRELLLEDGYNVYQS-----EAHGLPLH-----LPGNKSPHRDPAPRGPARF 164
SEQUENCE FROM N.A.
SPECIES=Mouse; STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SPECIES-Wouse, and Rat; TISSUE-Brain;
MEDLINE-99257141; PubMed-9602045;
Yamamoto S., Mikami T., Obbayashi N., Ohta M., Itoh N.;
"Structure and expression of a novel isoform of mouse FGF homologous factor (FHF)-4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.7%; Score 153; DB 11; Length 2 Best Local Similarity 32.7%; Pred. No. 5.2e-06; Matches 53; Conservative 21; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:100189; Fgf14.

GO; GO:0008083; F:growth factor activity; IEA.

InterPro; IPR008986; Cytok IL1_like.

InterPro; IPR00248; IL1_HBGF.

Pfint; PR00262; IL1HBGF.

PRINTS; PR00262; IL1HBGF.

PROMORN; PR00481; IL1 HBGF; 1.

SMART; SM00442; FGF; 1.

PROSITE; PS00247; HBGF FGF; 1.

PROSITE; PS00247; HBGF FGF; 1.
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-2001) to the EMBL/GenBank/DDBJ
EMBL, BC018238; AAH18238.1; -.
MGD, MG1.1091/196; FGf13.
OGC GO:0008083; F:growth factor activity, IEA.
InterPro; IPR008996; Cytok_ILI_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochim. Biophys. Acta 1398:38-41(1998).
EMBL; AK035974; BAC29263.1; --
EMBL; AK079100; BAC3740.1; --
EMBL; AB008908; BAA31544.1; --
EMBL; AB008907; BAA31543.1; --
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169 GLPPALP 175
                    191 VDPSKLP 197
                                                                                 086YN7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 30
                                                          RESULT 29
Q86YN7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 SFRELLLEDGYNVYQSEAHGLPLHLPGNK----SPHRDPAPRGPAR-----FLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                           76 SPESILIQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVY 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 ADSPGFLNERL-----GQIEGKLORGSPTDFAHL---KGILRRRQLYC----RTGFFLLE 74
                                                                                                                                                                                                         25 ACQAHPIPDSSPLLQFGGQVRQRY-----LYTDDAQQTEAHLEIREDGTVGGAADQ- 75
                                                                                                                                                                                                                                           -----QSEAHGLPLHL-----PGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                                                                                                                                                                                                                                  156 SSMIYRQQQSGRGWYLGLNKEGEIMKGNHVKKNKPA----AHFLPKP-LKVAMYKEPSL 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHLE
                                                                                                                                                                   37 SCDKNKLNVFSRVKLÅGSKKRRRRRPEPQLKGIVTKLYSRQGYHLOLOADGTIDGTKDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.6%; Score 151.5; DB 11; Length 207; 32.6%; Pred. No. 5.6e-06; tive 20; Mismatches 75; Indels 31; Gaps
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                       29;
                                                                                              13.7%; Score 152.5; DB 11; Length 245; 29.6%; Pred. No. 5.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Heart;
Sontag D.P., Cattini P.A.;
Sontag D.P., Cattini P.A.;
"Cloning and biological function of FGF-16 in the heart.";
"Cloning and biological function of refr-16 in the heart.";
submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF292104; AAG29501.1; -.
HSSP; P31371; 1G82.
                                                                                                                       72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00167; FGF; 1.
PRINTS; PR00262; IL1HBGF.
Pr0D0m; PD000831; IL1 HBGF; 1.
SMART; SM00442; FGF; 1.
SROO247; HBGF FGF; 1.
SRQUENCE 207 AA; 23739 MW; E28004DED598A2C6 CRC64;
                 Pfam; PF00167; FGF; 1.

PRINTS; PR00262; ILIHBGF.

PRODOM; PD000831; ILI HBGF; 1.

SMART; SM00442; FGF; 1.

PROSITE; PS00247; HBGF FGF; 1.

SEQUENCE 245 AA; 27587 MW; 5B96D41AC3A3DF78 CRC64;
                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1931627; Fgf16.
GO; GO:0006083; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok III_like.
InterPro; IPR002348; III_HEGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Mismatches
                                                                                                                                                                                                                                                                                                                                 207 AA
                                                                                                                         25; Mismatches
                                                                                                                                                                                                                                                                                                                                  PRT;
       InterPro; IPR002348; ILL HBGF
                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 32.6%
nes 61; Conservative
                                                                                                                          53; Conservative
                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                               FGF-16 protein.
                                                                                                   Query Match
Best Local S:
Matches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                09ERQ5;
                                                                                                                                                                                                                                                                                                                                    Q9ERQ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                              RESULT 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 BACSFRELLLEDGYNVYQS-----BAHGLPLH----LPGNKSPHRDPAPRGPARF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 HIBIREDGTVGGAADQSPES-ILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-20112823; PibMed=10644718;
Munoz-Sanjuan I., Smallwood P.M., Nathans J.;
Munoz-Sanjuan I., Smallwood P.M., Nathans J.;
"Isoform Diversity among Fibroblast Growth Factor Homologous Factors
Is Generated by Alternative Promoter Usage and Differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Gaps
                                                                          01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 14 isoform 1B.
Fibroblast growth factor 14 isoform 1B.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 252;
                                                                                                                                                                                                                                                                                                                                                                 Bonner T.I.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AT198178; AA031806 1; -
CO; GO:0080818; F:growth factor activity; IEA.
InterPer; IPR008996; Cytok III_like.
InterPer; IPR008996; LILHBGF.
Pfam; PF00167; FGF9; I.
PRINTS; PR00167; FGF9; I.
SWART; SM00442; FGF9; I.
PROSITE; PS00247; HBGF FGF; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.6%; Score 151; DB 4; Length 25; Best Local Similarity 32.7%; Pred. No. 8e-06; Matches 53; Conservative 20; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   091AII;
091AII;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor homologous factor 4 isoform 1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 LPLPGLPPALPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 LPKP-LEVAMYREPSL----HDVGETVPKPGVTPSKSTSAS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28462 MW; 305B0B9A3F56D577 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 AA.
  Z
252
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J. Biol. Chem. 275:2589-2597(2000).
EMBL; AF199606; AAF31393.1; -.
                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
PRT;
                                                        L-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken)
     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 AA;
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9IAI5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus
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156 PAPR---GPARFLPL 167
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9ERW3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9ERW3
                                                                                                                                                     095K97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 33
Q9ERW3
                                                                                                         RESULT 32
Q95K97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID DTT ACCOON SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING 
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                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 GOVRORYLYTDDAQOTEAHLEIREDGTVGGAADQS-PESILIQLKALKPGVIQILGVKTSR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 FLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQS---EAHGLPLH--LPGNKSPHRD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 HLEIREDGTVGGAADQSPES-LLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDP 118
                                                                                                                                                                                                                                                                                                                                                                                                                     119 EACSFRELLLEDGYNVYQS-----EAHGLPLH-----LPGNKSPHRDPAPRGPARF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 GDVRWRKLFS----FTKYFLKIEKNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSNY
                                                                                                                                                                                                                                                                                                                                                            26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                       cch 13.6%; Score 151; DB 13; Length 253; al Similarity 32.1%; Pred. No. 8e-06; 52; Conservative 23; Mismatches 61; Indels 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
13.5%; Score 150; DB 4; Length 170;
Best Local Similarity 30.4%; Pred. No. 6e-06;
Matches 41; Conservative 31; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 LPKP-LEVAMYREPSL----HDIGETVPKAGVTPSKSTSAS 237
                  mose; clivity is considered activity; IEA.

G0.00080803; F:growth factor activity; IEA.

InterPro; IPR008996; Cytok ILL_like.

InterPro; IPR002348; ILL_HBGF.

PEMP; PF00167; FGF.

PRODM; PF000821; ILLHBGF.

PRODM; MO0402; RGF; I.

PROSITE; PS00247; HGFF; I.

PROSITE; PS00247; HGFF FGF; I.

SEQUENCE 253 AA; 28640 MW; 5AEFD9F9D6E74305 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 AA; 19195 MW; 4EA43515F758327A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 LPLPGLPPALPEPPGILAPOPPDVGSSDPLSMVGPSQGRSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 10 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS, PR00262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00247; HBGF FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 52; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=11923311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rissum=Bladder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OBNF19
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42 GQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQS-PESLLQLKALKPGVIQILGVKTSR 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Medulla oblongata; Osada N., Hida M., Kuaba J., Tanuma R., Iseki K., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.; "Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                         Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. TISSUE-borsal root ganglion; Xiao H., Huan Z., Zhang X.; Xiao H., Huang Q., Zhang F., Guo C., Chen Z., Han Z., Zhang X.; "Rattus norvegicus fibroblast growth factor 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
13.5%; Score 150; DB 6; Length 208;
Best Local Similarity 30.4%; Pred. No. 7.8e-06;
Matches 41; Conservative 31; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         libraries.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
BHBL; AB063051; BAB60779.1;
GO; GO: 0000083; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok ILI_like.
InterPro; IPR008996; ILI_HBGF.
PEAM: PF00167; F:GF; ILI_HBGF.
PRINTS; PR001621; ILI_HBGF.
PRODOM; PD000831; ILI_HBGF; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00247; HBGF_FGF; 1.
Hypothetical protein.
SEQUENCE 208 AA; 23466 MW; 0766A787609B3661 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1.MXR-2001 (TrEMBLrel. 16, Created)
(1.MXR-2001 (TrEMBLrel. 16, Last sequence update)
(1.CCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 13.
                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein.
                                                                                                                                                          208 AA
                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 PAPR---GPARFLPL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 OKTRRKNTSAHFLPM 204
152 OKTRRKNTSAHFLPM 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                              PRELIMINARY;
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63 IREDGTVGGAA-DQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 IFPNGTVHGTRHDHSRFGILEFISLAVGLISİRĞVDSGLYLGMNERĞELYĞSKKLTRE-C 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 SFRELLLEDGYNVYQSEAHGL----PLHLPGNKSPHRDPAPRGPAR-----FLPL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 AIGGVQTKLYLANMSBGYLYTSEHFTPE-CKFKESIFENYYVTYSSMIYRQQGGRGWYL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SDETGFEHSGIMVSVLAGILLGACÇAHPIPDSSPLLOFGGOVRORYLYTDDAQQTEAHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 ADSPGFINERL-----GQIEGKLQRGSPIDFAHL---KGILRRRQLYC----RTGFHLE
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.3%; Score 147.5; DB 11; Length 207; 32.4%; Pred. No. 1.3e-05; Indels 33; ive 19; Mismatches 75; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Itoh N.;

"Mus musculus mRNA for FGF-16 (FGF16).";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

BMBL, AB049219; BAB16405.1; -.

HSSP; P31371; IGB2.
                                                                                              145 HL-----PGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                                                                                                   126 GLNKEGEIMKGNHVKKNKPA---AHFLEKP-LKVAMYKEPSL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 AA; 23751 MW; 68BD03EBDAA1D84E CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Keratinocyte growth factor 2.
                                                                                                                                                                                                                                                                                                                                                                                                        01-WAR-2001 (TrEMBLrel. 16, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Fibroblast growth factor 16.
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GO; GO:0008083; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok ILL like.
InterPro; IPR002348; ILL HBGF.
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SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF FGF; 1.
SEQUENCE 207 AA; 23751 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 32.4%; 61, Conservative 1
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                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 PVDPSKLP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
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Best Local
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Matches
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Q9ESL8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 EACSFRELLLEDGYNVY-----QSEAHGLPLHL-----PGNKSPHRDPAPRGPARF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E-CKFKESVFENYYVTYSSMIYRQQSGRGWYLGINKEGEIMKGNHVKKNKPA----AHF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 HLEIREDGTVGGAADQ-SPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 HLOLQADGTIDGTKDEDSTYTLFNLIPVGLRVVAİQGVQTKLYLAMNSEGYLYTSEHFTP
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE-20112833; PubMed=10644718;
Munoz-Sanjuan I., Smallwood P.M., Nathans J.;
Munoz-Sanjuan I., Smallwood P.M., Nathans J.;
Munoz-Sanjuan I., Smallwood P.M., Nathans J.;
Munoz-Sanjuan I., Smallwood P.M., Nathans J.;
Is Generated by Alternative Promoter Usage and Differential
Splicing...
J. Blol. Chem. 275:2589-2597 (2000).
BENBL; AF199610; AAF31397.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                        13.3%; Score 148.5; DB 11; Length 192; 33.8%; Pred. No. 9.7e-06; Live 17; Mismatches 52; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor homologous factor 2 isoform 10+1Y'
                            Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF271786; AAG15492.1; -.
HSSP; P31371; 1G82.
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PROSITE; PS00247; HBGF FGF; 1.
SEQUENCE 199 AA; 22316 MW; FCEC93ABFCEDE22C CRC64;
                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00247; HGGF FGF; 1.
SEQUENCE 192 AA; 21604 MW; 7736A3671677B263 CRC64;
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                                                                                                                    GO, GO:000803; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok III_like.
InterPro; IPR002348; III_HBGF.
Pfam; PF00167; FGF; 1.
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ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                    PRINTS; PR00262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
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142 LPKP-LKVAMYKEPSL 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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OPIAI3;

RESULT 34 O9IAI3

Matches

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212 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rissum=Endometrium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                            042407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E-CKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVKKNKPA----AHF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 HIEIREDGTVGGAADQ-SPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 GOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQS-PESLLQLKALKPGVIQILGVKTSR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 FLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQS---EAHGLPLH--LPGNKSPHRD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauxia; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.0%; Score 144.5; DB 13; Length 236; 33.1%; Pred. No. 2.9e-05; tive 18; Mismatches 52; Indels 21;
                     A SEQUENCE FROM N.A.

A Langy Y., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.;
Zhang Y., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL, AF411527; AAL05875.1; -.

R GG; GG: 0080803; F:growth factor activity; IEA.

R InterPro; IPR002348; IL1_HBGF.

R PRINTS; PR00265; IL1_HBGF.

R PRINTS; PR00265; IL1_HBGF.

R PRODOM; PD000831; IL1_HBGF; 1.

R SWART; SW00242; RGF; 1.

R PROSITE; PS00247; HBGF FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
13.2%; Score 147; DB 4; Length 208;
Best Local Similarity 29.6%; Pred. No. 1.5e-05;
Matches 40; Conservative 32; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 236 AA; 26670 MW; 748ED02C414DDC01 CRC64;
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Last annotation update)
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EMBL, AF540440; AA032391.1; -.

GO, GO:0008083; F:growth factor activity; IEA.

InterPro; IPR008996; Cytok ILL like.

InterPro; IPR00149; ILL HBGF.

Pfam; PF00167; PGF; I.

PRINTS; PR00262; ILHBGF.

ProDom; PD000831; ILL HBGF; I.

PROMITE: PS00247; HBGF; I.

NON_TER.
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"FHF-2 in the turkey (Meleagris gallopavo).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0TW-2003 (TrEMBLrel. 24, Created)
01-0TW-2003 (TrEMBLrel. 24, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
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Best Local Similarity 33.1%
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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42 GQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQS-PESLLQLKALKPGVIQILGVKTSR 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 GDVRKRXLXS----YNKYFLKIEKNGKVSGTKKENCPFSILEITSVEIGVVAVKSIKSNY 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Obuchi H., Nakagawa T., Yamamoto A., Araga A., Ohta T., Ishimaru Y., Yoshioka H., Kuwana T., Yohno T., Yamasaki M., Itoh N., Noji S., "The mesenchymal factor, FGF10, initiates and maintains the outgrowth of the chick limb bud through interaction with FGF8, an apical ectobermal factor.";
                                                                                                                                                                                                                                                                                                                                     Fibroblast growth factor 10.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metaza, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.9%; Score 144; DB 13; Length 212; 28.9%; Pred. No. 2.8e-05; tive 30; Mismatches 52; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23631 MW; AB4C0B32C72A0D90 CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                     212 AA
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                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05, Created)
01-JUN-1998 (TrEMBLrel. 06, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=97330690; PubMed=9187149;
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EMBL; D86333; BAA24945.1; -.
HSSP; P31371; 1G82.
                              156 PAPR---GPARFLPL 167
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Les 39; Conservative
165 LPLPGLPPALPEPPGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKP-GVIQILGVKTS 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 GOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQS-PESLLQLKALKPGVIQILGVKTSR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 FLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQS---EAHGLPLH--LPGNKSPHRD
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Ciona intestinalis.
Bukaryota, Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
                    A Chem C. Spencer T.E., Bazer F.W.;

Chem C.C., Spencer T.E., Bazer F.W.;

I "Fibrolast growth factor-10: A stromal mediator of epithelial function in the ovine uterus.";

Embl: Reprod. 63:959-96 (2000).

R BASP: P31311; 1082.

R GO; 60:008083; F:growth factor activity; IEA.

R InterPro; IPR002948; ILI_HBGF.

R InterPro; IPR002948; ILI_HBGF.

R Probom; P000631; ILI_HBGF.

R Probom; P000631; ILI_HBGF.

R PRINTS; R000442; RGF; 1.

R SMART; SM00442; RGF; 1.

R SMART; SM00442; RGF; 1.

R SRQUENCE 213 AA; 23768 MW; C347149A81C15634 CRC64;
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Best Local Similarity 29.3%; Pred. No. 6.5e-05;
Matches 44; Conservative 23; Mismatches 50; Indels 33;
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Best Local Similarity 31.1%; Pred. No. 3.2e-05;
Matches 42; Conservative 30; Mismatches 48; Indels 15;
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MEDLINE=22259793; PubMed=12373588;
Satou Y., Imai K.S., Satoh N. S.

Satou St., Imai K.S., Satoh N. S.

Fog genes in the basal chordate Ciona intestinalis.";

Dev. Genes Evol. 212:432-438(2002).

EMBL, AB086094; BAC22066.1; ---

EMBL, AB086094; BAC22066.1; ---

GO, GO.0008093; F:Growth factor activity; IEA.

InterPro; IPR008996; Cytok ILI_like.

InterPro; IPR002348; ILI_HBGF.
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Pr0010m; PD000831; ILL HBGF; 1.
SWART; SM00442; FGF; 1.
SEQUENCE 268 AA; 30873 MW; 9187484AEBB5457D CRC64;
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01-WAR-2003 (TYEMBLrel. 23, Last sequence update)
01-OCT-2003 (TYEMBLrel. 25, Last annotation update)
Fibroblast growth factor 3/7/10/22.
CI-FGF3/7/10/22.
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MEDLINE=20411101; PubMed=10952944;
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238 WYIGIDKRGRSKKGRNVKPESSSAHFLPLP 267
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158 -----PRGPAR-----
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Search completed: March Job time: 89.0833 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March 2, 2004, 15:51:17; Search time 20.0292 Seconds (without alignments) 543.341 Million cell updates/sec Run on:

US-10-060-765-4 1113 1 MDSDETGFEHSGLWVSVLAG......SSDPLSMVGPSQGRSPSYAS 209

BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence:

Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                 Hayashizaki Y.;
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SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-Pancreas;

KRAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Adachi J., Fukuda S.,

Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Baito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.P., Suuki R., Tomita M., Wagner L., Washio T.,

Rochim L. Lewis S., Matsudo I., Nikaido I., Pesole G., Quackenbush J.,

Rochim L., Boffelli D., Bojunga N., Canninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Austincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchiguni L., Mashima J., Manazarelli J., Mombaerts P.,

Lyons P., Marchiguez I., Sakamoto N.,

Rosaski H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

By Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
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MEDLINE-20461777; PubMed=10858549;
Mishimura T., Nakatake Y., Konishi M., Itoh N.;
"Identification of a novel FGF, FGF-21, preferentially expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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FIBROBLAST GROWTH FACTOR-21.
FIBROBLAST GROWTH FACTOR-21.
71925C52A0023823 CRC64;
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16-OCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-21 precursor (FGF-21)
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                                Pfam; PF, CARE, LD. HBGF.
PRINTS, PRO0262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF-FGF; FALSE_NEG.
Growth factor; Signal.
SIGNAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 GLWYRILLAVFLLGVYQAXPIPDSSSPLLQFGGQVRQRYLYTDDDQDTEAHLEIREDGTVV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 GAAHRSPESILEIKALKPGVIQILGVKASRFICQQPDGALYGSPHFDPEACSFREILIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 GYNVYOSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPLPGLPPALPEPPGILAPQPPDVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLWVS-VLAGLLLGACQAHPIPDSSPLLQFGGQVRQRXIYTDDAQQTEAHLBIREDGTVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLED
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Nishimura T., Utsunomiya Y., Hoshikawa M., Ohuchi H., Itoh N.;
"Structure and expression of a novel human FGF, FGF-19, expressed in
                                    Nature 409:685-690(2001).
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- TISSUE SPECIFICITY: Most abundantly expressed in the liver, also expressed in the thymus at lower levels.
-!- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Fibroblast growth factor-19 precursor (FGF-19) (UNQ334/PRO533).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1, Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 210 FIBROBLAST GROWTH FACTOR-21.
210 AA; 23237 MW; AB02AABA6477B6F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 793.5; DB 1
Pred. No. 1.8e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prodom; PD000831; IL1 HBGF; 1.
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
PROSITE; Signal.
SIGNAL
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, P03968; IBAR.
MGD; MGI:1861377; FGf21.
InterPro; IPR008996; Cytok IL1_like.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 SDPLSMVEPLÓGRSPSYAS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 SDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB025718; BAA99416.1; -.
EMBL; AK007574; BAB25115.1; -.
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78.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00262; ILLHBGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=2228825; Furnwen=1247/9342,
Attausperg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Attausperg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Attausperg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
Attachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
Brapleton M., Jodin T.B., Pochlyuki S., Carninci P., Prange C.,
Braba S.S., Moclean P.J., McKernan K.J., Mallek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Butkerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Channa and mouse cophs sequences.",
Decoration and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 embryogenesis.
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUB SPECIFICITY: Expressed only in fetal brain.
--- TISSUB SPECIFICITY: Expressed only in fetal brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a
                                                                                                                                                    PGR-19, a novel fibroblast growth factor with unique specificity for
                                                                                                                                                                                                                                                       MEDLINE=2288726; PubMed=12975309; ABCLINE=2288726; PubMed=12975309; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Clan J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Edhen J., Chow B., Chimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Saeshagiri S., Simmons L., Liao D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                        SEQUENCE FROM N.A. Xie M.-H., Holcomb I., Deuel B., Dowd P., Huang A., Vagts A., Foster J., Brush J., Gu Q., Liang J., Hillan K., Goddard A., Gurney A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. Ü.S.A. 99:16899-16903(2002).
-!- FUNCTION: May be involved in brain development during
                                                                                                                                                                                                      Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
the fetal brain.";
Biochim. Biophys. Acta 1444:148~151(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 603891; -.
GO; GO:0007399; P:neurogenesis; TAS.
InterPro; IPR008996; Cytok_IL1_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
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EMBL, AF110400; AA045973.1; --
EMBL, AX358302; AA088669.1; --
EMBL, BC017664; AAH17664.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 LEDGYNVYQSEAHGLFLHLPGNKSPHRDPAPRGPARFLPLPGLPPALP----EPPGI--- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 RPDGYNVYRSEKHRLPVSLSSAKQ-RQLYKNRG---FLPLSHFLPMLPWVPEFPEDLRGH 182
                                                                                                                                                                                                                                                                                                                                                                         68 TVGGAADQSPESILIQLKALKPGVIQILGVKTSRFLCQRPDGALYGSIHFDPEACSFRELL 127
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MEDLINE=20490027; PubMed=11032749;
Yamashita T., Yoshioka M., Itoh N.;
"Identification of a novel fibroblast growth factor, FGF-23,
preferentially expressed in the ventrolateral thalamic nucleus of the
                                                                                                                                                                                                                                                                                                                                                                                                               67 VVDCARGOSAHSILLEIKAVALRTVAİKGVHSVRYLCMGADGKMQGILLQYSEEDCAFEEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                           11 SGLWVSVLAGLLIGACQAHPIPDSSPLLQF--GGQVRQRYLYTDDAQ-QTEAHLBIREDG
                                                                                                                                                                                                                                                                                                                    14 AGLWLAV-AGRPLA-----FSDAGPHVHYGWGDPIRLRHLYTGGPHGLSSCFLRIRADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nat. Genet. 26:345-348 (2000).
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- TISSUE SPECIFICITY: Mainly expressed in the brain and thymus at low levels. In brain; preferentially expressed in the ventrolateral thalamic nucleus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BALB/C; TISSUE=Embryo; MEDLINE=20517346; PubMed=11062477; MEDLINE=20517346; PubMed=11062477; Mathite K.E., Bvane W.E., O'Kiordan J.L.H., Speer M.C., Econs M.J., Mahite K.E., Bvane W.E., O'Kiordan J.L.H., Speer T., Strom T.M.; Mattinger T., Strom T.M.; "Autosemal dominant hypophosphataemic rickets is associated with
                                                                                                                                                                                                               Length 216;
                                                                                                                                      POTENTIAL.
FIBROBLAST GROWTH FACTOR-19.
                                                                                                                                                                                                                                                       82; Indels
                                                                                                                                                   CHAIN 23 216 FIBROBLAST GROWTH FACTOR-: SEQUENCE 216 AA; 24002 MW; BOBCBC9C220F9832 CRC64;
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                                                                                                                                                                                                                  Query Match 23.8%; Score 265; DB 1; Best Local Similarity 36.3%; Pred. No. 8.5e-13; Matches 77; Conservative 27; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-23 precursor (FGF-23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ----LAPOPPDVGSSDPLSMV-GPSQGRSPSY 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 LESDMFSSPLETDSMDPFGLVTGLEAVRSPSF 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
        Pfam; PF001G7; FGF; 1.
PRINTS; PR00262; ILIHBGF.
ProDom; PD000831; ILI HBGF; 1.
SMRAT; SM04427; FGF; I.
PROSITE; PS00247; HBGF_FGF; 1.
Growth factor; Signal.
InterPro; IPR002348; IL1_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutations in FGF23.
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Gaps

23;

Indels

86:

58

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67 GTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFREL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 LLEDGYNVYQSBAHGLPLHLPGNK---SPHRDPAPRGPARFL-----PLPGLPPALPEP 177
                                                                                                                                                                                                                                                                                                                                                                                                                          12 GLWVSVLAGLLLGACQ---AHPIPDSSPLL--OFGGQVRQRYLYTDDAQQTEAHLEIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20490027; PubMed=11032749; MEDLINE-20490027; PubMed=11032749; Mamshita T., Yoshioka M., Itoh N.; "Identification of a novel fibroblast growth factor, FGF-23, preferentially expressed in the ventrolateral thalamic nucleus of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GACLRLLVGALCTVCSLGTARAYSDTSPLLGSNWGSLT---HLYTATARNS-YHLQIHRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., VARIANTS ADHR GLN-176; GLN-179 AND TRP-179, AND
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MEDLINE=22887296; PubMed=12975309;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20517346; PubMed=11062477;
White K.E., Evans W.E., O'Riordan J.L.H., Speer M.C., Econs M.J.,
Lorenz-Depiereux B., Grabowski M., Meitinger T., Strom T.M.;
"Autosomal dominant hypophosphataemic rickets is associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21267444; PubMed-11344269; Shimada T., Hino R., Takeda S., Shimada T., Mizutani S., Muto T., Yoneya T., Hino R., Takedi Y., Pujita T., Fukumoto S., Yamashita T.; "Cloning and characterization of FGF23 as a causative factor of
                                                                                                                                                                                                                                                                                         Score 235.5; DB 1; Length 251; Pred. No. 1.4e-10;
                                                                                                                                                                POTENTIAL.
FIBROBLAST GROWTH FACTOR-23
                                                                                                                                                                                    25 251 FIBROBLAST GROWTH FACTOR-:
251 AA; 27911 MW; 35A229E1B3900593 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MR-2004 (Rel. 43, Last annotation update)
15-MR-2004 (Rel. 43, Last annotation update)
15-MR-2019 (Rel. 43, Last annotation update)
15-MR-2019 (Rel. 43, Last annotation update)
15-MR-2019 (Rel. 43, Last annotation update)
16-OCT-2019 (Rel. 43, Last annotation update)
17-OCT-2019 (Rel. 43, Last annotation update)
17-OCT-2019 (Rel. 43, Last annotation update)
18-OCT-2019 (Rel. 43, Last annotation update
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                                                                                                                                                                                                                                                                            21.2%; Sco...
34.1%; Pred. No. 1...
''ve 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prodom, PD000831, IL1 HBGF; 1.
SMART; SM00442; FGF, I.
PROSITE; PS00247; HBGF-FGF; FALSE_NBG.
Growth factor; Signal.
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                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 34.1%
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
Pfam; PF00167; FGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 ILEDGYNVYQSEAHGLPLHLPGNK---SPHRDPAPRGPARFL-----PLPGLPPALPEP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLWVSVLAGLLLGACQ---AHPIPDSSPLL--OFGGOVRORYLYTDDAQQTEAHLEIRED
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-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- SIMILARITY: Belongs to the heparin-binding growth factors family.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 24 POTENTIAL.
25 251 FIBROBLAST GROWTH FACTOR-23.
251 AA, 27757 MW, 110C1F2C735DC360 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 22.4%; Score 249.5; DB 1
Best Local Similarity 35.1%; Pred. No. 1.4e-11;
Matches 73; Conservative 27; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fibroblast growth factor-23 precursor (FGF-23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 AA
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                                                                                                                                                                                                                       HSSP, P03968; IBAR.
MGD; MGI:1891427; Fgf23.
INTEAFRO; IPR002996; Cytok ILL like.
InteaFro; IPR002489; ILL HBGF.
Pfam; PF00167; FGF; 1.
PRINTS; PR00262; ILLHBGF.
PRODOM; PD000831; ILLHBGF. I.
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF FGF; FALSE NEG.
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InterPro, IPR008996; Cytok ILI_like.
InterPro, IPR002348; ILI_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                      EMBL; AB037889; BAB13478.1; -. EMBL; AF263536; AAG09916.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Growth factor; Signal.
SIGNAL 1
                                                                                                                                                                                           PIR; JC7513; JC7513.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- DISEASE: Defects in FGF23 are the cause of autosomal dominant hypophosphateamic rickets (ADHR) [MIM:193100]. ADHR is characterized by low serum phosphorus concentrations, rickets, osteomalacia, leg deformities, short stature, bone pain and dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47; Gaps
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Scheenfeld J., Seshagris S., Simmons L., Singh V., Sminson J., Vagts A., Vandlen R., Watanabe C., Waieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                            "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."; Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the heparin-binding growth factors family.
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20.0%; Score 222.5; DB 1; Length 251;
Best Local Similarity 30.8%; Pred. No. 1.3e-09;
Matches 68; Conservative 36; Mismatches 70; Indels 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
FIRNCHALAST GROWTH FACTOR-23.
R -> Q (in ADHR).
R -> Q (in ADHR).
R -> Q (in ADHR).
PTId=VAR_010717.
R -> W (in ADHR).
R -> W (in ADHR).
FTId=VAR_010718.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00247; HBGF FGF; FALSE_NEG.
Growth factor; Signal; Disease mutation; Polymorphism.
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GO; GO:0005615; C:extracellular space; NAS.
GO; GO:0030154; P:cell differentiation; NAS.
InterPro; IPR008996; Cyrck III like.
InterPro; IPR002348; ILI_HBGF.
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Α -- Ε
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EMBL, AF263537; AAG09917.1; -.
EMBL, AB047859; BAB55889.1; -.
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PRINTS, PR00262; IL1HBGF.
ProDom; PD000831; IL1 HBGF; 1.
SMART; SM00442; FGF; 1.
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RA Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
R. Kawai U., Shinagawa A., Shibata K., Yoshino H., Adachi J., Fukuda S.,
R. Arakawa T., Hara A., Fukumishi Y., Konno H., Adachi J., Fukuda S.,
R. Arakawa T., Itawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
R. Asaito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
R. Kadota K., Matsuda H.A., Ashburnar M., Batalov S., Casavan T.,
R.A Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
R.A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
R.A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Wagner I., Washio T.,
R.A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
R.A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
R. Bornstein M.J. Bult C., Fletcher C., Fujita M., Gariboldi M.,
R. Bornstein M.J. Bult C., Fletcher C., Fujita M., Gariboldi M.,
R. Bornstein M.J., Bult C., Fletcher C., Fujita M., Ramiya M., Lee N.H.,
R. Morndore P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
R. Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
R. Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
R. Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
R. Havachizaki Y.
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KAUSINELS 2388257; PubMed=12477932;

RA Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A lepkins R.F., Jordan H., Moorer T., Max S.I., Wang J., Hsieh F.,

A piechenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Biechenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldon M.F., Carninci P., Prange C.,

RA Raha S.S., Loquilano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rohas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rodards S., Worley K.C., Hales, Garcia A.M., Gay L.J., Hulyk S.M.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Ran and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDILINE=974542; PubMed=9310317; MEDILINE=974542; PubMed=9310317; Ghun J., Murre C.; McWhirter J.R., Goulding M., Weiner J.A., Chun J., Murre C.; McWhirter J.R., Goulding M., Weiner J.A., Chun J., Murre C.; McMirter J. R., anyel fibroblast growth factor gene expressed in the developing nervous system is a downstream target of the chimeric homeodomain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                       165 PLIHFNTPIPRRHTRSAEDDSERDPLNVLKPRARMTPAPAS 205
179 ---GILAPOP-----PDVGSSDPLSMVGPSQGRSPSYAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2003 (Rel. 42, Last annotation update)
Fibroblast growth factor-15 precursor (FGF-15)
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                                                                                                                                                                                                                                                                                218 AA
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                                                                                                                                                                                                                                                                                        STANDARD;
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MEDLINE=88296404; PubMed=2841106;
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65
                                                                                      growth factors.
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                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: May play an important role in regulating cell division and patterning within specific regions of the embryonic brain, spinal cord and sensory organs.
                                                                                                          -1- TISSUE SPECIFICITY: Expressed in the developing brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
28-FSB-2015 (Rel. 41, Last annotation update)
(RGF-3) (HBGF-3).
FGF-3 (HBGF-3).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYNQYRSMKHHLHIIFIQAK-PREQLQDQKPSNFIPV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 GYNVYOSEAHGLPLHLPGNKSPHRDPAPRGPARFLPL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 18.6%; Score 206.5; DB 1
Best Local Similarity 33.8%; Pred. No. 1.6e-08;
Matches 53; Conservative 29; Mismatches 70
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MGD, MGI:1096383; Egf15.
InterPro; IPR008996; Cytok III_like.
InterPro; IPR002348; III_HEGF.
Pfam; PF00167; FGF; 1.
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                                                                                                 SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                EMBL, AF007268, AAB63197.1; -.
EMBL, AK017829, BAB30961.1; -.
EMBL, BC021328, AAH21328.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probom; PD000831; III HBGF; 1.
SMART; SM00442; FGF; I.
PROSITE; PS00247; HBGF_FGF; 1.
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SEQUENCE OF 1-73 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00262; IL1HBGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 FLCQRPDGALYGSLHPDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSP--HRDPAP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 YLAMNKRĠRLYASDHYNAE-CEFVERIHELGYNTYASR----LYRTGSSGPGAQRQPGA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 RGP-----ARFLPLPGLPPALPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 ORPWYVSVNGKGRPRRĞFKTRRTQKSSLFLPRVLGHKDHEMVRLLQSSQPRAPGRGS 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family.";
J. Cell Sci. Suppl. 13:87-96(1990).
-- FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.
-- FUNCTION: BY INTEGRATION OF MOUSE MAMMARY TUMOR VIRUS.
-- INDUCTION: BY INTEGRATION OF MOUSE MAMMARY TUMOR VIRUS.
-- SIMILARITY: Belongs to the heparin-binding growth factors family.
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01-0CT-1989 (Rel. 12, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1NT-2 proto-oncogene protein precursor (Fibroblast growth factor-3) (FGF-3) (HBGF-3).
FGF-3 (HBGF-3).
FGF3 (HURZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith R., Peters G., Dickson C.; "Multiple RNAs expressed from the int-2 gene in mouse embryonal carcinoma cell lines encode a protein with homology to fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
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N-LINKED (GLCNAC. . .).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70D94FD6A7837C79 CRC64;
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1 Similarity 28.8%; Pred. No. 1.9e-06;
51; Conservative 30; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 AA.
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                                                                                                                                                                                                               EMBO J. 7:1013-1022(1988)
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65
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P10767;
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                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as a long as its content is n no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 YLAMNKAGRLYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTFGAR---RQPSAER 151
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10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41; Gaps
                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 IMYVSVNGKGRPRRGFKTRRTOKSSLFLPRVLDHRDHEMVROLOSGLPRPPG 203
                                                                                                                   MEDLINE-89239468; PubMed-2470007;
Brooks S., Smith R., Casey G., Dickson C., Peters G.;
Sequence organization of the human int-2 gene and its expression
teracocarcinoma cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fibroblast growth factor-4 precursor (FGF-4) (Heparin secretory transforming protein) (HST) (HBGF-4).
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Proto-oncogene; Growth factor; Mitogen; Signal; Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.9%; Score 177.5; DB 1; Length 2 29.7%; Pred. No. 2.4e-06; tive 23; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INT-2 PROTO-ONCOGENE PROTEIN.
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 164950; -
GO; GO:000576; C:extracellular; TAS.
GO; GO:000576; P:growth factor activity; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
GO; GO:0007185; P:histogenesis and organogenesis; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR008996; Cytok ILL like.
InterPro; IPR02248; ILL HBGF.
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                                                                                                                                                                                                                        Oncogene 4:429-436(1989).
-!- FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.
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ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X14445; CAA32615.1; -. PIR; S04742; RSSP; P31371; 1G82. Genew; HGNC:3681; FGF3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239
                                                                                                                                                                                                     teratocarcinoma cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                 SEQUENCE FROM N.A.
                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGF4 OR HST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOVIN
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 WVSVLAGILLGACQAHPIPDSSPLLQFGGQV-----RQRYLYTDDAQQTEAHLEIRBDGT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 WESLVARSLIAGLEVAAQPKEAAVQSGAGDYLLGIKRLRRLYCNVG--IGFHLQVLPDGR
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                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Gaps
                                                                                                                                                                                                                                                                                             An unexpected transforming gene in calf-thymus carrier DNA: bovine
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
MCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1989 (Rel. 11, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fibroblast growth factor-6 precursor (FGF-6) (HBGF-6) (HST-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 206;
                                                                                                                                                                                                        MEDLINE-96032369; PubMed=7557455;
Yu J.C., Deseabra A.J., Wang L.M.; Fleming T.P., Chedid M.,
Miki T., Heidaran M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 206 FIBROBLAST GROWTH FACTOR-4.
206 AA; 22041 MW; F9B7AB6066E56613 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 EDGYNVYQSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.9%; Score 177; DB 1; 32.1%; Pred. No. 2.2e-06; iive 23; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE, PS00247; HBGF FGF; 1.
Proto-oncogene; Growth factor; Mitogen; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR008996; Cytok III_like.
InterPro; IPR002348; III_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00262; IL1HBGF.
ProDom; PD000831; IL1 HBGF; 1.
SMART; SM00442; FGF; 1.
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HSSP; P31371; 1G82.
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Best Local Similarity 32...
Best Local Similarity
Lacan S2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   Gene 162:333-334(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00167; FGF; 1.
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82 IKRQRRLYCNVG--IGFHLQVLPDGRISGTHEENPYSLLEISTVERGVVSLFGVRSALFV 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48; Conservative
                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00167; FGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                        FGFA XENLA
P48805;
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                                                                                                                                                                                      FGFA_XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - SIMILARITY: Belongs to the heparin-binding growth factors family.
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                                                                                                                                                                                                                             MEDLINE=89201880; PubMed=2649847;
Marics I., Adelaide J., Raybaud F., Mattei M.-G., Coulier F.,
Planche J., de Lapeyriere O., Birnbaum D.;
"Characterization of the HST-related FGF.6 gene, a new member of the tibroblast growth factor gene family.";
Oncogene 4:335-340(1989).
                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: CAN TRANSFORM NIH 3T3 CELLS. EXHIBITS STRONG MITOGENIC AND ANGIOGENIC PROPERTIES.
                                                     SEQUENCE OF 11-208 FROM N.A.
MEDLINE-92195660; PubMed=1549352;
MIDD.INE-92195660; T., Naito K., Sakamoto H., Katoh O., Hirohashi S.,
Sato T., Onda M., Sugimura T., Terada M.;
"Human hst-2 (FGF-6) oncogene: cDNA cloning and characterization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
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N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 LWVSVLAGLLLGACQAHP-----IPDS---SPLLQ-----FGGQV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00442; FGF; I.
PROSITE; PS00247; HBGF-FGF; 1.
Proto-oncogene; Growth factor; Mitogen; Angiogenesis; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.9%; Score 176.5; DB 1; Length 208; 29.1%; Pred. No. 2.4e-06; artive 27; Mismatches 52; Indels 33.
                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: Leukemia cell lines with platelet/
megakaryocytic differentiation potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 V -> G (IN REF. 3).
22904 MW, 79EF44685B324322 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 134921; -
GO; 0005576; C:extracellular; TAS.
GO; GO:0008083; F:growth factor activity; TAS.
GO; GO:0008283; F:eell proliferation; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR002996; Cytok III_like.
InterPro; IPR002349; III_HBGF.
PFINITS; FR00265; ILHBGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PD000831; IL1 HBGF; 1.
3M00442; FGF; 1.
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SEOUENCE OF 81-208 FROM N.A.
              Oncogene 6:1437-1444(1991).
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                                                                                                                                                                 Oncogene 7:303-309(1992).
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208
45
157
100
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HSSP; P09038; 1BFG.
Genew; HGNC:3684; FGF6.
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SIGNAL
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MIM; 13
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              SOLITIFIER WERE REPRESENTED TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 DSDYLL---GIKRQRRLYCNVG--IGFHIQVLPDGRINGMHSBNRYSLLELSPVEVGVVS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 LYGVKSGMFVAMVAKGKLYGSRYFN-EECKFKETLLFUNYNAYESRKYPGMYIALGKNGR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 DSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQ 92
                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor 1 (XERGF-1) (HBGF-4-I) (Embryonic fibroblast growth factor 1).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopus.
Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Development 114:711-720(1992).

-!- FUNCTION: GOOD CANDIDATE FOR AN INDUCING FACTOR WITH POSSIBLE ROLES BOTH IN MESODERM INDUCTION AT THE BLASTULA STAGE AND IN THE FORMATION OF THE ANTEROPOSTERIOR AXIS AT THE GASTRULA STAGE.

-!- SUBCELLULAR LOCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDILINE=92215916; PubMed=1618138; Isaacs H.V., Tannahill D., Slack J.M.W.; Expression of a novel FGF in the Xenopus embryo. A new candidate inducing factor for mesoderm formation and anteroposterior specification.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL 1 22 POTENTIAL.
CHAIN 23 187 FIBROBLAST GROWTH FACTOR-4-I.
SEQUENCE 187 AA; 21223 MW; AAR63D65E82AD1BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57; Indels
103 CORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
                                    | || : | | || : || 115 || 140 AMNSKGRLYATPSFQ-EECKFRETLLPNNYNAYESDLY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.6%; Score 174; DB 1;
34.8%; Pred. No. 3.3e-06;
tive 23; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, P31371, 1G82.
InterPro, IPR008996; Cytok IL1_like.
InterPro, IPR002348; IL1_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 -KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0262; ILLHBGF.
PRODON; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; I.
PROSITE; PS00247; HBGF FGF; 1.
Growth factor; Mitogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X62593; CAA44479.1; -. PIR; S23595; S23595.
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102 LCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
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CARBOHYD
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Best Local
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         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: CAN TRANSFORM NIH 3T3 CELLS. EXHIBITS STRONG MITOGENIC PUNCTION: CAN TRANSFORM (BY SIMILARITY).
-!- SUBSCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: Embryos, adult muscles and adult testis.
-!- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90295275; PubMed=2193291;

Me Lapeyriere O., Rosnet O., Benharroch D., Raybaud F.,

Marchetto S., Planche J., Galland F., Mattei M.-G., Copeland N.G.,

Jenkins N.A., Coulier F., Birnbaum D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure, chromosome mapping and expression of the murine Fgf-6
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                               Ollendorf V., Rosnet O., Marics I., Birnbaum D., Delapeyriere O., "Isolation and sequence of the murine Fgf6 cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . .) (POTENTIAL)
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1 Similarity 36.4%; Pred. No. 6.7e-06;
36; Conservative 21; Mismatches 39; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00147; HGGF FGF; 1.
Proto-oncogene; Growth factor; Mitogen; Anglogenesis; Signal;
                                                                                                                     01-MAY-1991 (Rel. 18, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fibroblast growth factor-6 precursor (FGF-6) (HBGF-6) (HST-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
FIBROBLAST GROWTH FACTOR-6.
N-LINKED (GLCNAC. . .) (POT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 37 POTENTIAL.
38 208 FIBROBLAST GROWTH FACTOR-6
45 N-LINKED (GLCNAC. . .) (PC
90 157 POTENTIAL.
208 AA; 22798 MW; BBF7B9301BB79A1B CRC64;
                                                                                   208 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, M92415; AAA62260.1; ---
EMBL, M92416; AAA62261.1; ---
EMBL, SS1552; CAA35925.1; ---
PIR; S14192; S14192.
HSSP, P09038; 1BFG.
MGD; MGI:95520; FGFG.
InterPro; IPR008996; Cytok ILL like.
InterPro; IPR00898; ILL HBGF.
                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Embryo;
MEDLINE=93120244; PubMed=1477139;
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PRODOM; PD000831; ILL HBGF; 1.
SMART; SMO0442; PGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochimie 74:1035-1038(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 11-208 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oncogene 5:823-831(1990)
                                                                                       STANDARD;
                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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SIGNAL
                                                                                                                                                                                                                         FGF6 OR FGF-6.
                                                                                     FGF6 MOUSE
P21658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
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                                              RESULT 13
                                                                                                              $\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2
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42 GQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRF 101

Matches

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R EMBL; D64086; BAA10967.1; -.
R EMBL; D64086; BAA10967.1; -.
R PIR; S68144; S68144.
PIR; S68144; S68144.
R PIR; S68145; S68146.
R InterPro; IPR008396; Cytok IL1_like.
R InterPro; IPR008396; Cytok IL1_like.
R InterPro; IPR002348; IL1_HBGF.
R PFONG; PR00081; IL1_HBGF.
R PRINTS; PR000262; IL1HBGF.
R SWART; SM00442; FGF; 1.
R SWART; SM00442; FGF; 1.
R PROSITE; PS00247; HBGF_FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 SSPLLQFGGQVRQRYLYTDDAQQTEA-----HLEIREDGTVGGAADQSPESLLQLK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Short; Synonyms=FGF-58; IsoId=P48807-2; Sequence=VSP_001522, VSP_001523; IsoId=P48807-2; Sequence=VSP_001522, VSP_001523; -:- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hattori Y., Yamasaki M., Itoh N.; "The rat FGF-5 mRNA variant generated by alternative splicing encodes "The rat FGF-5 mRNA variant generated by
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-SER.
LINKED (GLCNAC. .) (POTENTIAL)
ILEI -> QIYR (in isoform Short).
/FIId=VSP_001522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.0%; Score 167; DB 1; Length 266; 30.3%; Pred. No. 1.6e-05; Pred. 26; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Missing (In isoform Short). /FTIG=VSP_001523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIBROBLAST GROWTH FACTOR-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95B0A0CA7C0A200C CRC64;
                                                                                                                                                          P48807; Q63402; OC. PRI; CED AA. D48807; Q62402; 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Pibroblast growth factor-5 precursor (FGF-5) (HBGF-5).
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Mismatches
                                                                                                                                                     266 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Long;
Isold=P48807-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a novel truncated form of FGF-5.",
Biochim. Biophys. Acta 1306:31-33(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Wistar;
MEDLINE=96201703; PubMed=8611621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 AA; 29264 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266
59
108
121
                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54
108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
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                       97 KTSRFLCQRPDGALYGSLHFDPBACSFRELLLEDGYNVYQSBAH-GLPLHLPGN---KSP 152
                                                                                            120 RSGLFVAMNSKGKLYGSTHVNDE-CKFKEILLENNYNAYESRIYPGMYIALSKNGRTKKG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECURNCE FROM N.A. (ISOFORM LONG).
MEDLINE=90201563; PubMed=2318343;
Hebert J.M., Babilico C., Goldfarb M., Haub O., Martin G.R.;
Hachert J.M., Babilico C., Goldfarb M., Haub O., Martin G.R.;
"Isolation of cDNAs encoding four mouse FGF family members and characterization of their expression patterns during embryogenesis.";
Dev. Biol. 138:454-463(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Short; Synonyms=FGF-5S;
IsoId=P15656-2; Sequence=VSP_001520, VSP_001521;
SIMILARITY: Belongs to the heparin-binding growth factors family.
LLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM SHORT).
MEDLINE=99003286; PubMed=9786939;
Ozawa K., Suzuki S., Asada M., Tomooka Y., Li A.J., Yoneda A.,
Komi A., Imamura T.;
"An alternatively spliced fibroblast growth factor (FGF) -5 mRNA is
abundant in brain and translates into a partial agonist/antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene in the
                                                                                                                                                                                                                                                                                      FGF5_MOUSE STANDARD; PRT; 264 AA. P1565; OB8825; OB8825; O1-APR-1990 (Rel. 14, Created) O1-APR-1990 (Rel. 14, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Fibroblast growth factor-5 precursor (FGF-5) FGFS OR FGF.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haub O., Drucker B., Goldfarb M.;
"Expression of the murine fibroblast growth factor 5-adult central nervous system.";
proc. Natl. Acad. Sci. U.S.A. 87:8022-8026(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Long;
IsoId=P15656-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGF-5 neurotrophic activity.";
J. Biol. Chem. 273:29262-29271(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, M30643, AAA96698.1; ---
EMBL, M37821, AAB02660.1; ---
EMBL, M37821, AAB02660.1; JOINED.
EMBL, M37822, AAB02660.1; JOINED.
EMBL, M37822, AAB02660.1; ALT_SEQ.
EMBL, AB016516; BAA33737.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM LONG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6;
MEDLINE=91045929; PubMed=1700424;
                                                                                                                                                    153 HRDPAPRGPARFLP 166
                                                                                                                                                                                            179 NKVSPTMTVTHFLP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AB016516; BAA
PIR, A36207; A36207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=10090;
       37
                                           65
                                                                                                                                                                                                                                                    RESULT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AALLPALLLGLLWPGAVRGRPPPGRLPPGPRQRRWDAALFARSVARLPAERRDAARDGDY 64
                                                                                                     178
                                                                                                                                       182 TGREWYVALNK---RGKAKRGCSPRVKPQHVSTHFLPRFKQSEQPELSFTVTVPEKKKPP 238
                           ALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH---- 140
                                                      Nature 371:609-612 (1994).

-!- FUNCTION: MAY BE THE ENDOGENOUS RIDGE SIGNAL FOR LIMB DEVELOPMENT.

-!- FUNCTION: MAY BE THE ENDOGENOUS RIDGE SIGNAL FOR LIMB DEVELOPMENT.

BETTWERN SONIC HEDDEHOG (SHH) AND FGF4.

-!- TISSUE SPECIFICITY: POSTERIOR RIDGE.

-!- INDUCTION: By retinoic acid.

-!- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                     141 -GLPLHLPGNKSPHRDPAPRG------PARFLP-----LPGLP----PALPEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95021713; PubMed=7935/94;
Makander L., Jeffrey S., Martin G.R., Tickle C.;
NA positive feedback loop coordinates growth and patterning in the vertebrate limb.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.8%; Score 165; DB 1; Length 194; 27.3%; Pred. No. 1.6e-05; tive 29; Mismatches 68; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
FIBROBLAST GROWTH FACTOR-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 AA; 21642 MW; 5D44245BE97E664A CRC64;
                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-201 (Rel. 40, Last annotation update)
Fibroblast growth factor-4 precursor (FGF-4) (HBGF-4).
                                                                                                                                                                                                                                                                                                                   194 AA.
                                                                                                                                                                                                         ---RPWKPKV----PLS---PSR-RSPS 255
                                                                                                                                                                                  179 GILAPQPPDVGSSDPLSMVGPSQGRSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P09038; 1BFF.
InterPro; IPR008996; Cytok_ILI_like.
InterPro; IPR002348; ILI_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 SGLWVSVLAGLLL-GACQAHPIP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; Irkvozzy,
Pfam; PF00167; FGP; 1.
PRINTS; PR00262; ILLHBGF.
ProDom; P0000831; ILL HBGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00442; FGF; I.
PROSITE; PS00247; HBGF FGF; 1.
Growth factor; Mitogen; Signal SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U14654; AAA58706.1; -. PIR; S78506; I50710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53; Conservative
                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                 FGF4 OR FGF-4.
                                                                                                                                                                                                                                                                                                                     FGF4 CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                   P48804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus
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modified and this statement is not removed. entities requires a license agreement (See h
                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1988 (Rel. 08, Last sequence Up
10-OCT-2003 (Rel. 42, Last annotation
Fibroblast growth factor-4 precursor
Fibroplast growth factor-4
                                                                       HSSP, P31371; 1G82.
InterPro; IPR008996; Cytok IL1_like.
InterPro; IPR002348; IL1_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=87301716; Pubmed=2957062;
                                                                                                                                 ProDom; PD000831; ILLI HBGF; 1.
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF FGF; 1.
Growth factor; Mitogen; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGF4 OR HST OR HSTF1 OR KS3.
                                               EMBL; X62594; CAA44480.1; -. PIR; S54407; S54407.
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                     PRINTS; PR00262; ILIHBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens (Human)
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                             Pfam; PF00167; FGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                            FGF4 HUMAN
P08620;
                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                 FGF4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ношо
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                                                                                                                                                                                                                                                                                                                                                      85 ALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSRAH---- 140
                                                                                                                                                                                                                                                                                                                                                                                                                             182 TGREWYVALNK---RGKAKRGCSPRVKPOHVSTHFLPRFKQSEQPELSFTVTVPEKKKPP 238
                                                                                                                                                                                                                                                                                                                    63 ASPGSQGSGSEHSSFQWSPSGRRIGSLYCRVGIGFHLQIYPDGKVNGSHEASVLSILEIF 122
                                                                                                                                                                                                                                                                                                                                                                                                       183
                                                                                                                                                                                                                                                                                                     34 SSPILQFGGQVRQRYLYTDDAQQTEA-----HLEIREDGTVGGAADQSPESILQLK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                     141 -GLPLHLPGNKSPHRDPAPRG-----PARFLP-----LPGLPPALPEPPGILAP
               MGD; MGI:95519; Fgf5.
InterPro; IPR008996; Cytok IL1_like.
InterPro; IPR002348; IL1_HBGF.
InterPro; IPR002548; IL1_HBGF.
Pran; PR00167; RGF; IL1_HBGF.
PRODOM; PR000631; IL1_HBGF; I.
PROSITE; PR00442; FGF; I.
PROSITE; PR0442; FGF; I.
PROSITE; PROSITE; PROFF II.
PROSITE; PROSITE; PROFF II.
PROFCO-ONCOGENE; Growth factor; Mitogen; Signal; Alternative splicing.
SIGNAL.
I 77 POTENTIAL.
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=92315916; PubMed=1618138;
Inaacs H.V., Tannahill D., Slack J.M.W.;
"Expression of a novel FGF in the Xenopus embryo. A new candidate inducing factor for mesoderm formation and anteroposterior pression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-4-II precursor (FGF-4-II) (HBGF-4-II)
Fibroblast growth factor II) (XEFGF-II).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi,
                                                                                                                                                         POLY-SER.
LINKED (GLCNAC. . ) (POTENTIAL)
ILEI -> QIYG (in isoform Short).
/FTId=VSP_001520.
                                                                                                                                                                                                                                                                                42;
                                                                                                                                                                                                                                                     Length 264;
                                                                                                                                                                                                                                                                                78; Indels
                                                                                                                                                                                                     122 264 Missing (In isoform Short).
/FIId=VSP 001521.
264 AA, 29103 MW, F6A9C8153EE923D1 CRC64;
                                                                                                                                           FIBROBLAST GROWTH FACTOR-5.
                                                                                                                                                                                                                                                        14.7%; Score 164; DB 1;
28.6%; Pred. No. 2.6e-05;
tive 25; Mismatches 78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 QPPDVGSSDPLSMVGPSQGRSPS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 VKPKVPLSQP-----RRSPS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                     58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                               264
59
108
121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kenopodinae; Xenopus.
                                                                                                                                                                                                                                                                          Similarity
              HSSP; P09038; 1BFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8355;
                                                                                                                                                                                   118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGFB_XENLA
                                                                                                                                                             DOMAIN
CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                              VARSPLIC
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FGFB_XENLA
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                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    loved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: CAN TRANSFORM NIH 3T3 CELLS PROM A HUMAN STOMACH TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transforming protein) (HST-1) (HST) (Transforming protein KS3) (HBGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "CDNA sequence of human transforming gene hat and identification of the coding sequence required for transforming activity."; proc. Natl. Acad. Sci. U.S.A. 84:2980-2984(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINES-8804-1096; Pubmed-2959959;
YOSHida T., Miyagawa K., Odagiri H., Sakamoto H., Little P.F.R.,
Terada M., Sugimura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 ACSFRELLLEDGYNVYQSEAH-GLPLHLPGN----KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Heparin secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Delli Bovi P., Curatola A.M., Kern F.G., Greco A., Ittmann M.
Basilico C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genomic sequence of hst, a transforming gene encoding a protonomologous to fibroblast growth factors and the int-2-encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
FIBROBLAST GROWTH FACTOR-4-II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-87204251; PubMed=2953031;
Taira M., Yoshida T., Miyagawa K., Sakamoto H., Terada M.,
Sugimura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              23 192 FIBROBLAST GROWTH FACTOR-
192 AA; 21903 MW; 2B01B0BBB8824E3B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      roc. Natl. Acad. Sci. U.S.A. 84:7305-7309(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGF4 HUMBER (Rel. 08, Created)
10.40G-1988 (Rel. 08, Last sequence update)
01.40G-1988 (Rel. 08, Last amnotation update)
11.40G-1988 (Rel. 42, Last amnotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.7%; Score 163.5; DB 32.4%; Pred. No. 2e-05; tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 IQILGYKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH-----GLPLH 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 PGAAQLAHLHGILRRRQLYC----RTGFHLQILPDGSVQGTRQDHSLFGILBFISVAVGL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 VSİRGVDSGLYLGMNDKGELYGSEKLTSE-CIPREQFEENWYNTYSSNIYKHGDTGRRYF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGA-ADQSPESLLQLKALKPGV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
              -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE-96204005; PubMed=8622866; Kiefer P., Strahle U., Mason I., Dickson C.; Meder P., Strahle U., Mason I., Dickson C.; Mason I., Dickson C.; Mason I., Dickson C.; Mason I., Dickson C.; Mason I., Dickson I.; Secretion and Mitogenic activity of zebrafish FGF3 reveal intermediate properties relative to mouse and Xenopus homologues."; Oncogene 12:1503-1511(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.5%; Score 161; DB 1; Length 211; illarity 33.1%; Pred. No. 3.4e-05; Conservative 19; Mismatches 64; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 AA; 23498 MW; AB04608C16060CC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Fibroblast growth factor-3 precursor (FGF-3) (HBGF-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 LPGNKSPHRDPAPRGPAR-----FLPLPGLPPALPE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 VALNK----DGTPRDGARSKRHOKFTHFLPRPVDPERVPE 202
SUBCELLULAR LOCATION: Secreted (Potential).
                                                                                                                                                                                                                                                                                                                                                                    MIM; 605558; -...
GO; GO:0005576; C:extracellular; TAS.
GO; GO:0005525; C:soluble fraction; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR008996; Cytok_ILl_like.
InterPro; IPR003348; ILl_HBGF.
PFGM; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                    EMBL; AB044277; BAB03533.1; -. EMBL; AB030648; BAB03530.1; -. PIR; JC7353; JC7353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00247; HBGF_FGF; 1.
Growth factor.
SEQUENCE 211 AA; 23498 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                  HSSP; P31371; 1G82.
Genew; HGNC:3677; FGF20.
MIM; 605558; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGF3 OR FGF-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGF3 BRARE
P48802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
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                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 HLEIREDGTVGGAADQSPESILLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIJINE=20374469; PubMed=10913340;
Kirikoshi H., Sagara N., Saitoh T., Tanaka K., Sekihara H.,
Shiokawa K., Katoh M.;
"Molecular cloning and characterization of human FGF-20 on chromosome
                                                   -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                  GO: 00:005576; C:extracellular; TAS.
GO: 00:0005576; C:extracellular; TAS.
GO; GO:0008284; F:growth factor activity; TAS.
GO; GO:0008284; P:cell-cell signaling; TAS.
GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
GO; GO:0001165; P:signal transduction; TAS.
InterPro; IPR002996; Cytok ILL like.
InterPro; IPR002948; ILL HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 ACSFRELLLEDGYNVYQSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 -CTFKEILLPNNYNAYESYKYPGMFIALSKNGKTKKGNRVSPTMKVTHFLP 204
         (HST) AND FROM KARPOSI'S SARCOMA (KS3). IT HAS A MITOGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.7%; Score 163.5; DB 1; Length 206; 36.9%; Pred. No. 2.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000831, III HBGF; 1.
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF FGF; 1.
Procto-oncogene; Growth factor; Mitogen; Signal; 3D-structure.
SIGNAL 1 27 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Itch N.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. FIBROBLAST GROWTH FACTOR-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 AA; 22047 MW; C7FD54A0272A1569 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 274:337-343 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last amnotation update)
Fibroblast growth factor-20 (FGF-20).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Mismatches
                                                                                                                                                                                                                                                                                              EMBL; J02986; AAB59555.1; -. EMBL; M17446; AAA59473.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00262; ILLHBGF
                                                                                                                                                                                                                                                                                                                                        PIR, A28417; TVHUHS.
PDB; 11JT; 15-AUG-01.
Genew; HGNC:3682; FGF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8p21.3-p22
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Matches

d à

SO DE RESERVA MARIA DE LA RESERVA DE LA RESE

FGFK HUMAN

RESULT 19

9

Gaps

24;

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between the Swiss Institute of Bioinformatics and the EMBL outstation-
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQ-SPESILQLKALKPGVIQILGVKTS 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=2226935; PubMed=12364586;
MEDLINE=2226935; PubMed=12364586;
Mederrahim H., Bougueleret L., Barry C., Tanaka H., La Rosa P.,
Abderrahim H., Bougueleret L., Barry C., Tanaka H., La Rosa P.,
Puech A., Tahri N., Cohen-Akenine A., Delabroses S., Lissarrague S.,
Picard R.-P., Maurice K., Essioux L., Millasseau P., Grel P.,
Debailleul V., Simon A., Caterina D., Dufaure I., Malekzadeh K.,
Belova M., Luan J.-J., Bouillot M., Sambucy J.-L., Primas G.,
Saumier M., Boubkiri N., Martin-Saumier S., Nasroune M., Peixoto H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smallwood P.M., Munoz-Sanjuan I., Tong P., Macke J.P., Hendry S.H., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J., "Fibroblast growth factor (FGF) homologous factors: new members of the FGF family implicated in nervous system development."; Proc. Natl. Acad. Sci. U.S.A. 93:9850-9857(1996).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Fibroblast growth factor-14 (FGF-14) (Fibroblast growth factor homologous factor 4) (FHF-4).
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 28.1%; Pred. No. 4.5e-05;
Matches 47; Conservative 22; Mismatches 47; Indels 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 GPARFLPLPGLPPALPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL. FIBROBLAST GROWTH FACTOR-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 RYLAMNEKGRLYASEVFNRE-CEFLERIHELGYNTYASRHHA----
                                                                                                                                                                                                                                                                                                                                                                                      CEBAIC72A170BBDC CRC64;
                                                                                                                                                                                                                                                                                                                 PROSITE, PS00247; HBGF FGF; 1.
Growth factor; Mitogen; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 AA
                                                                                                                                 EMBL, Z48714, CAA88596.1; -.
PIR, JC4627, JC4627.
HSSP, P09038, LBFG.
ZFIN, ZDB-GENE-980526-178, Fgf3.
InterPro, IPR008996; Cytok ILI_like.
InterPro, IPR002348; ILI_HBGF.
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                                                                                                                                                                                                                                                                                 ProDom; PD000831; IL1 HBGF; 1.
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                          28923 MW;
                                                                                                                                                                                                                                          Pfam; PF00167; FGF; 1.
PRINTS; PR00262; IL1HBGF.
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                                                                                                                                                                                                                                                                                                                                                                         256
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                                                                                                                                                                                                                                                                                                                                                                         19 2
256 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGF14 OR FHF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGFE HUMAN
ID FGFE HUMAN
AC Q92915;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 NVYQS------EAHGLPIH-----LPGNKSPHRDPAPRGPARFLPLPGLPPALPEPP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 GACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQ-----QTEAHLEIREDGTVGGAA 73
Delaye A., Pinchot V., Bastucci M., Guillou S., Chevillon M., Sainz-Fueres R., Meguenni S., Aurich-Costa J., Chevillo., Gimalac A., Van Duijn C., Gauvreau D., Ouelette G., Fortier I., Realson J., Sherbatich T., Riazanskay N., Rogew E., Raeymaekers P., Aerssens J., Konings F., Luyten W., Macciardi F., Sham P.C., Straub R.E., Weinberger D.R., Cohen N., Cohen D.; Heinberger D.R., Cohen N., Cohen D.; The gene for D-amino acid oxidase in schizophrenia."; Proc. Natl. Acad. Sci. U.S.A. 99:13675-13680(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 VIYSSMLYRQQESGRAWFLGLNKEGQAMKGNRVKKTKPA----AHFLPKP-LEVAMYREP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 GLCNGNLVDIFSKVRIFG--LKKRRLRRQDPQLKGIVTRLYCRQGYYLQMHPDGALDGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 DOSPES-LLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPBACSFRELLLEDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 DDSTNSTLFNLIPVGERVVALQGVKTGLYIAMNGBGYLYPSBLFTPE-CKFKESVFENYY
                                                                                                                                                                                                                                -i- TISSUE SPECIFICITY: Nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1993 (Rel. 26, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
FGF-9) (HBGF-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 14.3%; Score 159; DB 1; Length 24 Local Similarity 29.8%; Pred. No. 5.6e-05; as 62; Conservative 27; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 AA; 27702 MW; 427C3373198B967E CRC64;
                                                                                                                                                                                                           -i- SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0008083; F:growth factor activity; TV GO; GO:0007267; P:cell-cell signaling; TAS. GO; GO:0007399; P:neurogenesis; TAS. GO; GO:0007165; P:signal transduction; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 GILAPOPPDVGSSDPLSMVGPSQGRSPS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 SL----HDVGETVPKPGVTPSKSTSAS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR008996; Cytok_IL1_like.
Interpro; IPR002348; IL1_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00247; HBGF_FGF; 1. Growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE014303; AAN16025.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U66200; AAB18916.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:3671; FGF14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P31371; 1G82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGF9_HUMAN
P31371;
                                                                                                                                                                                                 function
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Kurokawa T.;

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63 IREDGTVGGA-ADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEAC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- 
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R InterPro; IPR008996; Cytok ILL like.

R pfam; PF00167; FGF; 1.

R PRINTS; PR00262; ILL HBGF.

R PRODOM; PD000831; ILL HBGF; 1.

R PROSTE; PG00247; HBGF; 1.

R PROSTE; PG00247; HBGF; 1.

R PROSTE; PG00247; HBGF; 1.

R Growth factor; Differentiation; Mitogen; Heparin-binding; Glycoprotein; 3D-structure.

T CHAIN 4 208 GLIA-ACTIVATING FACTOR.

T CHAIN 79 79 N-LINNED (GLCNAC. . .).

T CONFLICT 24 26 VLP -> SLL (IN REF. 2).

T CONFLICT 34 34 S -> A (IN REF. 2).

T TURN 62 62

STRAND 63 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.1%; Score 157; DB 1; Length 208; 31.2%; Pred. No. 6:5e-05; Live 20; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23440 MW; F32A0E7106EF59C9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 PVDPDKVPE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 AA;
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                                                                                                                                                                                                                                                                                                      122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.60 ANGSTROMS).

MEDLINE=21127675; PubMed=11223514;

MEDLINE=21127675; PubMed=11223514;

MECH H.J., Adar R., Hofmann B., Bogin O., Weich H., Yayon A.;

Heacht H.J., Adar R., Hofmann B., Bogin O., Weich H., Yayon A.;

Structure of fibroblast growth factor 9 shows a symmetric dimer with unique receptor and heparin-binding interfaces.";

Acta Crystallogr. D 7:378-384 (2001).

Act Crystallogr. D 7:378-384 (2001).

I. FUNCTION: May have a role in glial cell growth and differentiation during development, gliosis during repair and regeneration of brain tissue after damage, differentiation and survival of neuronal cells, and growth stimulation of glial tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FTM: N-glycosylated.
-!- DISEASE: The continuous overexpression of GAFS may lead to malignant cell growth caused by an autocrine loop.
--- SIMILARITY: Belongs to the heparin-binding growth factors family.
-!- SIMILARITY: Belongs to the heparin-binding growth factors family.
-!- DATABASE: NAME-RED Systems' cytokine source book: FGF9;
WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=199".
                                                                                                                                                                                                                                                                                                      "Molecular cloning of a novel cytokine cDNA encoding the ninth member of the fibroblast growth factor family, which has a unique secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Secreted.

TISSUE SPECIFICITY: Glial cells.

PIN: Three molecular species were found (30 kDa, 29 kDa and 25 kDa), cleaved at Leu-4, Val-13 and Ser-34 respectively. The smaller ones might be products of proteolytic digestion.

Furthermore, there may be a functional signal sequence in the 30 kDa species which is uncleavable in the secretion step.
                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Novel secretory heparin-binding factors from human glioma cells (glia-activating factors) involved in glial cell growth.

Purification and biological properties.";
J. Biol. Chem. 268:2857-2864(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IISSUB=Glial tumor;
MEDLINE=93155105; PubMed=8428960;
Naruo K.-I., Seko C., Kuroshima K.-I., Matsutani E., Sagada R.,
Kondo T., Kurokawa T.;
                                                                                                                                                                                                                                                    Miyamoto M., Naruo K.-I., Seko C., Matsumoto S., Kondo T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 600921; -. Gextracellular space; TAS. GO:0008615; C:extracellular space; TAS. GO:0008083; F:growth factor activity; TAS. GO:0007267; P:cell-cell signalling; TAS. GO:0007165; P:signal transduction; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Cell. Biol. 13:4251-4259(1993).
                                                                                                                                                                                                           IISSUE=Foreskin;
MEDLINE=93309459; PubMed=8321227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D14838; BAA03572.1; -.
EMBL; AL139378; CAC17692.1; -.
PIR; A48137; A48137.
PDB; 1G82; 07-MAR-01.
PDB; LIHK; 02-MAY-01.
Genew; HGNC:3687; FGF9.
MIM; 600921; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 4-26 AND 34-54.
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                 NCBI_TaxID=9606;
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8

38; Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 IFPNGTIQGTRKDHSRFGILEFISIAVGLVSIRGVDSGLYLGMNEKGELYGSEKLTQE-C 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 SFRELLLEDGYNVYQSEAH----GLPLHLPGNKSPHRDPAPRGPAR-----FLPL 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75
                                                                                                                                                                                                       PLOYELY, 'Sol. 13:4251-4259(1993).

-1 FUNCTION: May have a role in glial cell growth and differentiation during development alloss during repair and regeneration of brain tissue after damage, differentiation and survival of neuronal cells, and growth stimulation of glial tumors.

-1 SUBSCELULIAR LOCATION: Secreted.

-1 TISSUE SPECIFICITY: Brain and kidney.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 SPHLGOSEAG-----GLPRG-----PAVTDLDHLKGILRRRQLYC----RTGFHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                   "Molecular cloning of a novel cytokine cDNA encoding the ninth member of the fibroblast growth factor family, which has a unique secretion
                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
01-NOV-1997 (Rel. 35, Last annotation update)
Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
(FGF-9) (HBGF-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 3 BY SIMILARITY.
4 208 GLIA-ACTIVATING FACTOR.
79 79 N-LINKED (GLCNAC. . .) (POTENTIAL)
208 AA; 23413 MW; 4A3CE894DFF643EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
14.1%; Score 157; DB 1; Length 208;
Best Local Similarity 31.2%; Pred. No. 6.5e-05;
Matches 59; Conservative 20; Mismatches 72; Indels
                                                                                                                                            Miyamoto M., Naruo K.-I., Seko C., Matsumoto S., Kondo T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00262; IL1HBGF.
PRODOM; PD000831; IL1 HBGF; 1.
SMART; SM00442; FGF; I.
PROSITE; PS00247; HBGF FGF; 1.
Growth factor; Differentiation; Mitogen; Heparin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P31371; 1G82.
InterPro; IPR008996; Cytok_IL1_like.
InterPro; IPR002348; IL1_HBGF.
                                                                                                                                     MEDLINE=93309459; PubMed=8321227;
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D14839; BAA03573.1; -.
                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 PGLPPALPE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : | |
PVDPDKVPE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00167; FGF; 1.
                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein.
                                         FGF9 OR FGF-9
                                                                                                                            rissue=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P31371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191
                                                                                                                                                               Kurokawa T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDIATE=96192599; PubMed=8619928;
MEDIATE=96192599; PubMed=8619928;
MEDIATE=96192599; PubMed=8619928;
"Identification of fibroblast growth factor 9 (FGF9) as a high
affinity, heparin dependent ligand for FGF receptors 3 and 2 but not
for FGF receptors 1 and 4";
Growth Factors 12:223-233(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Retinoic acid induces gene expression of fibroblast growth factor-9 during induction of meuronal differentiation of meuse embryonal
                                              01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
(FGF-9) (HBGF-9)
                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                   Santos-Ocampo S., Colvin J.S., Chellaiah A.T., Ornitz D.M.; Santos-Ocampo S., Colvin J.S., Chellaiah A.T., Ornitz D.W.; Expression and biological activity of mouse fibroblast growth
208 AA
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InterPro; IPR008996; Cytok III_like.
InterPro; IPR002348; III_HBGF.
Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; S82023; AAB36429.1; --
EMBL; AF144626; AAD49222.1; --
EMBL; AF144624; AAD49222.1; JOINED.
EMBL; AF144625; AAD49222.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 271:1726-1731(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95385801; PubMed=7656983;
Seo M., Noguchi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96139512; PubMed=8576175;
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ProDom; PD000831; ILI_HBGF; 1.
SMART; SM00442; FGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EBS Lett. 370:231-235(1995)
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carcinoma P19 cells."
                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1G82.
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                                                                                                                                                                                                   FGF9 OR FGF-9.
     FGF9 MOUSE
P54130;
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48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       FGF1 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             P10935;
  Matches
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                                                                                                                                                                                                                                                                                                            23 LGACQAHPIPDS---SPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGA-ADQSPE 78
                                                                                                                                                                                                                                                                                                                                                                  92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90200291; PubMed=1693366; Mansson P.E., Zhou H., Harris S.E.; Hall U.A., Harris M.A., Malark M., Mansson P.E., Zhou H., Harris S.E.; Hall U.A., Harris M.A., Malark M., Mansson P.E., Zhou H., Harris S.E.; Hall U.A., Harris M.A., Malark M., Mansson P.E., Zhou H., Harris S.E.; J. Cell. Biochem. 43:17-26(1990).

-1. FUNCTION: The heparin-binding growth factors are angiogenic agents in vivo and are potent mitogens for a variety of cell types in vitro. There are differences in the tissue distribution and concentration of these 2 growth factors.
                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast growth factor) (AFGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: Monomer.
-!- MISCELLANBOUS: This protein binds heparin, although less strongly than does bFGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1. SIMILARITY: Belongs to the heparin-binding growth factors family. PIR; A60721; A60721.
HSSP: P05200; IRML.
HISSP: P05200; IRML.
InterPro; IPR002348; IL1_HBGF.
PRINTS; PR00252; IL1HBGF.
PRINTS; PR00262; IL1HBGF.
PRODOM; PR000831; IL1_HBGF; 1.
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 AH----GLPLHLPGNKSPHRDPAPRGPAR------FLPLPGLPPALPE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27;
                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 155.5; DB 1; Length 155; Pred. No. 6.1e-05;
                                                                                                                                                                                                         Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEPARIN-BINDING GROWTH FACTOR
             PROSITE; PS00247; HBGF_FGF; 1.
Growth factor; Differentiation; Mitogen; Heparin-binding;
                                                                                                                                                                                                                                                              Indels
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41E5EC760E412CC5 CRC64;
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PROSITE; PS00247; HBGF_FGF; 1.
Growth factor; Mitogen; Angiogenesis; Heparin-binding.
                                                                                BY SIMILARITY.
GLIA-ACTIVATING FACTOR.
N-LINKED (GLCNAC. . .) (PC.
; B&DEIEEDFB70979E CRC64;
                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                 69;
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                                                                                                                                                                                                         14.1%; Score 156.5; DB 1
ilarity 32.0%; Pred. No. 7.1e-05;
Conservative 21; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 AA.
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                                                                                                                                                              208 AA; 23440 MW;
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116
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208
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                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                Glycoprotein
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CARBOHYD
SEQUENCE
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FGF1_MESAU
                                                                                     PROPEP
                                                                                                                                                                                                                                                                    Matches
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14.0%; 35.0%;

Query Match Best Local Similarity

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                                                                                                                  100 RFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPR 159
                                                                                                                                                          78 OYLAMDIDGLLYGS-QIPNEECLFLERLEENHYNIYISKKHAEKNWFVGLKK--NGSCKR 134
                                   41 GGQVRQRYLYTDDAQQTBAHLEIREDGTVGGAADQSPESL-LQLKALKPGVIQILGVKTS 99
                                                                            17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of the 1B promoter of fibroblast growth factor 1 and its expression in the adult and developing mouse brain.";
J. Biol. Chem. 271:30263-30271(1996)
-!- FUNCTION: The heparin-binding growth factors are angiogenic agents in vivo and are potent mitogens for a variety of cell types in vitro. There are differences in the tissue distribution and concentration of these 2 growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90201563; PubMed=2318343;
Hebert J.M., Basilico C., Goldfarb M., Haub O., Martin G.R.;
Hsolation of cDNAs encoding four mouse FGF family members and
"Isolation of cDNAs encoding four mouse FGF family members and
electrication of their expression patterns during embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                !- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                              21 GNYKKPKLLYCSNGGH---FLRILPDGTVDGTRDRSDQHIQLQLSAESAGEVYIKGTETG
                                                                                                                                                                                                                                                                                                                                                                                        01-07U-1989 (Rel. 11, Created)
01-07U-1989 (Rel. 11, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast growth factor) (AGF).
FGF1 OR FGF-1
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ractus "Activestrue" (Nordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metazoa; Chordata; Criurognathi; Muridae; Murinae; Mus
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89240051; PubMed=2470029;
Goodrich S., Yan G.C., Bahrenburg K., Mansson P.E.;
"The nucleotide sequence of rat heparin binding growth factor 1
  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97094746; PubMed=8939980;
Alam K.Y., Frostholm A., Hackshaw K.V., Evans J.E., Rotter A.,
Chiu I.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIAINE-97128312; PubMed-8972905;
Madiai F., Hackshaw K.V., Chiu I.M.;
"Cloning and characterization of the mouse Fgf-1 gene.";
    62; Indels
                                                                                                                                                                                                                                                                                                                                                    155 AA
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mucleic Acids Res. 17:2867-2867(1989).
                                                                                                                                                                                                                                                                                                                                                    PRT;
      12;
                                                                                                                                                                                                         160 GPAR------FLPLP 168
                                                                                                                                                                                                                                               135 GPRTHYGOKAILFLPLP 151
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    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse), and
                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090, 10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 179:231-236(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Monomer.
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Mus musculus (Mouse)
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202 AA;
                                                                                                             DEVELOPING LIMB.
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       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDILE=90201563; PubMed=2318343;
Hebert J.M., Basilico C., Goldfarb M., Haub O., Martin G.R.;
Hisolation of coNAs encoding four mouse FGF family members and characterization of their expression patterns during embryogenesis.";
Dev. Biol. 138:454-463(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Gaps
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01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
28-FEB-2003 (Rel. 11, Last annotation update)
Fibroblast growth factor-4 precursor (FGF-4) (K-fibroblast growth factor-1 precursor (FGF-4) (K-fibroblast growth factor-1 precursor (FGF-4) (K-fibroblast growth factor-1 precursor (FGF-4) (K-fibroblast growth factor-1 precursor (FGF-4) (K-fibroblast growth factor-1 precursor (FGF-4) (K-fibroblast growth factor-1 precursor (FGF-4) (K-fibroblast growth factor-1 precursor (FGF-4) (K-fibroblast growth factor-1 precursor (FGF-4) (K-fibroblast growth factor-1 precursor (FGF-4) (K-fibroblast growth factor-1 precursor (FGF-4) (K-fibroblast growth factor-1 precursor (FGF-4) (K-fibroblast growth factor-1 precursor (FGF-4) (K-fibroblast growth factor-1 precursor (FGF-4) (K-fibroblast growth factor-1 precursor (FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast growth FGF-4) (K-fibroblast gr
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 155;
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34.3%; Pred. No. 7.2e-05;
tive 13; Mismatches 64; Indels
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HEPARIN (POTENTIAL).
, 8880E4FF0FBA4161 CRC64;
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SWART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; 1.
Growth factor; Mitogen; Anglogenesis; Heparin-binding
                                                                                                                                                                        EMBL; X14232; CAA32448.1; ---
EMBL; M30641; AAA37618.1; ---
EMBL; M30645; AAC52969.1; ---
EMBL; U36459; AAC52969.1; ---
EMBL; U36458; AAC52969.1; JOINED.
EMBL; U36458; AAC52907.1; ---
FIR; D37360; D37360.
PIR; S04147; S04147.
HSSP; P05230; IRML.
MGD; MG195515; F9f1.
InterPro; IPR008996; Cytok ILI_like.
InterPro; IPR008998; ILI_HBGF.
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PRINTS; PR00262; ILIHBGF.
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28
116
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155 AA;
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Best Local S:
Matches 48
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FUNCTION: IS ESSENTIAL FOR SURVIVAL OF THE POSTIMPLANTATION MOUSE EMBRYO AND AT LATER EMBRYONIC STAGES, IS AN ESSENTIAL COMPONENT OF SIGNALING NETWORK REQUIRED FOR GROWTH AND PATTERNING OF THE
                                                                                                                                                                                                                                   TISSUE SPECIFICITY: EXPRESSED IN THE BLASTOCYST INNER CELL MASS AND LATER IN DISTINCT EMBRYONIC TISSUES. SIMILARITY: Belongs to the heparin-binding growth factors family.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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10-CCT-2003 (Rel. 42, Last sequence update)
Fibroblast growth factor-14 (FGF-14) (Fibroblast growth factor-homologous factor 4) (FHF-4).
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MGD; MGI:95518; Fgf4.

GO; GO:0042475; P:odontogenesis (sensu Vertebrata); IDA.
InterPro; IPR008996; Cytok IL1_like.
InterPro; IRR00348; IL1_HBGF.

Pfam; PF00167; FGF; 1.
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FIBROBLAST GROWTH FACTOR-4.
A -> S (IN REF. 2).
; 62D456231047CA31 CRC64;
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ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF FGF; 1.
PROSITE; PS00247; HBGF FGF; 1.
Proto-oncogene; Growth factor; Mitogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 13.8%; Score 153.5; DB 1 Local Similarity 34.2%; Pred. No. 0.00011; les 38; Conservative 21; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X14849; CAA32967.1; -. EMBL; M30642; AAA37619.1; -. PIR; S04741; TVMSHS. HSSP; P09038; 1BFG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 B-CKFKESUFENYYUYSSMLYRQDESGRAWFLGLNKEGQVMKGNRVKKTKPA---AHF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 BACSFRELLLEDGYNVYQS-----EAHGLPLH-----LPGNKSPHRDPAPRGPARF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 HLEIREDGTVGGAADQSPES-LLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 YLQMHPDGALDGIKDDSINSTLFNLIPVGLRVVAIQGVKTGLYIAMNGEGYLYPSELFTP
                                                                                                                                                                                                         Isoda=P70379-1; Sequence=Displayed;
Name=2; Synonyms=FGF-14C;
Isola=P70379-2; Sequence=VSP 001530;
Isola=P70379-2; Sequence=VSP 001530;
--- TISSUE SPECIFICITY: Brain and testis; widely distributed in the developing nervous system. In adult, high levels in the granular layer of the cerebellum, less in hippocampus and olfactory bulb.
--- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26; Gaps
        Yamamoto S., Mikami T., Konishi M., Itoh N.,
"Stage-specific expression of a novel isoform of mouse FGF-14 (FRF-4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                    Biochim, Biophys. Acta 1490:121-124(2000).
-!- FUNCTION: Probably involved in nervous system development and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1989 (Rel. 12, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Fibroblast growth factor-5 precursor (FGF-5) (HBGF-5) (Smag-82)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.7%; Score 153; DB 1; Length 247; 32.7%; Pred. No. 0.00015; tive 21; Mismatches 62; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 LPKP-LEVAMYREPSL----HDVGETVPKAGVTPSKSTSAS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 247 AA; 27764 MW; 372C6FC0BDC72FDA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 LPLPGLPPALPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPS
                                                                                                                              -!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, P31371, 1682.
MGD, MGI:109189, F9f14.
InterPro; IPR008996; Cytok_IL1_like.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE, PS00247; HBGF FGF; 1.
Growth factor; Alternative splicing.
MEDLINE=20246297; PubMed=10786625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB029498; BAA89483.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 53; Conserv
                                                     in spermatocytes."
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11D FGF85 H
AC P12053
DT 10-OCT
DT 10-OCT
DE FIDEOB
GN FGF5.
OC BURNALY
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OX NCBI_T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Short; Synonyms=FGF-5S; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2
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Imamura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translates into a partial agonist/antagonist for FGF-5 neurotrophic
                                                                                            Haub O., Drucker B., Goldfarb M.;
"Expression of the murine fibroblast growth factor 5 gene in the adult central nervous system.";
Proc. Natl. Acad. Sci. U.S.A. 87:8022-8026(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "An alternatively-spliced FGF-5 mRNA is abundant in brain and
                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM LONG).
SEQUENCE FROM N.A. (ISOFORM LONG).
Zhoun X., Bates B., Hu X., Goldfarb M.;
Zhan X., Bates B., Hu X., Goldfarb M.;
"The human FGF-5 oncogene encodes a novel protein related to fibroblast growth factors.";
Mol. Cell. Biol. 8:3487-3495(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005615; P:cell proliferation; TAS.
GO; GO:0007267; P:cell cell signaling; TAS.
GO; GO:0008543; P:FGF receptor signaling pathway; TAS.
GO; GO:0007369; P:
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EMBL; M23536; AAB60699.1; -.
EMBL; M23534; AAB60699.1; JOINED.
EMBL; M23535; AAB60699.1; JOINED.
EMBL; M23534; AAB60699.1; ALT.SEQ.
EMBL; AB016517; BAA33738.1; -.
EMBL; AF171928; AAF89742.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM SHORT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM SHORT)
[1]
STOTE FROM N.A. (ISOFORM LONG).
TISSUE-Brain stem;
MEDLINE-91045929; PubMed=1700424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00262; ILLHBGF.
ProDom; PD000831; ILL_HBGF; 1.
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Genew; HGNC:3683; F
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                                                                                                                                                                                                                                                                                                                                                                           81 IQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPFACSFRELLLEDGYNVYQSEAH 140
                                                                                                                                                                                                                                                                                                                                                                                                141 ----GLPLHLPGNKSPHRDPAPRG-----PARFLP-----LPGLPPALPEPPG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 RIEKTGREWYVALNK---RGKAKRGCSPRVKPQHISTHFLPRFKQSEQPELSFTVTVPEK 236
                                                                                                                                                                                                                                                                                                              34 SSPLLQFGGQ----VRQRYLYTDDAQQTEA-----HLEIREDGTVGGAADQSPESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- TISSUE SPECIFICITY: Brain, eye and heart; in embryonic brain, present in all divisions of the central and peripheral nervous system and it is at least 5 times more abundant than other FHFB.
                                                                                                                                                                                                                                                                                    Gaps
SWART; SW00442; FGF; 1.
PROSITE; PS00247; HBGF FGF; 1.
Proto-oncogene; Growth factor; Mitogen; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smallwood P.M., Munoz-Sanjuan I., Tong P., Macke J.P., Hendry S.H., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.; Frendry S.H., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.; Frebelar growth factor (FGF) homologous factors: new members of the FGF family implicated in nervous system development."; Proc. Natl. Acad. Sci. U.S.A. 93:9850-9857(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goldfarb M.;
"Murine FGF-12 and FGF-13: expression in embryonic nervous system,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mech. Dev. 64:31-39(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGFD MOUSE STANDARD; PRT; 245 AA.
P70377; 035338;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1999 (Rel. 35, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Fibroblast growth factor-13 (FGF-13) (Fibroblast growth factor homologous factor 2) (FHF-2).
                                                                           POLY-SER.
POLY-SER.
N-LINKED (GLCNAC. . .) (POTENTIAN VLEI -> QVHR (in isoform Short).
/FTId=VSP 001519.
Missing (in isoform Short).
/FTIG=VSP 001519.
R -> I (IN REF. 1).
PSGR -> LGA (IN REF. 2).
                                                                                                                                                                                                                                                   13.7%; Score 153; DB 1; Length 268; 28.1%; Pred. No. 0.00017; Live 27; Mismatches 74; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hartung H., Feldman B., Lovec H., Coulier F., Birnbaum D.,
                                                              FIBROBLAST GROWTH FACTOR-5
                                                                                                                                                                                                                         08F4268B26781E9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-Eye;
MEDLINE-96382556; PubMed-8790420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=97376484; PubMed=9232594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  connective tissue and heart.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | : | | | | 237 KNPPSP--IKSKIPLS 250
                                                                                                                                                                                                                             29526 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 ILAPOPPDVGSSDPLS 195
                                                                                                                                                                                                                                                                          Similarity 28.19
55; Conservative
                                                                                                                                                              268
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52
62
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83
268 AA;
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49
55
110
120
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                                                                                                                                                                                             CONFLICT
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Best Local
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-: FUNCTION: Induces heparcocallular proliferation. Has no biological effect on the heart (By similarity).

-: SUBCELIULAR LOCATION: Secreted (By similarity).

-: SUBCELIULAR Elongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 ACQAHPIPDSSPLLQFGGQVRQRY-----LYTDDAQQTEAHLEIREDGTVGGAADQ-
In adult, most abundant in hippocampus. SIMILARITY: Belongs to the heparin-binding growth factors family.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 13.7%; Score 152.5; DB 1; Length 245; 1 Similarity 29.6%; Pred. No. 0.00017; 53; Conservative 25; Mismatches 72; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 MISSING (IN REF. 2).
199 L -> Q (IN REF. 2).
27617 MW, 5B96D41C190975DD CRC64;
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15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-16 (FGF-16).
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MGD; MGI:109178; FGF1.
InterPro; IPR008996; Cytok III_like.
InterPro; IPR008988; III_HBGF.
Pfam; PF00167; FGF; 1.
ProDom; P000801; III_HBGF.
ProDom; P000801; III_HBGF; 1.
SMART; SM00442; FGF; 1.
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MEDLINE=98139883; PubMed=9473496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.5%; Score 150.5; DB 1; Length 207; 32.6%; Pred. No. 0.00019; ative 20; Mismatches 75; Indels 31; Gaps
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15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Fibroblast growth factor-10 precursor (FGF-10) (Keratinocyte growth
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"Structure and expression of human fibroblast growth factor-10.";
J. Biol. Chem. 272:23191-23194(1997).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Katsumata T., Negoro T., Nakatsuka M., Birnbaum D., Coulier F.,
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SEQUENCE 207 Aa; 23759 MW; D8AD160BDABDB5F8 CRC64;
                                                                                                                                                                                                                                                             Oct. 0.001615; C:extracellular space; TAS.

GO; GO:0008615; F:growth factor activity; TAS.

GO; GO:0007267; P:cell-cell signaling; TAS.

GO; GO:0007397; P:istcgenesis and organogenesis; TAS.

GO; GO:0008152; P:istcgenesis and organogenesis; TAS.

GO; GO:000266; P:response to temperature; TAS.

GO; GO:0007165; P:signal transduction; TAS.

InterPro; IPR008996; Cytok III_like.

InterPro; IPR002348; III_HBGF.
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MEDLINE=97435285; PubMed=9287324;
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ProDom; PD000831; IL1 HBGF; 1.
SMART; SM00442; FGF; 1.
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                                                                                                                                                     EMBL; AB009391; BAA24956.1; -
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                                                                                                                                                                                                                         Genew; HGNC:3672; FGF16.
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                                                                                                                                                                           PIR; JC5941; JC5941.
HSSP; P31371; JG82.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.5%; Score 150; DB 1; Length 208;
30.4%; Pred. No. 0.00021;
tive 31; Mismatches 49; Indels 14; Gaps
                                                                                                                                                                                                                                                 -!- SIMCIARAL LOCATION: Secreted (Potential).
-!- SIMCIBLIUMAR LOCATION: Secreted (Potential).
-!- SIMILARITY: Belongs to the heparin-binding growth factors family.
Huddleston K.A., Teliska M., Alfonso P., Florence C., Blunt A., Huddleston K.A., Teliska M., Alfonso P., Coleman T.A., Ornitz D.M., Dilon P.A., Duan R.D.;
"Cutaneous wound healing by keratinocyte growth factor 2.";
Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
-!-FUNCTION: COULD BE A GROWTH FACTOR ACTIVE IN THE PROCESS OF WON
HEALING. ACTS AS A MITGGEN IN THE LUNG. MAY ACT IN A MANNER
SIMILAR TO FGF-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-SEK.
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB002097; BAA22331.1; -.
EMBL; U67918; AAB61991.1; -.
PDB; IMNN; 04-MAR-03.
Genew; HGNC.366; FGF10.
MIM; 602115; -.
GO; GO:0005645; C:extracellular space; TAS.
GO; GO:0000094; P:growth factor activity; TAS.
GO; GO:0000074; P:regularion of cell cycle; TAS.
InterPro; IRR002348; ILI_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIBROBLAST GROWTH FACTOR-10.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 208 POLY-SER.
52 62 N-LINKED (GLCNAC. ..) POT 156 196 N-LINKED (GLCNAC. ..) (POT 156 196 N-LINKED (GLCNAC. ..) (POT 150 196 196 N-LINKED (GLCNAC. ..) (POT 1508 AA; 23436 MW; COA0705C108680B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00167; FGF; 1.
PRINTS; PR00262; IL1HBGF.
ProDom; PD000831; IL1 HBGF; 1.
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF FGF; 1.
SGROWTH factor; Glycoprotein; Signal; 3D-structure.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-10 precursor (FGF-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 PAPR---GPARFLPL 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
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                                                                                                                                     MOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-10 precursor (FGF-10) (Keratinocyte growth
                                                                                    Yamasaki M., Miyake A., Tagashira S., Itoh N.;
"Structure and expression of the rat mRNA encoding a novel member of
the fibroblast growth factor family.";
J. Biol. Chem. 271:15918-15921(1996).
-!- FUNCTION: COLLD BE A GROWTH FACTOR ACTIVE IN THE PROCESS OF WOUNI
HEALING. ACTS AS A MITOGEN IN THE LUNG. MAY ACT IN A MANNER
SIMILAR TO FGF-7.
         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                    -i- SUBCELLULAR LOCATION: Secreted (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.5%; Score 150; DB 1; Length 21: 30.4%; Pred. No. 0.00022; tive 31; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
FIBROBLAST GROWTH FACTOR-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (P. 93778EFA6FC0866A CRC64;
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                                                                                                                                                                                                                                                                                                                                                InterPro; IPR008996; Cytok ILI_like.
InterPro; IPR002348; ILI_HBGF.
Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0262; ILIHBGF.
PRODOM; PRO00831; ILI HBGF; 1.
SWART; SMO0442; PGF; 1.
PROSITE; PS00247; HBGF FGF; 1.
Growth factor; Glycoprotein; Signal.
                                                                               MEDLINE=96279129; PubMed=8663172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 1
24029 MW;
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                                                                                                                                                                                                                                                                                                                            EMBL; D79215; BAA11468.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41; Conservative
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215
69
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
50
203
215 AA;
                                                            SEQUENCE FROM N.A.
                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                          HSSP; P31371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGFA MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor 2).
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                                                                                                                                                                                                                                                                                                                                13.3%; Score 148; DB 1; Length 209;
30.4%; Pred. No. 0.0003;
tive 30; Mismatches 50; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBSCELLULAR LOCATION: Secreted (Potential).
-!- TISSUE SPECIFICITY: Expressed abundantly in embryos and the lung, and at much lower levels in brain and heart.
-!- SIMILARITY: Belongs to the heparin-binding growth factors family.
               Tagashira S., Harada H., Katsumata T., Itoh N., Nakatsuka M.; "Cloning of mouse FGF10 and up-regulation of its gene expression during wound healing."; Gene 197:399-404(1997).
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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MGD; MGI:1099809; Fgf10.
GO; GO:0001989; P:induction of an organ; IMP.
GO; GO:0009887; P:organogenesis; IMP.
InterPro; IPRO08996; Cytok IL1_like.
InterPro; IRR002348; IL1_HBGF.
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Growth factor; Glycoprotein; Signal
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MEDLINE=97473538; PubMed=9332392;
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P05230; P07502;
13-AUG-1987 (Rel. 05, Created)
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ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
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197 1
209 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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STRUCTURE BY NMR OF 24-155.
MEDLINE=22388257; PubMed=12477932; Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Straubberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Estapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., Morkan D.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
  13-AUG-1987 (Rel. 05, Last sequence update)
10-CCT-2003 (Rel. 42, Last amnotation update)
Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast
growth factor) (AFGF) (Beta-endothelial cell growth factor) (ECGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang W.P., Lehtoma K., Varban M.L., Krishnan I., Chiu I.M., Cloning of the gene coding for human class 1 heparin-binding growth factor and its expression in fetal tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain stem;
MEDLINE=90265618; PubMed=1693186;
MEDLINE=90265618; PubMed=1693186;
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"Alternative splicing generates two forms of mRNA coding for human heparin-binding growth factor 1.";
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"An acidic fibroblast growth factor protein generated by alternate
                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIJINE=22019819; PubMed=1717925; Wang W.P., Quick D., Balcerzak S.P., Needleman S.W., Chiu I.M.; Wang W.P., Quick D., Balcerzak S.P., Needleman S.W., Chiu I.M.; "Cloning and sequence analysis of the human acidic fibroblast gracefort gene and its preservation in leukemia patients."; Oncogene 6:1521-1529(1991).
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Li Y.L., Kha H., Golden J.A., Migchielsen A.A.J., Goetzl E.J.,
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                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=86261805; PubMed=3523756;
                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain stem;
MEDLINE=89343957; PubMed=2474753;
                                                                                                                                    Homo sapiens (Human).
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                                                                                                                                                                                              NCBI_TaxID=9606;
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SEQUENCE OF 16-49.

MEDLINE=86275260; PubMed=3732516;
Gautefoll P., Farter-Schroeder M., Boehlen P.;
Gautefoll P., Farter-Schroeder M., Boehlen P.;
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FEBS Lett. 204:203-207(1986).
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"K-ray crystal structure of human acidic fibroblast growth factor.";
Biochemistry 35:2086-2094(1996).
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Harper J.W., Strydom D.J., Lobb R.R.;
"Human class 1 heparin-binding growth factor: structure and homology
to bovine acidic brain fibroblast growth factor.";
Biochemistry 25:4097-4103 (1986).
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MEDLINE=94069734; PubMed=7504343;
Zhao X.M., Yeoh T.K., Hiebert M., Frist W.H., Miller G.G.;
Thao X.M., Yooh T.K., Hiebert M., Frist Well (heparin-binding growth factor (heparin-binding growth factor-1) and cytokine genes in human cardiac allografts and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEDLINE=86186784; PubMed=3964259; MEDLINE=86186784; PubMed=3964259; MEDLINE=86186706; Conn G., Hatcher V.B., Thomas K.A.; dimenez-Gallego G., Conn G., Hatcher V.B., Thomas prowth factors: "Human brain-derived acidic and basic fibroblast growth factors: amino terminal sequences and specific mitogenic activities."; Biochem. Biophys. Res. Commun. 135:541-548(1986).
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MEDLINE-94358885; PubMed-7521397;
Pineda-Lucena A., Jimenez M.A., Nieto J.L., Santoro J., Rico M.,
Gimenez-Gallego G.;
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MEDLINE=86295741; PubMed=3527167;
Gimenaz-Gallego G., Conn G., Hatcher V.B., Thomas K.A.;
Gimenaz-dallego G., Conn G., Hatcher V.B., Thomas K.A.;
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MEDLINE=87048871; PubMed=3778488;
Gautschi-Sova P., Mueller T., Boehlen P.;
"Amino acid sequence of human acidic fibroblast is Biochem. Biophys. Res. Commun. 140:874-880(1986)
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MEDLINE=90365758; PubMed=2393407;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 RFLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 QYLAMDTDGLLYGS-QTPNEECLFLERLEBNHYNTYISKKHAEKNWFVGLKK--NGSCKR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESL-LQLKALKPGVIQILGVKTS 99
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                                                                                               -1- SUBUNIT: Monomer.
-1- MISCELLANEOUS: This protein binds heparin, although less strongly than does DFGF.
                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
MEDLINE=97107535; PubMed=8950275;
Pineda-Lucena A., Jimenez M.A., Lozano R.M., Nieto J.L., Santoro J.,
Rico M., Gimenez-Gallego G.;
                                     "Three-dimensional structure of acidic fibroblast growth factor in solution: effects of binding to a heparin functional analog."; J. Mol. Biol. 264:162-178(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
13.2%; Score 146.5; DB 1
Best Local Similarity 34.3%; Pred. No. 0.00028;
Matches 47; Conservative 12; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M23087; AAA52638.1; -. M23086; AAA52638.1; JOINED. BC032697; AAA132697.1; -. S67291; AAB230657.2; -. X65778; CAA46661.1; -.
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M30491; AAA52446.1; JOINED.
M60515; AAA51672.1; --
M60516; AAA51673.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M13361; AAA79245.1; -.
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1AXM; 22-APR-98.
2AXM; 22-APR-98.
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EMBL; S67291;
EMBL; X65778;
PIR; A33665;
PDB; ZARG; 12
PDB; 2AXM; 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 SFRELLLEDGYNVYQSEAHGLPLHLPGNK----SPHRDPAPRGPAR-----FLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 IREDGTYGGAA-DQSPESLLQLKALKPGVLQ1LGVKTSRFLCQRPDGALYGSLHFDPEAC 121
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                                                                                                                                                                                                                                   28 ADSPGFINERL-----GQIEGKLQRGSFIDFAHL---KGIIRRRQLYC----RIGFHLE
                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=Wistar; TISSUB=Heart;
MEDLINE=98139883; PubMa=1473496;
Miyake A., Konishi M., Ma-tin F.H., Hernday N.A., Ozaki K.,
Miyake A., Kinishi M., Markawa T., Itoh N.;
Yamamoto S., Mikami T., Arakawa T., Itoh N.;
"Structure and expression of a novel member, FGF-16, on the fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHLE
                                                                                                                                                                                                                                                                                                                                                                                                             greatly after birth.
                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 78 N-LINKED (GLCNAC. . .) (POTENTIAL)
207 Aa; 23753 MW; 1C7A11C8BA3164BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.2%; Score 146.5; DB 1; Length 207; 32.1%; Pred. No. 0.00038; Artive 21; Mismatches 75; Indels 31;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
Fibroblast growth factor-16 (FGF-16).
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PIR, JC5940; JC5940.
HSSP, P31371; 1682.
InterPro; IPR006996; Cytok III_like.
InterPro; IPR002348; III_HBGF.
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PRINTS; PR00262; ILLHBGF.
ProDom; PD000831; ILL_HBGF; 1.
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                                                                          Rattus norvegicus (Rat)
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Best Local Similarity
                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Growth factor
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SEQUENCE
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207 AA.

STANDARD;

FGFG RAT ID FGFG RAT AC O54769;

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Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                         NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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9
                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Fibroblast growth factor-3 precursor (FGF-3) (HBGF-3) (INT-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.1%; Score 146; DB 1; Length 237; 35.6%; Pred. No. 0.00048; tive 19; Mismatches 40; Indel8
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=94038898; PubMed=8223431;
Kiefer P., Mathieu M., Close J.M., Peters G., Dickson C.;
"FGF3 from Xenopus laevis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIBROBLAST GROWTH FACTOR-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 RFICORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
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237 AA; 26984 MW; EDD31B0893567A2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE, PS00247; HBGF FGF; 1.
Growth factor; Mitogen; Signal; Glycoprotein.
                                                  237 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR008996; Cytok ILI_like.
InterPro; IPR002348; ILI_HBGF.
Pfam; PF00167; FGF; 1.
                                                                                                                                                                                 Xenopus laevis (African clawed frog)
                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS, PR00262; IIIHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z25539; CAA80987.1; -. EMBL; X65237; CAA46341.1; -. PIR; S39582. HSSP; P31371; 1G82.
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 39-137 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              EMBO J. 12:4159-4168(1993).
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                                                    STANDARD;
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Best Local Similarity
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                                                    FGF3 XENLA
P36386;
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                                                          SOTE THE SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH 
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FGF1 BOVIN P03968;

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FGF1_BOVIN

RESULT 38

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MEDLINE=89231704; PubMed=2714282; MEDLINE=89231704; Massberg M., Bernotat-Danielowski S., Luethe N., Sharma H.S., Schaper W.; Sharma H.S., Schaper W.; Isolation of heparin-binding growth factors from bovine, porcine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Halley C., Courtois Y., Laurent M.; "Nucleotide sequence of bovine acidic fibroblast growth factor cDNA."; Nucleic Acids Res. 16:10913-10913 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 2-155.
MEDILNE=87016918; PubMed=3532107;
Burgess W.H., Mehlman T., Marahak D.R., Fraser B.A., Maciag T.;
Burgess W.H., Mehlman T., Marahak D.R., Fraser B.A., Maciag T.;
Structural evidence that endothelial cell growth factor beta ais the precursor of both endothelial cell growth factor alpha and acidic fibroblast growth factor.";
Proc. Natl. Acad. Sci. U.S.A. 83:7216-7220(1986).
23-OCT-1986 (Rel. 02, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
48-perin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast growth factor) (Arganial cell growth factor)
6-perin and alpha.chains) (Acidic eye-derived growth factor II) (EDGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=86070224; PubMed=4071057; Mios-Candelore M., MEDLINE=86070224; PubMed=4071057; Bennett C., Rios-Candelore M., Disalvo J., Thomas K.; Incorplast growth factor: complete amino acid "Brain-derived acidic fibroblast growth factor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87026586; PubMed=3768327; Crabb J.W., Armes L.G., Carr S.A., Johnson C.M., Roberts G.D., Bordoli R.S., McKeehan W.L.; Pornoplete primary structure of prostatropin, a prostate epithelial cell growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laurent M.;
                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
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MEDLINE=86261806; PubMed=3425435;
Abraham J.A., Mergia A., Whang J.L., Tumolo A., Friedman J.,

Abraham J.A., Gospodarowicz D., Fiddes J.C.;
Hjerrild K.A., Gospodarowicz D., Fiddes J.C.;
"Nucleotide sequence of a bovine clone encoding the angiogenic protein, basic fibroblast growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alterio J., Halley C., Brou C., Soussi T., Courtois Y., Laus "Characterization of a bovine acidic FGF cDNA clone and its expression in brain and retina.";
FEBS Lett. 242:41-46(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=86055750; PubMed=4065099; Bobline=86055750; PubMed=4065099; Bobline P., Esch F., Baird A., Gospodarowicz D.; Acidic fibroblast growth factor (FGF) from bovine brain: amino-terminal sequence and comparison with basic FGF.";
                                                                                                                                                                                                                                                                                 FGF1 OR FGF-1 OR FGFA OR HBGF-1 OR AFGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 16-44, AND COMPOSITION.
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MEDLINE=89078619; PubMed=2849564;
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Science 230:1385-1388(1985).
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SUBUNIT: Monomer.
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FGF1 OR FGF-1
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                                                                                                                                    agents
                                                                                                                                                                              SUBUNIT: Monomer.
MISCELLANEOUS: This protein binds heparin, although less strongly
                                                                                                                                                                                               than does bFGF. SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SN00442; FGF; Ī.
PROSITE; PS00247; HBGF_FGF; 1.
Growth factor; Mitogen; Angiogenesis; Heparin-binding; Acetylation;
                                                                 MEDLINE=91095983; PubMed=1702556;
MEDLINE=91095983; PubMed=1702556;
Zhu X., Xomiya H., Chirino A., Faham S., Fox G.M., Arakawa T.,
Thu B.T., Rees D.C.;
"Three-dimensional structures of acidic and basic fibroblast growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENDOTHELIAL CELL GROWTH FACTOR BETA. HEPARIN-BINDING GROWTH FACTOR 1. ENDOTHELIAL CELL GROWTH FACTOR ALPHA. ACETYLATION.
                                                                                                                    factors.";
Science 251:90-93(1991).
Science 251:90-93(1991).
-!- FUNCTION: The heparin-binding growth factors are angiogenic
-!- FUNCTION: The heparin-binding for a variety of cell types in vivo and are potent mitogens for a variety of cell types vitro. There are differences in the tissue distribution and concentration of these 2 growth factors.
                             SEQUENCE OF 1-18 FROM N.A. Philippe J.M., Renaud F., Desset S., Laurent M.; Submitted (JUL-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEPARIN (POTENTIAL)
                                                                                                                                                                                                                                                                                                                               EMBL; M35608; AAA30517.1; EMBL; X66446; CAA47063.1; --
EMBL; X66446; CAA47063.1; --
EMBL; M97660; AAA30564.1; --
PIR; JH0613; GKBOA.
PDB; IBAR; 31-OCT-93.
PDB; IBAC; 31-OCT-93.
InterPro; IPR008996; Cytok III_like.
InterPro; IPR008998; III_HBGF.
     canine hearts.";
Eur. J. Biochem. 181:67-73(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                 Probom; Proof 57; FGF; 1.
PRINTS; PROO262; ILLHBGF; 1.
Probom; PD000831; ILL HBGF; 1.
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Eur. J. Biochem. The heparin-binding growth factors are angiogenic agents
-!- FUNCTION: The heparin-binding growth avariety of cell types in
in vivo and are pottent mittogens for a variety of cell types in
vitro. There are differences in the tissue distribution and
concentration of these 2 growth factors.
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MEDLINE-89231704; PubMed=2714282;
Quinkler W., Masaberg M., Bernotat-Danielowski S., Luethe N.,
Sharma H.S., Schaper W.;
"Isolation of heparin-binding growth factors from bovine, porcine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pictoria
01-FEB-1991 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast
growth factor) (AFGF) (Alpha-endothelial cell growth factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 LPLGNYKKPKLLYCSNGGY---FLRILPDGTVDGTKDRSDQHIQLQLCAESIGEVYIKST
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Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92062117; PubMed=1719973; Schaper W.; Schnidt M., Sharma H.S., Schott R.J., Schaper W.; Schnidt M., Sharma H.S., Schott R.J., Schaper W.; Amplification and sequencing of mRNA encoding acidic fibroblast growth factor (aFGE) from porcine heart.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17493 MW; F636641F189F9BFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.0%; Score 144.5; DB 1;
35.0%; Pred. No. 0.00039;
iive 12; Mismatches 64;
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TISSUE=Heart;
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Best Local Similarity
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CARBOHYD
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                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 RFLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 OYLAMDTSGILYGS-QTPSEECLFLERLEENHYNTYTSKKHAEKNWFVGLKK--NGSCKR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESL-LQLKALKPGVIQILGVKTS
-!- MISCELLANEOUS: This protein binds heparin, although less strongly
                                                               -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
(FGF-9) (HBGF-9) (XFGF-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEPARIN-BINDING GROWTH FACTOR 1.
ENDOTHBLIAL CELL GROWTH FACTOR ALPHA.
HEPARIN (FOTEWTIAL).
C -> S (IN REF. 2).
R -> Y (IN REF. 2).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=97006698; PubMed=8853991;
Song J., Slack J.M.W.;
XRGF-9: a new fibroblast growth factor from Xenopus embryos.";
Dev. Dyn. 206:427-436(1996);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: May have a role in muscle development and neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.9%; Score 143.5; DB 1; Length 152; 33.6%; Pred. No. 0.00045; tive 12; Mismatches 64; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IRR008996; Cytok III_like.
InterPro; IRR008996; Cytok III_like.
InterPro; IRR008348; III_HBGF.
PFam; PR00167; FGF; 1.
PRINTS; PR00262; III_HBGF; 1.
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF 7.
Growth factor; Mitogen; Angiogenesis; Heparin-binding.
PROSEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17103 MW; AE853B0A92F9ABF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 GPAR-----FLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 GPRTHYGOKAILFLPLP 151
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X60317; CAA42869.1; -.
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>152
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>152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; JH0476; JH0476.
PIR; S03954; S03954.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P05230; 2AXM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8355;
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091875:
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SEQUENCE
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FGF9_XENLA
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@ib.ch).
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                                                              patterning.
SUBCELIULAR LOCATION: Secreted.
SUBCELIULAR LOCATION: Baternal transcript is found mainly in the arisal hemisphere. Zygotic transcript is found around the blastopore and in the late gastrula stage, in the dorsal part. In later stages it is found along the dorsal part and head region. DEVELOPMENTAL STAGE: THE MATERNAL PROTEIN IS DETECTED UP TO THE BLASTULA STAGE BUT DECLINES BY THE BRALY GASTRULA. ZYGOTIC EXPRESSION STARTS AT AROUND EARLY GASTRULA; THE LEVEL OF EXPRESSION REACHED AT STAGE 15 PERSISTS DURING NEURULA AND TALLBUD STAGES, AND IS FURTHER INVERASED DURING THE TADPOLE STAGES.
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differentiation, has no specific role in anteroposterior
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InterPro; IPR002348; IL1_HBGF.
InterPro; IPR00148; IL1_HBGF.
PRIM: PR00167; FGF.
ProDom; PD000831; IL1_HBGF; 1.
SWART; SW00442; FGF; 1.
SWART; SW00442; FGF; 1.
Growth factor; Differentiation; Mitogen; Heparin-binding;
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GLIA-ACTIVATING FACTOR.
N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U47622; AAC59936.1; -.
HSSP; P31371; 1G82.
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PROPEP
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

2, 2004, 16:00:38 ; Search time 29.6083 Seconds (without alignments) 678.999 Million cell updates/sec March Run on:

US-10-060-765-4 1113 1 MDSDETGFEHSGLWVSVLAG......SSDPLSMVGPSQGRSPSYAS 209 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

283366

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		Description	fibroblast growth			fibroblast growth	H						н								acidic fibroblast					IlDroblast growth	acidic fibroblast	IlDroblast growen	transforming proce	ACIDIC LIDIODIASC	
SUMMARIES		ID	JC7513	TVMST2	S04742	S20102	S23595	JC4268	S14192	S68144	150710	A36207	S54407	TVHUHS	JC7353	JC4627	JC7511	S66486	A48137	A60721	S04147	D37360	TVMSHS	JC7082	JC5941	TVHUFS	A33665	JC5940	539582	GKBOA	JH0476
		DB	2	Н	Н	N	~	7	7	0	Ø	~	7	Н	N		7												Н		7
		Query Match Length	251	245	239	208	187	206	208	266	194	264	192	206	211	256	212	208	208	155	155	155	202	208	207	267	155	207	237	155	152
	æ	Query Match	22.4	16.1	15.9	15.9		15.5		15.0	14.8	14.7	14.7	14.7	14.5	14.4	14.4	14.1	14.1	14.0	13.9	13.9	13.8	•	. 13.5	13.3	13.2	13.2	13.1	13.0	12.9
		ore	249.5	179	177.5	176.5	174	173	170.5	167	165	164	163.5	163.5	161	160.5	160	157	157	155.5	154.5	154.5	153.5	153	150.5	148.5		146.5	***	144.5	143.5
		Result No.		2	ı	4	ľ	y v	7	· cc	0	10	Ξ	12	13	11	1 2	19	17	18	19	20	21	22	23	24	25	26	27	28	29

transforming protein (int-2) - mouse transforming protein (int-2) - mouse)
C.Species: Mis musculus (house mouse)
C.Species: Mis musculus (house mouse)
C.Accession: A23930; S08157
R.Moore, R.; Casey, G.; Brookes, S.; Dixon, M.; Peters, G.; Dickson, C.
RMBO J. S., 919-924, 1986
RMBO J. S., 919-924, 1986
RMBO J. S., 1919-924, 1986
RMBO J. S., 1919-924, 1986
RMBO J. S., 1919-924, 1986
RMBO J. S., 1919-924, 1986
A.Fitle: Sequence, topography and protein coding potential of mouse int-2: a putative on A.Fitle: Sequence number: A23930; MUID:86247582; PMID:3013624
A.Accession: A23930

RESULT 2 TVMST2

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194 220	194 194	194	189	155	155	155	164	413	154	154	168	137	146
12.8 12.8	2.7	2 2	2.4	2.1	1.8	1.5	11.4	1.1	11.0	11.0	11.0	6.01	6.01
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142	141	139	138	135	131.5	127.5	127	124	122	122	122	121	121
30	32	3.4	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

TRESULT 1 JUZIAN 11 JUZIAN 12
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embryonic fibroblast growth factor - African clawed frog c;Species: Xenopus lacvis (African clawed frog) C;Species: Xenopus lacvis (African clawed frog) C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999 C;Accession: S2395 R;Isaacs, H.V.; Tannahill, D.; Slack, J.W.W. Development 114, 711-720, 1992 A;Title: Expression of a novel FGF in the Xenopus embryo. A new candidate inducing fact
                                                                                                                                                                   fibroblast growth factor 6 precursor - human NiAltennate names: fibroblast growth factor related protein FGF.6; transforming protein NiAltennate names: fibroblast growth factor-related protein FGF.6; transforming protein C; Species: Home sapiens (man) C; Date: 18-Feb-1994 #sequence revision 12-Apr-1996 #text_change 21-Jul-2000 C; Date: 18-Feb-1994 #sequence revision 12-Apr-1996 #text_change 21-Jul-2000 C; Accession: S20102; S23739; S04204; S36910 R; Coulier, F.; Batoz, M.; Marics, I.; de Lapeyriere, O.; Birnbaum, D. Oncogene 6, 1437-1444, 1991 A; Marics, I.; de Lapeyriere, O.; Birnbaum, D. A; Title: Butative structure of the FGF6 gene product and role of the signal peptide. A; Reference number: S20102; MUID:91360279; PMID:1886714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X63454
A;Cross-references: EMBL:X63454
A;Note: it is uncertain whether Met-1 or Met-11 is the initiator
R;Marics, I.; Adelaide, J.; Raybaud, F.; Mattei, M.G.; Coulier, F.; Flanche, J.; de Lapinocegene 4, 335-340, 1989, A;Title: Characterization of the HST-related FGF.6 gene, a new member of the fibroblast A;Reference number: S04204; MUID:89201880; PMID:2649847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sato,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: not compared with conceptual translation
A;Residues: 1-208 <COU>
A;Cross-references: EMBL:X57075
A;Cross-references: EMBL:X57075
B;Ida, S.; Yoshida, T.; Naito, K.; Sakamoto, H.; Katoh, O.; Hirohashi, S.; Oncogene 7, 303-309, 1992
A;Title: Human hst-2 (FGF-6) oncogene: CDNA cloning and characterization.
A;Reference number: S23739; MUID:92195660; PMID:1549352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 LWALVFLGILVGMVVPSPAGTRANNTLLDSRGWGTLLSRSRAGLAGELAGVNWESGYLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 81-99,'G',101-208 <MAR>
A;Cross-references: EMBL:X14071; NID:G31354; PIDN:CAB37648.2; PID:g4467836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
: | | | | | | | 152 LWYVSVNGKGRPRRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references GDB:119908; OMIM:134921
A;Map position: 12p13-12p13
A;Introns: 115/3; 150/2
C;Superfamily: fibroblast growth factor
F;1-40/Domain: (or 11-40 or 34-40) signal sequence #status predicted
F;41-208/Product: fibroblast growth factor 6 #status predicted <MAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 LWVSVLAGLLLGACQAHP-----IPDS---SPLLQ----FGGQV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch
1 Similarity 29.1%; Score 176.5; DB 2; Length 2
1 Similarity 29.1%; Pred. No. 4.6e-07;
46; Conservative 27; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 CORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 AMSKGRLYATPSFQ-EECKFRETLLPNNYNAYESDLY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 46; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: GDB: FGF6; hst-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-208 <IID>
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S23595
                                                                                                                                                  RESULT
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N,Alternate names: transforming protein int-2

C;Species: Homo sapiens (man)

C;Accession: 504742

R;Brookes, S.; Smith, R.; Casey, G.; Dickson, C.; Peters, G.

A, Fitle: Sequence organization of the human int-2 gene and its expression in teratocarci
A;Reference number: 504742; MUD:89239468; PMID:2470007
          A;Residues: 1-245 <MOO>
A;Residues: 1-245 <MOO>
A;Cross-references: GB:Y00848; GB:MZ6284; GB:X68450; NID:G52716; PIDN:CAA68767.1; PID:G5
A;Cross-references: GB:Y00848; GB:MZ6284; GB:X68450; NID:G52716; PIDN:CAA68767.1; PID:G5
Nature 343, 662-665, 1990
A;Title: Subcellular fate of the Int-2 oncoprotein is determined by choice of initiation A;Reference number: S08157; MUID:90158795; PMID:2406607
A;Accession: S08157
A;Accession: S08157
A;Status: not compared with conceptual translation A;Nolecule type: mRNA
A;Residues: 'HSRAGIARGRVLPAPRIRETRAGAAAAGGRDAGM', 3-17 <ACL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 FLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAP-- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 YLAMNKRGRLYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGAR---ROPSAER 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 YLAMNKRGRLYASDHYNAE-CEFVERIHELGYNTYASR----LYRTGSSGPGAQRQPGA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 GGOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESILLQLKALKPGVIQILGVKTSR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 FICORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSBAHGLPIHLPGNKSP--HRDPAP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 GGAPRRKLYC----ATKYHLQIHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGR 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 GGAPRRKKLYC----ATKYHLQLHPSGRVNGSLENSAYSILEITAVEVGVVALKGLFSGR 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 RGP-----ARFLPLPGLPPALPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : : : : : | | | : | | 150 QRPWYVSVNGKGRPRRGFKTRRTQKSSLFLPRVLGHKDHEMYRLLQSSQPRAPGEGS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---- LPGLPPALPEPPG 179
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C;Keywords: growth factor
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-239/Product: transforming protein (int-2) #status predicted <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
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15.9%; Score 177.5; DB 1; Length 2
Best Local Similarity 29.7%; Pred. No. 4.5e-07;
Matches 51; Conservative 23; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
16.1%; Score 179; DB 1; Length 24
Best Local Similarity 28.8%; Pred. No. 3.5e-07;
Matches 51; Conservative 30; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Map position: 7
A, Introns: 74/1, 108/3
C; Superfamily: fibroblast growth factor
C;Keywords: growth factor; transforming protein
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A,Cross-references: GDB:120103; OMIM:164950
A,Map position: 11q13.3-11q13.3
A,Aintcons: 741, 108/3
C,Superfamily: fibroblast growth factor
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A; Residues: 1-239 < BRO>
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                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: int-2
                                                                                                                                                                                                                                                                                                                                                                                                    C, Genetics:
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fibroblast growth factor 5 - rat
fibroblast growth factor 5 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S68144
R;Hattori, Y:; Yamasaki, M.; Itoh, N.
Biochim. Biophys. Acta 1306, 31-33, 1996
A;Title: The rat FGF-5 mRNA variant generated by alternative splicing encodes a novel transference number: S68144; MUID:96201703; PMID:8611621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 GOVRORYLYTDDAQOTEAHLEIREDGTVGGAADQSPESILQLKALKPGVIQILGVKTSRF 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 -GLPIHLPGNKSPHRDPAPRG-----PARFLP-----LPGLP-----PALPEPP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGREWYVALNK---RGKAKRGCSPRVKPQHVSTHFLPRFKQSEQPELSFTVTVPEKKKPP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 ALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYOSEAH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:D64085; NID:g992952; PIDN:BAA10966.1; PID:g992953
C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 19-208 <RES>
A;Cross-treferences: GB:M92416; NID:g193288; PIDN:AAA62261.1; PID:g666915
A;Accession: 149664
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Cross-references: GB. M92415; NID: 9193286; PIDN: AAA62260.1; PID: 9193287
                                               A; Molecule type: DNA
A; Residues: 1-208 < LAP>
A; Residues: 1-208 < LAP>
A; Residues: 1-208 < LAP>
A; Cross references: EBBL:X51552
A; Cross references: EBBL:X51552
A; Note: it is uncertain whether Met-1 or Met-11 is the initiator
B; Ollendorff, V.; Rosnet, O.; Marics, I.; Birnbaum, D.; deLapeyriere,
Biochimie 74, 1035-1038, 1992
A; Title: Isolation and sequence of the murine Fgf6 CDNA.
A; Reference number: I49664; MUID:93120244; PMID:1477139
A; Accession: I49665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 LCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-266 <HAT>
A; Reference number: S14192; MUID: 90295275; PMID: 2193291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.3%; Score 170.5; DB 2; Best Local Similarity 36.4%; Pred. No. 1.4e-06; Matches 36; Conservative 21; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 GILAPQPPDVGSSDPLSMVGPSQGRSPS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Introns: 116/1; 150/3
C,Superfamily: fibroblast growth factor
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Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-18 <RE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:U15969
A;Note: The authors translated the codon GGC for residue 114 as Ser
C;Comment: This protein is a member of fibroblast growth factor family. The hstgene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fibroblast growth factor 6 - mouse
C,Species: Mus musculus (house mouse)
C,Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 17-Mar-2000
C;Accession: S14192; 149665; 149664
R;de Lapeyriere, O; Rosnet, O; Benharroch, D.; Raybaud, F.; Marchetto, S.; Planche, Oncogene 5, 823-831, 1990
A;Title: Structure, chromosome mapping and expression of the murine Fgf-6 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: transforming protein hst
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: JC4268
R;Yu, J.C.; DeSeabra, A.J.J.; Wang, L.M.; Fleming, T.P.; Chedid, M.; Miki, T.; Hs
Gene 162, 333-334, 1995
A;Title: An unexpected transforming gene in calf-thymus carrier DNA: Bovine hst.
A;Reference number: JC4268; MUID:96032369; PMID:7557455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 WESLVARSLIAGLPVAAQPKEAAVQSGAGDYLLGIKRLRRLYCNVG--IGFHLQVLPDGR 103
                                                                                                                                                                                                                                                                                                                                          54 DSDYLL---GIKRQRRLYCNVG--IGFHIQVLPDGRINGMHSENRYSLLELSPVEVGVVS 108
                                                                                                                                                                                                                                                                                                                                                                                                                  93 ILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH-GLPLHLPGN-- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                 68
                                                                                                                                                                                                                                                                                                        33 DSSPLLOFGGOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 WVSVLAGLLLGACQAHPIPDSSPLLQFGGQV----RQRYLYTDDAQQTEAHLEIREDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Gaps
                                                                                                                                                                                                                                                         Gaps
                                                                A;Molecule type: mRNA
*Residues: 1-187 <ISSA ;
A;Cross-references: EMEL:X62593; NID:g64692; PIDN:CAA44479.1; PID:g64693
C;Superfamily: fibroblast growth factor
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                                                                                                                                                                                                   Length 187;
                                                                                                                                                                                           Query Match 15.6%; Score 174; DB 2; Length 18
Best Local Similarity 34.8%; Pred. No. 6.5e-07;
Matches 48; Conservative 23; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 EDGYNVYOSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reference number: $23595; MUID:92315916; PMID:1618138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, Superfamily: IlDroblast Street Street C; Keywords: thymus; transforming protein
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C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 -KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 TKKGNRVSPTMTLTHFLP 185
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Best Local Similarity
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A, Molecule type: mRNA
A, Residues: 1-206 <YUJ>
                                       A; Accession: S23595
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7

Gaps

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embryonic fibroblast growth factor II - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 06-Sep-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000
C;Accession: S54407
R;Isaacs, H.V.; Tannahill, D.; Slack, J.M.W.
By-elopment 114, 711-720, 1992
A;Title: Expression of a novel FGF in the Xenopus embryo. A new candidate inducing fact.
A;Reference number: S23595; MUID:92315916; PMID:1618138
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C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 18-Jun-1999
C;Accession: A28417; A29876; A29649
R;Yoshida, T.; Miyagawa, K.; Odagiri, H.; Sakamoto, H.; Little, P.F.R.; Terada, M.; Sug A; Title: Genomic sequence of hst, a transforming gene encoding a protein homologous to A;Reference number: A28417; MUID:88041096; PMID:2959959
A;Residues: 1-206 <VOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: DDBJ:JO2986; NID:g184430; PIDN:AAB59555.1; PID:g386788
R;Talra, M.; Yoshida, T.; Miyagawa, K.; Sakamoto, H.; Terada, M.; Sugimura, T.
Proc. Natl. Acad. Sci. U.S.A. 84, 2980-2984, 1987
A;Title: cDNA sequence of human transforming gene hst and identification of the coding
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                                                                                                                                                                                                                                                                                                                                                  60 HLEIREDGTVGGAADQSPESILLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 ASPGSQGSGSEHSSFQWSPSGRRTGSLYCRVGIGFHLQIYPDGKVNGSHEASVLSILEIF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 TGREWYVALNK----RGKAKRGCSPRVKPOHVSTHFLPRFKQSEQPELSFTVTVPEKKKPP 238
                                                                                                                                                                                                             ---HLEIREDGTVGGAADQSPESLLQLK 84
                                                                                                                                                                                                                                                                                                                                                                                                                              -GLPLHLPGNKSPHRDPAPRG-----PARFLP-----LPGLPPALPEPPGILAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL:X62594; NID:9840919; PIDN:CAA44480.1; PID:9840920
C; Superfamily: fibroblast growth factor
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                   A;Cross-references: GB:M30643; NID:g193294; PIDN:AAA96698.1; PID:g309238
C;Superfamily: fibroblast growth factor
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                                                                                                     Length 264;
                                                                                                     Query Match
14.7%; Score 164; DB 2; Length 26.
Best Local Similarity 28.6%; Pred. No. 6.1e-06;
Matches 58; Conservative 25; Mismatches 78; Indels
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                                                                                                                                                                                                             34 SSPLLQFGGQVRQRYLYTDDAQQTEA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 VKPKVPLSQP-----RRSPS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fibroblast growth factor 4 - human
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Conservative 2
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nes 36; Conserv
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-192 < 1882
A;Residues: 1-264 <HEB>
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Best Local S:
Matches 36
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A,Residues: 1-194 <NIS>
A,Residues: 1-194 <NIS>
A,Cross-references: BMBL:U14654; NID:g609347; PIDN:AAB58706.1; PID:g609348
R,Niswander, L.; Jeffrey, S.; Martin, G.R.; Tickle, C.
Rature 371, 609-612, 1994
A)Title: A positive feedback loop coordinates growth and patterning in the vertebrate li
A,Reference number: 150710; MUID:95021713; PMID:7935794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-264 <HAU>
A;Residues: 1-264 <HAU>
A;Cross-references: GB:M37821; GB:M37822; GB:M37823; NID:g193280; PIDN:AAB02660.1; PID:
A;Cross-references: GB:M37821; GB:M37822; GB:M37823; NID:g193280; PIDN:AAB02660.1; PID:
B;Cross-references: GB:M37821; GB:M37821; GB:M37822; GB:M37823; NID:G138; 454-463; 1990
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                                                                                                                                                        C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: S78506; S50858; I50710
R;Niswander, L.
submitted to the EMBL Data Library, September 1994
A;Reference number: S78506
A;Reference number: S78506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Status: DNA
A;Residues: 1-136,'Q',137-194,'I' <NIW>
C;Genetics: EMBL:U14654; NID:g609347; PIDN:AAA58706.1; PID:g609348
C;Genetics:
A;Gene: FGF4
A;Gene: FGF4
C;Superfamily: fibroblast growth factor
C;Superfamily: transforming protein
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Status: preliminary; not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 165; DB 2;
Pred. No. 3.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29, Mismatches
  ---RPWKPKV----PLS---PSR-RSPS 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 SGLWVSVLAGLLL-GACQAHPIP----
                                                                                                                                    fibroblast growth factor 4 - chicken C; Species: Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.8%;
27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 HRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NKVSPTMTVTHFLP 192
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les 53; Conserv
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A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: S50858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
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fibroblast growth factor 3 - zebra fish
Cispecies: Brachydanio rerio (zebra fish)
Cipate: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 16-Jul-1999
CiAccession: JC4627
Riklefer, P:; Straehle, U:; Dickson, C.
Rene 168, 211-215, 1996
A;Title: The zebrafish Fgf-3 gene: cDNA sequence, transcript structure and genomic organ
A;Reference number: JC4627; MUID:96194899; PMID:8654946
                                                                                                                                                                                                                                                                                                                     A, Molecule type: mRNA
A, Residues: 1-256 < KIE>
A, Cross-references: EMBL: Z48714; NID: 9971333; PIDN: CAA88596.1; PID: 9971334
A, Experimental source: embryo
A, Note: The authors translated the codon TGG for residue 178 as His
C, Comment: This factor belongs to the fibroblast growth factor family which have the fun otein is a cell signalling molecule and plays the roles during the early stages of devel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rjohmachi, S.; Matanabe, Y.; Mikami, T.; Kusu, N.; Ibi, T.; Akaike, A.; Itoh, N. Biochem. Biophys. Res. Commun. 277, 355-360, 2000
A;Title: FGF-20, a novel neurotrophic factor, preferentially expressed in the substantia A;Reference number: JC7511; MUID:20490008; PMID:11032730
A;Contents: Brain
A;Accession: JC7511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: DNA
A,Residues: 1-212 coHM-
A,CTOSS-references: DDBJ:AB020021
C,Comment: This factor is secreted, and plays an important role as a neurotrophic factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 RFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 IQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH-----GLPLH 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 VSIRĠVDSGLYLGMNGKĠELYĠŚEKLTSĖ-CIFRĖQFEĖNWYNTYSŠNIYKHGDTĠRRYF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fibroblast growth factor-20 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 GGOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQ-SPESILQLXALKPGVIQILGVKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 PDSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGA-ADQSPESLLQLKALKPGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.4%; Score 160; DB 2; Length 212; 33.8%; Pred. No. 9.9e-06; Arive 17; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 GPARFLPLPGLPPALPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 14.4%; Score 160.5; DB 2; 1 Similarity 28.1%; Pred. No. 1.1e-05; 47; Conservative 22; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: fgf-20
C,Keywords: brain, growth factor; neurotrophic factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: embryo; fibroblast; growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Introns: 93/2; 127/3
C,Superfamily: fibroblast growth factor
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: Fgf-3
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fibroblast growth factor-20 - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 01-Dec-2000
C;Accession: JC7353
R;Kirikoshi, H.; Sagara, N.; Saitoh, T.; Tanaka, K.; Sekihara, H.; Shiokawa, K.; Katoh, Biochem Biophyas Res. Commun. 274, 337-343, 2000
A;Title: Molecular cloning and characterization of human FGF-20 on chromosome 8p21.3-p22
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: DDBJ:Ab044277
C;Comment: This factor is involved in physiological and pathological processes, playing
            A; Accession: A29876
A; Molecule type: mRNA
A; Residues: 1-206 cTAL?
A; Residues: 1-206 cTAL?
A; Residues: 1-206 cTAL?
A; Cross-references: 18:02986; GB:M16338; NID:g184430; PIDN:AAB59555.1; PID:g386788
B; PiDelli Bovi, P.; Curatola, A.M.; Kern, F.G.; Greco, A.; Ittmann, M.; Basilico, C.Cell 50, 729-737, 1987
A; Title: An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes a growth A; Reference number: A29649; MUID:87301716; PMID:2957062
                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: GB:M17446, NID:g186785, PIDN:AAA59473.1, PID:g307092
C,Comment: This protein is an oncogene for Kaposi's sarcoma. It is homologous to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 HLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 IQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH-----GLPLH 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 PDSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGA-ADQSPESLLQLKALKPGV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 ACSFRELLLEDGYNVYQSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 206;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Map position: 11q13.3-11q13.3
A;Introns: 114/1; 148/3
C;Superfamily: fiberblast growth factor
C;Keywords: growth factor; Kaposi sarcoma; transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 VALNK----DGTPRDGARSKRHOKFTHFLPRPVDPERVPE 202
number: A29876; MUID:87204251; PMID:2953031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.7%; Score 163.5; DB 1;
36.9%; Pred. No. 5e-06;
... Wiemmatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 14.5%; Score 161; DB 2; Similarity 33.1%; Pred. No. 8.2e-06; 53; Conservative 19; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GDB:120066; OMIM:164980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,Gene: fgf-20
Map position: 8p21.3-8p22
;Mapperfamily: fibroblast growth factor
;Keywords: angiogenesis; carcinogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 41; Conserva
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Best Local Similarity
Matches 53; Conserva
                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-206 <BOV>
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Accession: A60721 Apreciate number: A60721, MUID:90201; PMID:1693366 Appearation of the hamster hypering more transfer of transfer of the hamster of special segmence_revision 10-Sep-1999 #text_change 10-Sep-1999 (c) Accession: A60721 A.A.; Malark, M.A.; Mansson, P.E.; Zhou, H.; Harris, S.E. J. Cell. Biochem. 43, 17-26, 1990 A;Title: Characterization of the hamster DDT-1 cell aFGF/HGBF-I gene and cDNA and its A;Reference number: A60721, MUID:90270291; PMID:1693366 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A60721 A;Accession: A6072
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N'Alternate names: heparin-binding growth factor 1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 16-Jul-1999
C;Accession: S04147
C;Accession: G.C.; Bahrenburg, K.; Mansson, P.E.
Nucleic Acids Res. 17, 2867, 1989
A;Title: The nucleotide sequence of rat heparin binding growth factor 1 (HBGF-1).
A;Reference number: S04147; MUID:89240051; PMID:2470029
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                                                                                                                                                                                                                                                                                                                                  100 RFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 QYLAMDTÖGLLYGS-QTPNEECLPLERLEENHYNTYTSKKHAEKNWFVGLKK--NGSCKR 134
                                                                                                                                                               76 IFPNGTIQGTRXDHSRFGILEFISIAVGLVSIRGVDSGLXLGMNEKGELYGSEKLTQE-C 134
                                                                                                                                                                                                                                                                    ----FLPL 167
                                                                                      63 IREDGTVGGA-ADOSPESLLOLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEAC 121
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--PAVTDLDHLKGILRRQLYC----RTGFHLE 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 GGOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESL-LQLKALKPGVIQILGVKTS
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A;Residues: 1-155 <GGO>
A;Cross-references: EMBL:X14232; NID:g56351; PIDN:CAA32448.1; PID:g56352
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor; heparin binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 155;
                                                                                                                                                                                                                                                                         SFRELLLEDGYNVYQSEAH-----GLPLHLPGNKSPHRDPAPRGPAR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-155 <HAL>
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor; heparin binding
    ----GILPRG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 PGLPPALPE 176
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    34 SDHLGQSEAG--
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A; Molecule type: mRNA
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(Species: Homo sapiens (man)
(C)Species: Homo sapiens (man)
(C)Species: Homo sapiens (man)
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R;Seo, M.; Noguchi, K.
FEBS Lett. 370, 231-235, 1995
A;Title: Retinoic acid induces gene expression of fibroblast growth factor-9 during indu A;Reference number: S66486; MUID:95385801; PMID:7656983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Cross-references: EMBL:D38258; NID:g1107458; PIDN:BAA07410.1; PID:g1107459
C,Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                         fibroblast growth factor 9 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 IREDGTVGGA-ADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEAC
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A;Experimental source: foreskin
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                                                                   Cross-references: GDB:207221; OMIM:600921
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C;Superfamily: fibroblast growth factor
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              LPGNKSPHRDPAPRGPAR--
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Matches 59; Conservative
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A; Residues: 1-208 <SEO>
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fibroblast somatotropin-20 - African clawed frog
N;Alternate names: fibroblast growth factor-20
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: JC7082
R;Koga, C.; Adati, N.; Nakata, K.; Mikoshiba, K.; Furuhata, Y.; Sato, S.; Tei, H.; Sakak Biochem. Biophys. Res. Commun. 261, 756-765, 1999
A;Title: Characterization of a novel member of the FGF family, XFGF-20, in Xenopus laevi
A;Reference number: JC7082; MUID:99373151; PMID:10441498
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: JC5941
R;Myake, A.; Konishi, M.; Martin, F.H.; Hernday, N.A.; Ozaki, K.; Yamamoto, S.; Mikami, Biochem. Biochem. Biophys. Res. Commun. 243, 148-152, 1998
A;Title: Structure and expression of a novel member, FGF-16, of the fibroblast growth fa
                        A;Cross-references: GB:X14849; GB:M28516; NID:G52791; PIDN:CAA32967.1; PID:G52792
R;Hebert, J.M.; Basilico, C.; Goldfarb, M.; Haub, O.; Martin, G.R.
Bev. Biol. 138, 454-463, 1990
A;Title: Isolation of cDNAs encoding four mouse FGF family members and characterization A;Reference number: A37360; MUID:90201563; PMID:2318343
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C,Superfamily: fibroblast growth factor
C,Keywords: differentiation; fibroblast; growth factor; heparin binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 HLEIREDGTVGGAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 HLQVLPDGKIGGVHADTRDSLLELSPVQRGVVSIFGVASRFFVAMSSRGKLFGVPFFTDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-166,'S',168-202 <HEB>
A;Cross-references: GB:M30642; NID:9193290; PIDN:AAA37619.1; PID:g309237
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 ACSFRELLLEDGYNVYQSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.8%; Score 153.5; DB 1; 34.2%; Pred. No. 3.1e-05; iive 21; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.7%; Score 153; DB 2;
31.5%; Pred. No. 3.5e-05;
tive 22; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                          A,Gene: hst
C,Superfamily: fibroblast growth factor
C,Keywords: growth factor; transforming protein
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Best Local Similarity
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Matches 38; Conserv
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A; Residues: 1-208 < KOG>
       A; Residues: 1-202 <BRO>
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C;Comment: This protein is an inducer of neovascularization in angiogenic disease includ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome organization and location re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NiAlternate names: aFGF; FGF-1
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
C;Accession: D37360; UC5231
R;Hebert, J.M.; Basilico, C.; Goldfarb, M.; Haub, O.; Martin, G.R.
A;Title: Isolation of cDNAs encoding four mouse FGF family members and characterization
A;Reference number: A37360; MUID:90201563; PMID:2318343
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Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispaces: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 17-Mar-2000
Ciscossion: 804741; A37360
Ribrookes, S.; Smith, R.; Thurlow, J.; Dickson, C.; Peters, G.
Alticle: The mouse homologue of hst/k-FGF; sequence, genome organization and location relaterance number: 804741; MUID:89296455; PMID:2740210
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                                                                                                         97 KTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDP 156
                                                                                                                                                97 KTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDP 156
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18 LPLGNYKKPKLLYCSNGGH---FLRILPDGTVDGTRDRSDQHIQLQLSABSAGEVYIKGT 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Gaps
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Caross-references: GB: M30641; NID: g193284; PIDN: AAA37618.1; PID: g309236
R; Madiai, F.; Hackshaw, K.V.; Chiu, I.M.
A; Madiai, F.; Hackshaw, K.V.; Chiu, I.M.
A; Title: Cloning and characterization of the mouse Fgf-1 gene.
A; Reference number: JC5231; MUID: 97128312; FMID: 8972905
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1 Similarity 34.3%; Pred. No. 1.9e-05;
48; Conservative 13; Mismatches 64;
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C, Superfamily: fibroblast growth factor
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Best Local Similarity
Matches 48; Conserv
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C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 08-Dec-2000 C;Accession: A33665; A32316; $18217; A43804; A24662; JH0707; $35535; $35536; 139413; A2.8 A. Bibargia, A.; Tischer, E.; Graves, D.; Tumolo, A.; Miller, J.; Gospodarowicz, D.; Abraha Biochem. Biophys. Res. Commun. 164, 1121-1129, 1989 A;Title: Structural analysis of the gene for human acidic fibroblast growth factor. A;Reference number: A33665; MUID:90073637; PMID:2590193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: EMBL:M23086
R;Chiu, I.M.; Wang, W.P.; Lehtoma, K.
Rociogene 5, 755-762, 1990
A;Title: Alternative splicing generates two forms of mRNA coding for human heparin-bind:
A,Reference number: A43804; MUID:90265618; PMID:1693186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Mosterial Erype: mRNA
A; Residuces: 1-155 cCHT.
A; Cross-references: BMBL: X51943; NID: g32435; PIDN: CAA36206.1; PID: g32436
B; Jaye, M.; Howk, R.; Burgess, W.; Ricca, G.A.; Chiu, I.M.; Ravera, M.W.; O'Brien, S.J..
B; Jaye, M.; Howk, R.; Burgess, W.; Ricca, G.A.; Chiu, I.M.; Ravera, M.W.; O'Brien, S.J..
A; Jeine, E. 233, Asl.-1545, 1986
A; Reference number: A24662; MUID: 86261805; PMID: 3523756
A; A; Accession: A24662
A; Residuces: 1-155 cJAY>
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R;Yu, Y.L.; Kha, H.; Golden, J.A.; Migchielsen, A.A.J.; Goetzl, B.J.; Turck, C.W.
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A;Title: An acidic fibroblast growth factor protein generated by alternate splicing act: A;Reference number: JH0707; MUID:92202857; PMID:1372643
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A; Residues: 1-155 < YUY>
A; Cross-references: GB:X65778; NID:g396163; PIDN:CAA46661.1; PID:g396164
A; Cross-references: GB:X65778; NID:g396163; PIDN:CAA46661.1; PID:g396164
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Nucleic Acids Res. 21, 489-495, 1993
A; Title: Cloning of two novel forms of human acidic fibroblast growth factor (aFGF) mRN/A; Reference number: S35535; MUID:93181239; PMID:7680120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-155 <WAN>
A; Residues: 1-155 <WAN>
A; Cross-references: GB:M23087; NID:g183875; PIDN:AAA52638.1; PID:g386768
R; Wang, W.P.; Quick, D.; Balcerzak, S.P.; Needleman, S.W.; Chiu, I.M.
Rocogene 6, 1521-1529, 1991
A; Title: Cloning and sequence analysis of the human acidic fibroblast growth factor gent
A; Reference number: S18217; MUID:92019819; PMID:1717925
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R;Wang, W.P.; Lebtoma, K.; Varban, M.L.; Krishnan, I.; Chiu, I.M.
R;Wang, W.P.; Lebtoma, K.; Varban, M.L.; Krishnan, I.; Chiu, I.M.
Mol. Cell. Biol. 9, 2387-2295, 1989
A;Title: Cloning of the gene coding for human class 1 heparin-binding growth factor and A;Reference number: A32316; MUID:89343957; PMID:2474753
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R,Crumley, G.; Dionne, C.A.; Jaye, M.
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A;Title: The gene for human acidic fibroblast growth factor A;Reference number: 139412; MUID:90365758; PMID:2393407
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A,Molecule type: mRNA
A,Residues: 1-58 <PAY>
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A, Status: translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-155 <WA2>
                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Regidues: 1-155 < MER>
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A, Residues: 1-58 < PA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S18217
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A33665
acidic fibroblast growth factor 1 precursor [validated] - human
N;Alternate names: beta-ECGF; endothelial cell growth factor beta; heparin-binding growt
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CjAccession: A31194
R;Zhan, X.; Bates, B.; Hu, X.; Goldfarb, M.
Mol. Cell.: Biol.: 8, 3487-3495, 1988
Mol. Cell.: Biol.: 8, 3487-3495, 1988
A;Title: The human FGF-5 oncogene encodes a novel protein related to fibroblast growth A;Reference number: A31194; MUID:89096942; PMID:3211147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Cross-references: GB:M23536; GB:M21617; NID:9182539; PIDN:AAB60699.1; PID:9182542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                       8
                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-207 <MIY>
A;Coss-references: DDBJ:AB009391; NID:g2911169; PIDN:BAA24956.1; PID:g2911170
C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 HIRIREDGTVGGAADQSPESLIQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --PARF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 IFPNGTVHGTRHDHSRFGILEFISLAVGLISİRGVDSGLYLGMNERGELYĞSKKLTRE-C 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 IREDGTVGGAA-DQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 ADSPGFINERL-----GQIEGKLORGSPTDFAHL---KGILRRRQLYC----RTGFHLE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fibroblast growth factor 5 - human
N;Alternate names: transforming protein FGF5
C;Species: Homo sapiens (man)
C;Species: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                      SDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHLE
                                                                                                                                                                                                                                                                                                                                                       Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.3%; Score 148.5; DB 1; Length 267; 31.2%; Pred. No. 0.00011;
                                                                                                                                                                                                                                                                            ch 13.5%; Score 150.5; DB 2; Length 207; I Similarity 32.6%; Pred. No. 5.5e-05; 61; Conservative 20; Mismatches 75; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 SFRELLLEDGYNVYQSEAHGLPLHLPGNK----SPHRDPAPRGPAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 ACSFRELLLEDGYNVYQSEAH-----GLPLHLPGNKSPHRDPAPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 LP-----LPGLPPALPEPPGILAPOPPDVGSSDPLS 195
              A; Reference number: JC5940; MUID: 98139883; PMID: 9473496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
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Conservative 20; Mismatches
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C;Keywords: growth factor; transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GDB:119907; OMIM:165190
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C;Superfamily: fibroblast growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 VDPSKLP 197
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A; Residues: 1-267 <ZHA>
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Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A31194
                                                 A; Accession: JC5941
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                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 61
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A; Cross-references: GB:M60515; NID:g178226; PIDN:AAA51672.1; PID:g553170; GB:M60516; NL
A; Molecule type: mRNA
A; Residues: 1-40 <RES>
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exons

two upstream

encodes

8;

74

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A;Title: Developmental expression of the Xenopus int-2 (FGF-3) gene: activation by mesod A;Reference number: S25713; MUID:93048831; PMID:1425349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 GGAPRNRKLYC----ATKYHLQIHLNGKINGTLERNSVFSILEITAVDVGIVAIKGLFSG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IREDGTVGGAA-DQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 SFRELLLEDGYNVYQSEAHGLPLHLPGNK----SPHRDPAPRGPAR-----FLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-207 <MIY>
A;Cross-references: DDBJ:AB002561; NID:g2911149; PIDN:BAA24947.1; PID:g2911150
C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 IPPNGTVHGTRHDHSRFGILEFISLAVGLISIRGVDSGLYLGMNERGELFGSKKLTRE-C 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.Alternate names: FGF-3 protein; fibroblast growth factor 3
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 GGQVRQRYLYIDDDAQQTEAHLEIREDGTVGGAADQ-SPESILLQLKALKPGVIQILGVKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 ADSPGFLNERL-----GQIEGKLORGSPTDFAHL---KGILRRROLYC----RTGFHLE
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A; Residues: 1-237 <KIE>
A; Cross-references: EMBL: 225539; NID: 9396830; PIDN: CAA80987.1; PID: 9396831
A; Cross-references: EMBL: 225539; NID: 9396830; PIDN: CAA80987.1; PID: 9396831
B; Tannahill, D; Isaacs, H.V.; Close, M.J.; Peters, G.; Slack, J.M.W.
Development 115, 695-702, 1992
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C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                  Length 207;
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R;Kiefer, P.; Mathieu, M.; Close, M.J.; Peters, G.; Dickson, EMBO J. 12, 4159-4168, 1993
A;Title: FGF3 from Kenopus laevis.
A;Reference number: $39582; MUID:94038898; PMID:8223431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 RFLCQRPDGALYGSLHFDPBACSFRELLLEDGYNVYQSEAH 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 146; DB 1;
Pred. No. 0.00015;
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35.6%; Pred. No. v...
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transforming protein int-2 - African clawed frog
C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNÅ
A;Residues: 39-137 <TAN>
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Best Local Similarity
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                                                                                                                                                                         A;Accession: JC5940
A;Status: preliminary
A;Molecule type: DNA
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A,Status: preliminary
A,Molecule type: mRNA
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A,Residues: 16-155 <HAR>
R;Gimenez-Gallego, G.; Conn, G.; Hatcher, V.B.; Thomas, K.A.
Biochem. Biophys. Res. Commun. 138, 611-677, 1986
A;Title: The complete amino acid sequence of human brain-derived acidic fibroblast growt
A;Reference number: A24820; MUID:86295741; PMID:3527167
                                                                                                                                                                                                                                                                                       A,Molecule type: protein
A,Residues: 16-155 <GIM>
R,Gimenez-Gallego, G.; Conn, G.; Hatcher, V.B.; Thomas, K.A.
Biochem. Biophys. Res. Commun. 135, 541-548, 1986
A;Title: Human brain-derived acidic and basic fibroblast growth factors: amino terminal
A;Reference number: A90122; MUID:86186784; PMID:3964259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: protein
A,Residues: 16-30,'X',32-38;73-75,'X',77-97,'X',99-101;128-131,'X',133-140,'X',142-152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               endothelial cell mitogens from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Inferaction of nucleotides with acidic fibroblast growth factor (FGF-1). A;Reference number: A53639; MUID:94271773; PMID:7516183
A;Accession: A53639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GNYKRPKLLYCSNGGH---FIRILPDGTVDGTRDRSDQHIQLQLSABSVGEVYIKSTETG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESL-LQLKALKPGVIQILGVKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Rolecule type: protein
A;Residues: 16-30, X',32-49 <GAU>
R;Gautschi-Sova, P.; Muller, T.; Bohlen, P.
R;Gautschi-Sova, P.; Muller, T.; Bohlen, P.
B;Gautschi-Sova, P.; Muller, T.; Bohlen, P.
A;Title: Amino acid sequence of human acidic fibroblast growth factor.
A;Reference number: A26386; MUID:87048871; PMID:3778488
A;Molecule type: protein
A;Recession: A26386
A;Molecule: 16-155 <GA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Keywords: alternative splicing; growth factor; heparin binding F;16-155/Product: fibroblast growth factor 1 #status experimental F;129/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 16-47 <G12>
A; Experimental source: brain
R; Gautschi, P.; Frater-Schoder, M.; Bohlen, P.
FRBS Lett. 204, 203-207, 1986
A; Title: Partial molecular characterization of endotheli
     R;Harper, J.W.; Strydom, D.J.; Lobb, R.R.
Biochemistry 25, 4097-4103, 1986
A;Reference number: A23553; MUID:86296647; PMID:2427112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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34.3%; Pred. No. 8.2e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: GDB:FGF1; FGFA
A;Cross-references: GDB:119909; OMIM:131220
A;Map position: 5G31.3-5G33.2
A;Introns: 57/1; 91/3
C;Superfamily: fibroblast growth factor
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fibroblaвt growth factor 16 - rat
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Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                  A; Accession: A24820
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                                                                                        A; Accession: A23553
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A,Molecule type: protein
A,Residues: 16-30, X',32-40 «KUO>
A,Residues: 16-30, X',32-40 «KUO>
A,Residues: 16-30, X',32-40 «KUO>
A,Residues: 16-30, X',32-40 «KUO>
A,RHill, C.E.; Belford, D.A.; Godovac-Zimmermann, J.; Hendry, I.A.
Brain Res. Dev. Brain Res. 63, 13-19, 1991
Brain Res. Dev. Brain Res. 63, 13-19, 1991
A,Title: Class I heparin binding growth factor promotes the differentiation but not the A,Reference number: A61198; MUID:92164087; PMID:1724209
A,Accession: A61198
A,Accession: A61198
A,Rociente type: protein
A,Residues: 11-26;28-50;53-110, "H',112, 'NTY';134-155 «HIL>
R;Philippe, J.M.; Renaud, F.; Desset, S.; Laurent, M.; Mallet, J.; Courtois, Y.; Edwarde Biochem: Biophys Res. Commun. 188, 843-850, 1992
A,Title: Cloning of two different 5' untranalated exons of bovine acidic fibroblast grow A,Reference number: 146024; MUID:93075172; PMID:1280126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Molecule type: procein
A, Residues: 16-24;121-127;134-143 <SAS>
A, Residues: 16-24;121-127;134-143 <SAS>
C, Experimental source: heart
C, Comment: The acidic and basic fibroblast growth factors are the major endothelial-cell
ell types in vitro (although bFGF is 30-100 times more potent than aFGF in stimulating t
f these two growth factors.
C, Comment: This procein binds heparin, although less strongly than does bFGF.
C, Comment: There are some sequence similarities between residues 117-126 (a region flank
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R;Sasaki, H.; Hoshi, H.; Hong, Y.M.; Suzuki, T.; Kato, T.; Sasaki, H.; Saito, M.; Youki, J. Biol. Chem. 264, 17606-17612, 1989
A;Title: Purification of acidic fibroblast growth factor from bovine heart and its local A;Reference number: A34477; MUID:90008933; PMID:2677012
A;Accession: A34477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Note: this form was designated alpha endothelial cell growth factor
R;Strydom, D.J.; Harper, J.W.; Lobb, R.R.
Biochemistry 25, 945-951, 1986
A;Title: Amino acid sequence of bovine brain derived class 1 heparin-binding growth fact
A;Reference number: A24539; MUID:86187766; PMID:2421762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Protein Chem. 6, 163-171, 1987
A,Title: Primary structure and mitogenic and angiogenic activities of brain-derived acid
A,Reference number: A60884
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A;Residues: 16-155 <TRO:
K;Kuo, M.D.; Huang, S.S.; Huang, J.S.
J. Biol. Chem. 265, 16455-4643, 1990
A;Title: Acidic fibroblast growth factor receptor purified from bovine liver is a novel
A;Reference number: A37892; MUID:90375514; PMID:2168890
                                R;Burgess, W.H.; Mehlman, T.; Marshak, D.R.; Fraser, B.A.; Maciag, T.
Proc. Natl. Acad. Sci. U.S.A. 83, 715-7220, 1986
A;Title: Structural evidence that endochelial cell growth factor beta is the precursor A;Reference number: A94127; MUID:87016918; PMID:3532107
                                                                                                                                                                                                                                                        A,Molecule type: protein
A,Residues: 2-155 <BUX>
A,Note: this form was designated beta endothelial cell growth factor
A,Aocession: C25043
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A;Residues: 16-155 <STR>
R;Thomas, K.A.; Gimenez-Gallego, G.; Rios-Candelore, M.; DiSalvo,
                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: protein
A,Residues: 16-155 <BU2>
A,Note: this 16-10m was designated acidic fibroblast growth factor
A,Accession: A25043
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A,Residues: 22-30, XY, 32-38 <KUZ>
A,Note: this form was designated brain-derived growth factor A
A,Accession: 13789.
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A;Molecule type: mRNA
A;Residues: 1-18 <PH2>
2,'GE',5-155 <CRA>
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                                                                                                                                                                 acidic fibroblast growth factor precursor - bovine

NyAlternate names: aFGF; eye-derived growth factor II; heparin-binding growth factor I;
C;Species: Bos primigenius taurus (cattle)
C;Accession: JH0613; S02102; S02661; S22065; B24663; A94281; S03953; A91010; A24477; B25
R;Renaud, F.; Desset, S.; Bugra, K.; Halley, C.; Philippe, J.M.; Courtois, Y.; Laurent,
Biochem: Blophys. Res. Commun. 184, 945-952, 1992
A;Title: Heterogeneity of 3' untranslated region of bovine acidic FGF transcripts.
A;Reference number: JH0613; MUID:92246990; PMID:11374244
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R;Abraham, J.A.; Mergia, A.; Whang, J.L.; Tumolo, A.; Friedman, J.; Hjerrild, K.A.; Gosg
Science 233, 545-548, 1986
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A,Residues: 16-56 <ABR>
R;Gimenez-Gallego, G.; Rodkey, J.; Bennett, C.; Rios-Candelore, M.; DiSalvo, J.; Thomas,
Science 230, 1385-1388, 1985
A;Title: Brain-derived acidic fibroblast growth factor: complete amino acid sequence and
A;Reference number: A94281; MUID:86070224; PMID:4071057
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A;Residues: 16-155 <GIM>
R;Quinkler, W.; Maæbberg, M.; Bernotat-Danielowski, S.; Luethe, N.; Sharma, H.S.; Schape
Eur. J. Blochem. 181, 67-73, 1989
A;Title: Isolation of heparin-binding growth factors from bovine, porcine and canine hea
A;Reference number: S03953; MUID:89231704; PMID:2714282
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Reference number: A91010; MUID:86055750; PMID:4065099
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;Residues: 16-30, X', 33-34, X', 36-44 <BOH>
;Residues: 16-30, X', 32-34, X', 36-44 <BOH>
;Residues: 16-30, X', 18-30, X', 19-30, Y', Yohnson, C.M.; Roberts, G.D.; Bordoli, R.S.; MCK
lochemistry 25, 4988-4993, 1986
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R;Alterio, J.; Halley, C.; Brou, C.; Soussi, T.; Courtois, Y.; Laurent, M.
FBBS Lett. 242, 41-46, 1988
A;Title: Characterization of a bovine acidic FGF cDNA clone and its expression in brain A;Reference number: S02661; MUID:89078619; PMID:2849564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title: Complete primary structure of prostatropin, a prostate epithelial cell growth Reference number: A24477; MUID:87026586; PMID:3768327 A24477
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A;Residues: 58-155 (REN>
R;Halley, C.; Courtois, Y.; Laurent, M.
Nucleic Acids Res. 16, 10913, 1988
A;Title: Nucleotide sequence of bovine acidic fibroblast growth factor CDNA.
A;Reference number: S02102; MUID:89083506; PMID:3205724
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A;Residues: 1-155 <ALT>
A;Cross-references: EMBL:X14032; NID:g322; PIDN:CAA32192.1; PID:g323
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A;Residues: 16-45 <QUI>
R;Bohlen, P.; Esch, F.; Baird, A.; Gospodarowicz, D.
B;BRO J. 4, 1951-1956, 1985
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ibmitted to the EMBL Data Library, May 1992
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A;Residues: 1-155 <HAL>
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Residues: 1-18 <PHI>
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C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 16-Jul-1999 C;Accession: S26649; S78446
R;Yan, G:, Nikolaropoulos, S:; Wang, F:; McKeehan, W.L.
In Vitro Cell. Dev. Biol. 27, 437-438, 1991
A;Title: Sequence of rat keratinocyte growth factor (heparin-binding growth factor type A;Reference number: S26049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fibroblast growth factor 3 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 17-Mar-2000
C;Accession: 150588
                                                                                                                                                                                                                                                                                                                                                                                         A,Accession: S78446
A,Molecule type: MRNA
A,Residues: 1-16, 'P, 18-100, 'M',102-123,'Q',125-150,'S',152-194 <YAW>
A,Residues: 1-16, 'P, 18-100, 'M',102-123,'Q',125-150,'S',152-194 <YAW>
A,Cross-references: EMBL:X56551; NID:956707; PIDN:CAA39892.1; PID:956708
C,Superfamily: fibroblast growth factor
C,Keywords: extracellular protein; growth factor; heparin binding; mitogen
E,1-31/Domain: signal sequence #status predicted <SIG>
F;32-194/Product: fibroblast growth factor 7 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: mRNA
A,Residues 1-220 cMAH-
A,Cross-references: EMBL:Z47555; NID:g623215; PIDN:CAA87635.1; PID:g623216
C,Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAAD-QSPESLLQLKALKPGVIQILGVKTS
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 27.5%; Pred. No. 0.00024;
Matches 39; Conservative 30; Mismatches 47; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 220;
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A;Title: Multiple roles for FGF-3 during cranial neural dev A;Reference number: 150588; MUID:95309122; PMID:7789270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
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                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, February 1991
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Best Local Similarity 34.7%
Marches 35, Conservative
                                                                                                                                                                                         A,Accession: S26049
A,Molecule type: mRNA
A,Residues: 1-194 <XAN>
A;Cross-references: EMBL:X56551
R;Yan, G.
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                                                                                                                 A; Introns: 57/1; 91/3
C; Superfamily: fibroblast growth factor
C; Superfamily: fibroblast growth factor
C; Keywords: acetylated amino end; anglogenesis; growth factor; heparin binding; mitogen
C; Keywords: acetylated amino end; anglogenesis; growth factor #status experimental «ECB»
F; 2-155/Product: acidic fibroblast growth factor #status experimental «MAT»
F; 22-155/Product: alpha endothelial cell growth factor #status experimental «ECR»
F; 24-28, 113-116/Region: heparin binding #status predicted
F; 2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acidic fibroblast growth factor - pig (fragment)

acidic fibroblast growth factor - pig (fragment)

c;Species Sus scrofa domestica (domestic pig)

c;Decies 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999

c;Accession: JH0476; S20072

R;Schmidt, M.; Sharma, H.S.; Schott, R.J.; Schaper, W.
Biochem: Biophyrs, Res. Commun. 180, 853-859, 1997

A;Hile: Amplification and sequencing of mRNA encoding acidic fibroblast growth factor
A;Reference number: JH0476; MJID:92062117; PMID:1719973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: the hydrophobic core residues are packed around the internal symmetry axis C;Comment: This protein belongs to the fibroblast growth factor family. C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 LPLGNYKKPKLLYCSNGGY---FLRILPDGTVDGTKDRSDQHIQLQLCAESIGEVYIKST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Residues: 1-152 <SCH>
A,Cross-references: EMBL:X60317; NID:g1873; PIDN:CAA42869.1; PID:g1874
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                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 155;
                                                                                                                                                                                                                                                                                                                                                                       13.0%; Score 144.5; DB 1; Length 1 ilarity 35.0%; Pred. No. 0.00012; Conservative 12; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64; Indels
                             sidues 18-27) and bovine substance P beta (residues 98-107)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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F;22-28/Region: nuclear location signal
F;133/Binding site: heparin (Ly8) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fibroblast growth factor 7 precursor - rat N;Alternate names: keratinocyte growth factor C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 APRGPAR-----FLPLP 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                      49;
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Best Local
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Matches
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A;Molecule type: protein
A;Residues: YX, 33-44 «RUB»
A;Residues: YX, 33-44 «RUB»
A;Residues: YX, 33-44 «RUB»
A;Residues: YX, 33-44 «RUB»
B;Relley, M.J.; Pech, M.; Seuanez, H.N.; Rubin, J.S.; O'Brien, S.J.; Aaronson, S.A.
B;Relley, M.J.; Pech, M.; Seuanez, H.N.; Rubin, J.S.; O'Brien, S.J.; Aaronson, S.A.
B;Reci. Natl., Acad. Sci. U.S.A. 89, 9287-9221, 1992
A;Title: Emergence of the Keratinocyte growth factor multigene family during the great A;Reference number: A46289; MUID:93028449; PMID:1409637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: sequence extracted from NCBI backbone (NCBIN:115887, NCBIP:115889)
R;Aaronson, S.A.; Bottaro, D.P.; Miki, T.; Ron, D.; Finch, P.W.; Fleming, T.P.; Ahn, J.,
Mnn. N. Y. Acad. Sci. 634, 62-77, 1991
A;Title: Keratinocyte growth factor. A fibroblast growth factor family member with unust
A;Reference number: 151958; MUID:92152720; PMID:1664700
                                                                                                                                                              A,Molecule type: mRNA
**Residues: 1-194 <FINA
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A;Title: Human KGF is FGF-related with properties of a paracrine effector of epithelial
A;Reference number: A36301; MUID:89368897; PMID:2475908
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A;Note: the human genome contains about 16, intron-containing, partial copies C;Superfamily: fibroblast growth factor
C;Keywords: extracellular protein; growth factor; heparin binding; mitogen F;1-31/bomain: signal sequence #status predicted <81G>
F;1-31/bomain: signal sequence #status predicted <81G>
F;2-194/Product: fibroblast growth factor 7 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Daccession: A48834; S2536;
C;Accession: A48834; S2536;
Berja, A.Z.; Meijers, C.; Zeller, R.
A;Tille: Expression of alternatively spliced bFGF first coding exons and ant A;Reference number: A48834; MUID:93246053; PMID:7683281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAAD-QSPESLLQLKALKPGVIQILGVKTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 RFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GDB:131444; OMIM:148180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPGNKSPHRDPAPRGPARFLPL 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 97-194 < KEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Status: preliminary
A, Molecule type: nuclei
A, Residues: 1-189 < BOR>
A, Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-194 <AAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Accession: 151958
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                                                                                                                  A; Accession: A36301
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(Species: Mus musculus (house mouse)
(Species: Mus musculus (house mouse)
(Species: Musculus) (house mouse)
(Species: Musculus) (1996
(Spacession: 148610; S33227
(Spacession: 148610; S33227
(Spacession: 148610; S33227
(Spacession: 148610; Mullor-bace, F.; Smith, R.; Dickson, C.
Mch. Dev. 45, 15-30, 1994
A;Title: FGF-7 (keratinocyte growth factor) expression during mouse development suggests A;Accession: 148610
A;Accession: 148610
A;Status; preliminary; translated from GB/EMBL/DDBJ
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          20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999
                                                      CyAccession: S4950;
RyMitchell, J.E.A.; McInnes, C.J.
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A;Cross-references: EMBL:Z22703; NID:g297755; PIDN:CAA80403.1; PID:g297756
C;Superfamily: fibroblast growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 RFLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQS-
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Best Local Similarity 26.8%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 38; Conserv
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NyAlternate names: endothelial cell growth factor
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 0.3-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 16-Jul-1999
C;Accession: A60130; 802639
R;Schnuerch, H.; Risau, W.
Development 111, 1143-1154, 1991
A;Fitle: Differentiating and mature neurons express the acidic fibroblast growth factor (A;Reference number: A60130; MUID:91347925; PMID:1715259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:S63263; NID:g234372; PIDN:AAB19629.1; PID:g234373
R;Risau, W.; Gautschi-Gova, P.; Boehlen, P.
B;Bsau, W.; Gautschi-Gautschi-BsB
A;Title: Endothelial cell growth factors in embryonic and adult chick brain are related the A;Reference number: S02639; MUID:88296438; PMID:3402441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 39
S31622
basic fibroblast growth factor - short-tailed opossum (Monodelphis domestica) (fragment)
C;Species: Monodelphis domestica
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C;Accession: S31622
                                                                                                              comment: This protein is a potent mitogenic factor for NIH 3T3 fibroblasts in the absens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
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                                                                                                                                                                                                                                                                         ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 KISRFLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLP---LHLPGNKSPH 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 ETGQFLAMDTNGLLYGS-QTPSEECLFLERLEENHYNTYISKKHAEKNWFIGLKKNGSSK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74
                                                                                                                                                                                                                                                                                                                               38 LOFGGOVRORYLYTDDAQOTEAHLEIREDGTVGGAADQSPESL-LQLKALKPGVIQILGV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 LQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESL-LQLKALKPGVIQILGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 LPLGNYKKPKLLYCSNGGH---FLRILPDGKVDGTRDRSDQHIQLQLSAEDVGEVXIKST
                                                                                                                                                                                                                                                                                                                                                                                           18 LPLGNYKKPKLLYCSNGGY---FLRILPDGRVDGTKDRSDQHIQLQLYARESIGEVYIKST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                             11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
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11.5%; Score 127.5; DB 2; Length 155;
Best Local Similarity 32.6%; Pred. No. 0.0027;
Matches 45; Conservative 15; Mismatches 67; Indels 11
                                                                                                                                                                                                          Length 155;
                                                                                                                                                                                                                                                                             Indels
   A;Reference number: JW0055; MUID:98262939; PMID:9600090
                                                                                                                                                                                                                Score 131.5; DB 2;
Pred. No. 0.0013;
4; Mismatches 67;
                                                                                                                                                                                                                                                                             14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 22-30,'X',32-44,'X',46-48 <RIS>
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acidic fibroblast growth factor - chicken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 LGPRTHYGOKAILFLPLP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 RDPAPRGPAR---FLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 LGPRTHFGOKALLFLPLP 151
                                                                                                                                                                                                                       11.8%;
                                                                                                                                                                                                                                                Best Local Similarity 33.3%
Matches 46; Conservative
                                  A;Accession: JW0055
A;Molecule type: mRNA
A;Residues: 1-155 <GRI>
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A;Residues: 1-155 <SCH>
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                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-Jan-2001
C;Accession: JW0055
R;Grieb, T.W.; Ring, M.; Brown, E.; Palmer, C.; Belle, N.; Donjerkovic, D.; Chang, H.; Y
Biochem. Biophys. Res. Commun. 246, 182-191, 1998
A;Title: Primary structure of ovine fibroblast growth factor-1 deduced by protein and cD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell 51, 869-877, 1987
A;Title: Synergistic induction of mesoderm by FGF and TGF-beta and the identification of
A;Reference number: A29618; MUID:88052890; PMID:3479265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           natural
A;Note: sequence extracted from NCBI backbone (NCBIN:131000, NCBIP:131001)

B;Mitrani, E.; Gruenbaum, Y.; Shohat, H.; Ziv, T.

Development 109, 387-393, 1990

A;Title: Fibroblast growth factor during mesoderm induction in the early chick embryo. A;Reference number: S23636, MUID:90382254; PMID:2401202

A;Accession: S23636

A;Accession: Preliminary

A;Nolecule type: DNA

A;Nolecule type: AMT>

A;Residues: 95-128 <AMT>

A;Cross-references: EMBL:X56804; NID:g62855; PIDN:CAA40139.1; PID:g62856

C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-155 <KIM>
A;Cross-references: GB:M18067; NID:g214177; PIDN:AAA49726.1; PID:g214178; GB:M21092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   basic fibroblast growth factor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A40117; A25618
R;Kimelman, D.; Abraham, J.A.; Haaparanta, T.; Palisi, T.M.; Kirschner, M.W.
A;Title: The presence of fibroblast growth factor in the frog egg: its role as a 1A;Reference number: A40117; MUID:89058621; PMID:3194757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRINPDGRVDGVREKSDPHIKLQLQAEERGVVSIKGVSANRFLAMKEDGRLL-ALKCATE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LEIREDGTVGGAADQS-PESLLOLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 ECFFFERLESNNYNTYRSRKYS-DWYVALKRIGGYKPGPKIGPGGKALLFLPM 185
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.4%; Score 138; DB 2; Length 189;
Best Local Similarity 35.4%; Pred. No. 0.0005;
Matches 40; Conservative 18; Mismatches 47; Indels
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A, Residues: 95-110,112-155 <KI2>
C, Superfamily: fibroblast growth factor
C, Keywords: growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Kimelman, D.; Kirschner, M.
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A40117
A; Status: preliminary
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A,Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A,Reference number: A75000; MUID:99069613; PMID:9851916
A,Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A,Note: published errata appeared in Science 283, 35, 1999; $\overline{\text{G}}\end{\text{G}} = 0.03, 1999; and A,Accession: H88481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB:chr_III; PIDN: AAB53825.1; PID:9485091; GSPDB:GN00021; CESP: C05D1
R;Kusewitt, D.F.; Sabourin, C.L.K.; Budge, C.L.; Ley, R.D. submitted to the EMBL Data Library, September 1992
A;Description: Characterization of cDNA encoding basic fibroblast growth factor of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 ----DGSTRVKVH-------GTKEESSKFSIVEFVSVAMSLVSIRGVETKNFICMDPS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LEIREDGTVGGAADQS-PESTLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 YLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 GALYG--SLHFDPEACSFRELLLEDGYNVYQSEAHG---LPLHLPGNKS--PHRDP---A 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 GKLYATPSSNYSTE-CVFLEEMMENYVNLYASCAYGDRENPWYIELRRSGKPRRGPNSKK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein let-756 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: H88481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 DSDETG------PEHSGLWVSVLAGLLLGACQAHPI--PDSSPLLQFGGQVRQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         45; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 ECFFFERLESNNYNTYRSRKYSNWYVALKRTGQ---YKLGSKTGPGQKAILFLPM 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 ACSFRELLLEDGYNVYQSEAHG---LPLHLPGNKSPHRDPAPRGPAR----FLPL 167
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                                                                                                                                                                                                                                                                                                                                        Query Match
11.4%; Score 127; DB 2; Length 164;
Best Local Similarity 33.9%; Pred. No. 0.0032;
Matches 39; Conservative 19; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
11.1%; Score 124; DB 2, Length 413;
Best Local Similarity 24.6%; Pred. No. 0.016;
Matches 56; Conservative 28; Mismatches 66; Indels '
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                                                                                                                       A,Accession: S31622
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-164 <KUS>
A,Cross-references: BMBL:215154
C,Superfamily: fibroblast growth factor
                                                                                             A; Reference number: S31622
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A,Molecule type: DNA
A,Residues: 1-413 <STO>
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Gene: let-756
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Query Match 100.0%; Score 89; DB 4; Length 209; Best Local Similarity 100.0%; Pred. No. 5.9e-06; Matches 15; Conservative 0; Mismatches 0; Indels
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Sequence 31822, A
Sequence 22856, A
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Sequence 22, Appl Sequence 24, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22114, A Sequence 22114, A Sequence 22115, A Sequence 26115, A Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 20229, A Sequence 20229, A Sequence 20229, A Sequence 20229, A Sequence 28601, A Sequence 28601, A	lypeptides	<pre>Length 181; Indels 0; Gaps 0; Polypeptides</pre>
US-08-425-876-22 US-08-425-876-24 US-08-426-243-24 US-08-426-243-24 US-08-401-632-22 US-08-401-632-24 US-09-252-991A-22814 US-09-252-991A-22814 US-09-252-991A-22135 US-09-252-991A-22135 US-09-123-343A-7 US-09-431-573-4 US-09-431-573-4 US-09-431-573-6 US-09-431-573-6 US-09-252-991A-30229 US-09-252-991A-30229 US-09-252-991A-3750 US-09-252-991A-3750	ALIGNMENTS 2.6 5, Application US/09390207 3.6 10.6504530 3.1 INFORMATION: ANT: Thomson, Arlen ANT: Thomson, Arlen ANT: Thomson, Arlen CR. INVENTION: Phiroblast Growth Factor-Like Polypeptides BERERENCE: 99-371 TR. APPLICATION NUMBER: US/09/390,207 TY FILING DATE: 1999-09-07 TO SEQ ID NOS: 41 RE: PATHING PATE: 1999-09-07 NO S: THE PATE THE PATE THE THE PATE	ore 89; DB 4; Leed. No. 5.1e-06; Mismatches 0; Wth Factor-Like Po
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	A Application US/09390207 5. 4504530 NFORMATION: TI Thomason, Arlen TI: Liu, Benxian TI: Liu, Benxian TRENCE: 99-371 APPLICATION NUMBER: US/09/ APPLICATION NUMBER: US/09/ RILING DATE: 1999-09-07 PRING DATE: 1999-	100.0%; Sc Similarity 100.0%; Pr 5; Conservative 0; HLPGNKSPHRDPAR 15 HLPGNKSPHRDPAR 131 Application US/09390207 5504530 NRATION: Thomason, Arlen Liu, Benxian VENTION: Fibroblast Gro WENTION: Fibroblast Gro WENTION Fibroblast Gro VENTION Fibroblast Gro STRCE: 99-371 JING DATE: 1999-09-07 STROEN DATE: 1999-09-07
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Application Application CORMATION: Thomason, Ar Thum Benxian ILIU, Benxian FELICATION NUM FELICATION NUM FELICATION NUM FELICATION NUM FELICATION NUM FELICATION NUM FELICATION NUM FELING DATE: 19 SEQ ID NOS: 4 Patent In Ver. [81] F. Homo sapiens	natch 100 15; Conservative 101 11; Conservative 117 HIPGINKSPHENDPAPR 117 HIPGINKSPHENDPAPR 117 HIPGINKSPHENDPAPR 117 HIPGING 105, Application US/No. 6504530 INFORMATION: Thomason, Arlen NANT: Liu, Benxian OF INVENTION: Fibrob ERFERINGE: 99-371 THE APPLICATION WUMBER IT APPLICATION NUMBER IT APPLICATION NUMBER IT APPLICATION NUMBER IT APPLICATION NUMBER IT SEQ ID NOS: 41 100 PRINCE PREQ ID NOS: 41 100 PRINCE PREQ ID NOS: 41 100 PRINCE PREQ ID NOS: 41 100 PRINCE PREQ ID NOS: 41 100 PRINCE PREQ ID NOS: 41
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PACENT NO. 8-51/95
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29952
LENGTH: 286
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FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

NUMBER OF SEQ ID NOS: 33142
    TITLE OF INVENTION: ALCELIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18109
LENGTH: 187
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Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 53.3
Matches 8; Conservative
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US-09-252-991A-29952
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APPLICANT:
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Sequence 31822, Application US/09252991A

Sequence 31822, Application US/09252991A

Sequence 31822, Application US/09252991A

Sequence 31822, Application US/09252991A

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR PEDICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1988-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 1419
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: MATC J. Rubenfield et al.

APPLICANT: MATC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22856

LENGTH: 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 22856, Application US/09252991A ; Patent No. 6551795
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US-09-252-991A-31822
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Best Local Similarity 66.7'
Matches 10; Conservative
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Best Local Similarity
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US-09-252-991A-22856
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Sequence 23280 Application US/09252991A

Sequence 23280 Application US/09252991A

Sequence 23280 Application US/09252991A

Sequence 23280 Application US/09252991A

Patent No. 6521795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUGUST CACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AUGUST CACID AND THERAPEUTICS

FILE REFERENCE: 10716-136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 23280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARENTAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 60/094,190
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24235
LENGTH: 632
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Pred. No. 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ed. No. 63;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.3%; Score 45; 53.3%; Pred. No. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.6%;
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Best Local Similarity 55...
Best Accordance 8; Conservative
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Alonso, Jose
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81 PGGRATHPDPAP 92
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Matches 8; Conserv
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US-09-252-991A-24235
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                                                                                          RESULT 10
US-09-252-991A-23280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-819-288-3
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US-09-252-991A-30648

Sequence 30648, Application US/09252991A

Sequence 30648, Application US/09252991A

Sequence 30648, Application US/09252991A

Patent NO. 6551795

GENERAL INFORMATION:

APPLICATION WOLLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ALRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ALRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PLILNG DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
SEQ ID NO 25644
LENGTH: 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 4; Length 330;
Pred. No. 23;
                                                                                                                                        Score 46; DB 4; Length 307; Pred. No. 21;
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                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25664, Application US/09252991A Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                         TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                             Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity
'Lng 7; Conserv
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                                                                                                    US-09-252-991A-21588
                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-09-252-991A-25664
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              ; SEQ ID NO 21588
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APPLICANT:

3 PGNKSPHRDPAP 14

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Score 45; DB 4; Length 1294; Pred. No. 1.4e+02;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
              NAME: BEATCELL, ________34,293
RECISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3439
"WILEPAK: 215-568-3439
Beardell, Lori Y.
                                                                                                         TELEFAX: 215-568-3433
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1294 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                              50.68;
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Best Local Similarity 61.5'
Matches 8; Conservative
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Best Local Similarity 61.5'
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                                                                                                                                                                                                        TOPOLOGY: linear;
MOLECULE TYPE: protein
US-09-400-348-3
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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USA
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US-08-261-822A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-261-822A-3
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                                                                                                                                                                                                                                                                                                                                                                                                               임
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APPLICANT: Ecker, Joseph
APPLICANT: Alonso, Jose
TITLE OF INVENTION:
TITLE OF INVENTION: PLANT GENES FOR SENSITIVITY TO ETHYLENE
TITLE OF INVENTION: AND PATHOGENS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSES: Mondcock Washburn Kurtz Mackiewicz & No. 6355778ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STREET: PA
                            TITLE OF INVENTION: PLANT GENES FOR SENSITIVITY TO ETHYLENE TITLE OF INVENTION: AND PATHOGENS NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
STREEF: WoodGoock Washburn Kurtz Mackiewicz & No. 5955652ris STREET: One Liberty Place - 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 2; Length 1294;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOPTWARE: Patentin Release #1.0, Version #1.30 CURENT APPLICATION DATA: APPLICATION NUMBER: US/09/400,348
                                                                                                                                                                                                  ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CONTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/819,288
                                                                                                                                                                                                                                                                                                                                                                                                                                                            UPN-2949
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 3, Application US/09400348
; Patent No. 6355778
                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REPRENCE/DOCKET NUMBER: UPN-Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1294 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / TOPOLOGY: linear
// MOLECULE TYPE: protein
US-08-819-288-3
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US-09-400-348-3
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Sequence 3, Application US/08261822A
Sequence 3, Application US/08261822A
Patent NO. 5650553
GENERAL INFORMATION:
APPLICANT: ECKEY, JOSEPH R. et al.
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
TITLE OF INVENTION: and Pathogens
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5650553ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             °;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.6%; Score 45; DB 1; Length 1321; 61.5%; Pred. No. 1.4e+02; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/261,822A
FILING DATE: 17-UN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: Beardall, Lori Y.

REGISTRATION NUMBER: 34,293
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Sequence 27502, Application US/09252991A

Sequence 27502, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
THE REPREDICATION NUMBER:
TO SO (074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

WOWHER OF SEQ ID NOS: 33142

LENGTH: 441
                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                                 DB 4; Length 372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.4%; Score 44; DB 4; Length 372; 42.9%; Pred. No. 51;
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                                                                                                            Indels
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                                                            Query Match
Best Local Similarity 56.2%; Pred. No. 43;
Matches 9; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                  Sequence 23226, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 HLPGADRRHLHRAPHORPAGR 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32717
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216 PGGEDPHRRPRGPAPR 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GNKSPHRD----PAPR 15
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                                                                                                                                                               3 PGNKSPH---RDPAPR 15
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Best Local Similarity 56.2
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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US-09-252-991A-23226
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
APPLICANT: MAC J. RUBENFICH.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3217
TYPE: PRT
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                                                                                                                    APPLICANT: Trustees of The University of Pennsylvania TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene TITLE OF INVENTION: and Pathogens WUMBER OF SEQUENCES: 82 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                     ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris STREET: One Liberty Place, 46th floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLING DATE: 15-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 5; Le:
Pred. No. 1.4e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 32717, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,822
FILLING DATE: June 17, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
RELEGISTRATION NUMBER: 34,293
TELEPHONE: (215) 568-3100
TELEPRAY: (215) 568-310
INFORMATION FOR SEG ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                          PCT-US95-07744A-3; Sequence 3, Application PC/TUS9507744A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.6%;
ilarity 61.5%;
Conservative 2
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         939 HLPNNKSGYWDPS 951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                              19103
                                                                                                                                                                                                                                                                                             CITY: Phil
STATE: PA
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Pred. No. 77;
                                                               Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/07/999,280A
FILING DATE: 28-DEC-1992
CLASSIFICATION: 435
                                                             Score 44; DB 1;
Pred. No. 77;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHIRON CORPORATION Intellectual Property - R440, P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 28-DEC-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Philip L.
REGIGTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681.007
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                              Sequence 24, Application US/07999280A
Patent No. 5573930
GENERAL INFORMATION:
APPLICANT: LADNER, MARTHA B.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: MARSARIN, ENNEST S.
APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLC, NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22, Application US/08426279; Patent No. 5672343; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: n/a
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LADNER, MARTHA B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
                                                                   49.4%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          552 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 PASASPHQPPAP 213
                                                 Query Match 49.4
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                202 PASASPHOPPAP 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-07-999-280A-24
                                                                                                                                                  3 PCNKSPHRDPAP 14
, MOLECULE TYPE: protein US-07-999-280A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Emveryville STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 94662-8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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US-08-426-279-22
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                                                   Sequence 8325, Application US/09489039A

Sequence 8325, Application US/09489039A

Sequence 8325, Application US/09489039A

Sequence 8325, Application US/09489039A

PERENT No. 6610836

APPLICANT: APPLICANTON:
APPLICANTON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 2709,2004001

CURRENT PILLING DATE: US/09489,039A

CURRENT FILLING DATE: US/00-01-27

PRIOR FILLING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 8325

LENTH: 490
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APPLICANT: LADNER, MARTHA B.
APPLICANT: NOBLE, JANELLE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: COYNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: NEW FORMS OF COLONY STIMULATING FACTOR-1
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.4%; Score 44; DB 4; Length 490; 46.7%; Pred. No. 68; tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Intellectual Property - R440, P.O. Box 8097
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: BATEMIN PC-DOS/WS-DOS

SOFTWARE: PATEMIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/999,280A

FILING DATE: 28-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 28-DEC-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681.007
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/07999280A
Patent No. 5573930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHIRON CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (510) 601-2718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 YLSGERTPHNDPDAR 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 552 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 HLPGNKSPHRDPAPR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: n/a
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
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California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-489-039A-8325
                                                          US-09-489-039A-8325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 20
US-07-999-280A-22
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US-08-401-013-22

J Sequence 2.2, Application US/08401013

Patent No. 5681719

GENERAL INFORMATION:

APPLICANT: IADBLE, MARTHA B.

APPLICANT: MARTHA, GEORGE A.

APPLICANT: MARTHA, GEORGE A.

APPLICANT: MARTHA, GEORGE A.

APPLICANT: AMASAKI ERNEST S.

APPLICANT: KOYNE, WILE YEE

APPLICANT: ACONDE, MARTHA F.

APPLICANT: ACONDE, MARTHA B.

APPLICANT: ACONDE, MARTHA B.

APPLICANT: MARTHA, GEORGE A.

APPLICANT: MARTHA, GEORGE A.

APPLICANT: MARTHA, GEORGE A.

APPLICANT: ACONDE, MARTHA B.

APPLICANT: MARTHA, GEORGE A.

APPLICANT: MARTHA B.

APPLICANT: MARTHA B.

ANDRESSEE: CHIRON CORPORATION

STREE: California

COUNTY: Enveryville

STATE: California

CONFUTER: LIM PC COMPATIBLE

CONFUTER: LIM PC COMPATIBLE

CONFUTER: LIM PC COMPATIBLE

CONFUTER: LIM PC COMPATIBLE

CONFUTER: PATENTION BATA:

APPLICATION NUMBER: US 07/999,280

FILING DATE: 28-DEC-1992

ATTORNEY/AGENT: NUMBER: US 07/999,280

FILING DATE: 28-DEC-1992

ATTORNEY/AGENT: NUMBER: US PATIBLE

REGISTRATION NUMBER: 31,395

REGISTRATION NUMBER: 13,395

REGISTRATION NUMBER: 13,395

REGISTRATION NUMBER: 13,395

REFERENCE/POCKET NUMBER: 068-1007

PRICE APPLICANT NUMBER: 13,395

REFERENCE/POCKET NUMBER: 13,395
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                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,279
FILING DATE: 21-APR-1995
CLASSIFICATION: 530
ATTOMENYAGENT INPORMATION:
NAME: MCGARTIGHE JT. Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 31,395
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (510) 601-2718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION TELEPHONE: (510) 601-2718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: n/a
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (510) 655-3542
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INFORMATION FOR SEQ ID NO:
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Matches 7; Conservative
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MOLECULE TYPE: protein
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US-08-401-013-22
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| Sequence 24, Application US/08426279 |
| Patent No. 5672343 |
| GENERAL INFORMATION |
| APPLICANT: NOBLE, JANELLE A. |
| APPLICANT: MASTIN, GEORGE A. |
| APPLICANT: MASTIN, GEORGE A. |
| APPLICANT: MASTIN, GEORGE A. |
| APPLICANT: MAISTIN, GEORGE A. |
| APPLICANT: MAISTIN, GEORGE A. |
| APPLICANT: KOTHE, MAZIE YEE |
| APPLICANT: KOTHE, KIRSTON E. |
| TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1 |
| NUMBER OF SEQUENCES: 24 |
| NUMBER OF SEQUENCES: 24 |
| NUMBER OF SEQUENCES: 24 |
| STREET: Intellectual Property - R440, P.O. Box 8097 |
| STREET: Intellectual Property - R440, P.O. Box 8097 |
| STREET: MAISTING A. |
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| STREET: MAISTING A. |
APPLICANT: NOBLE, JANELLE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KORMSARI, ENDEST S.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: MAZIE YEE
TITLE OF INVENTION: UNW FORMS OF COLONY STIMULATING FACTOR-1
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORRESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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49.4%; Score 44; DB 1; Length 552;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Intellectua.

STREET: Emberyville

CITY: Emveryville

COMPUTER: California

COMPUTER: Toppy disk

COMPUTER: PADABLE FORM:

MEDUIM TYPE: Flopy disk

COMPUTER: DADABLE FORM:

MEDUIM TYPE: Flopy disk

COMPUTER: DADABLE FORM:

MEDUICATION NUMBER: US/08/426,279

FILING DATE: 21-APR-1995

CLASSIFICATION: 530

ATTORNEY/AGART INFORMATION:

NAME: McGarrigle Jr., Philip L.

REGISTRATION NUMBER: 0681.013

FELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (510) 655-3542
TELEK: n/a
INFORMATION FOR EXG ID NO: 22:
SEQUENCE CHARACTERISTICS:
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amino acid
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202 PASASPHQPPAP 213
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STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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TOPOLOGY:
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US-08-426-570-24
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                                                                                                    Score 44; DB 1; Length 552;
Pred. No. 77;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Intellectual Property - R440, P.O. Box 8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 0681.007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: McGarrigle Jr., Philip L. REGISTRATION NUMBER: 31,395
                                                                                                                                                                                                                                                                                                                        APPLICANT: LADNER, MARTHA B.
APPLICANT: NOBLE, JANELLE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: CONNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON E.
                                                                                                                                                                                                                                                                          Sequence 24, Application US/08401013; Patent No. 5681719; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHIRON CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: n/a
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                         Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 552 amino acids
amino acid
         LENGTH: 552 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-401-013-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : |||: |||
202 PASASPHQPPAP 213
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Matches 7; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                      3 PGNKSPHRDPAP 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Intellectucing CITY: Emveryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
COUNTRY: U.S.A.
ZIP: 94662-8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-401-013-24
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Gaps
                                                   GENERAL INFORMATION:
APPLICANT: LADNER, MARTHA B.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KAMASAKI, ERNEST S.
APPLICANT: KAMASAKI, ERNEST S.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1.
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
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APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.4%; Score 44; DB 3; Length 552; 58.3%; Pred. No. 77; ive 2; Mismatches 3; Indels
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Intellectual Property - R440, P.O. Box 8097
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.

ZIP: 94662-8097

ZIP: 94662-8097

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,570
FILING DATE: 21-APR-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 0661.012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Philip L.
REGISTRATION NUMBER: 31,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/08426570 Patent No. 6103224
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GENERAL INCORATION:
APPLICANT: IADNER, MARTHA B.
APPLICANT: NOBLE, JANELLE A.
APPLICANT: KAWASALI, ERNEST S.
APPLICANT: CAWASALI, ERNEST S.
APPLICANT: COUNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON E.
Sequence 22, Application US/08426570 Patent No. 6103224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 552 amino acids
amino acid
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Best Local Similarity 58.3 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: n/a
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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Gaps
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APPLICANT: NOBLE, JANELLE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KAMASKIT, ERNEST S.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: NOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

49.4%; Score 44; DB 3; Length 552;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 3; Length 552; Pred. No. 77;
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STREET: Intellectuat ...
CITY: Enveryville
STATE: California
COUNTRY: C.3.A.
ZIP: 94662-8097
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: 131-395
CLASSIFICATION NUMBER: US/08/425,876
FILING DATE: 21-APR-1995
CLASSIFICATION NUMBER: US/08/425,876
FILING DATE: 31-APR-1995
CLASSIFICATION NUMBER: 0581.011
REGISTRATION NUMBER: 0681.011
TELEPHANE: (510) 655-3542
TELEFAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/08425876 Patent No. 6117422 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (510,
TELEFAX: (510,
TELEX: n/a
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
"""": amino acid
"""": amino acid
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
(510) 601-2718
                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 PASASPHOPPAP 213
                                   (510) 655-3542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 PASASPHQPPAP 213
                                      TELEFAX: (510) 655-354
TELEX: n/a
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-425-876-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 PGNKSPHRDPAP 14
                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-08-425-876-22
   TELEPHONE:
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APPLICANT: NOBLE, JANELLE A.
APPLICANT: NOBLE, JANELLE A.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: KAMASAKI, ERBERT F.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON B.
APPLICANT: KOTHS, KIRSTON B.
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Pred. No. 77;
2; Mismatches 3; Indels
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STREET: Intellectual Property - R440, P.O. Box 8097
CITY: Enveryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,876
FILING DATE: 21-APR-1995
CLASSIFCATION: 435
ATTORNEY/A-TIVE
                                                                                                                                                           CAPIT: 94067-5037

CAPIT: 94067-5037

MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,570
FILING DATE: 21-APR-1995
CLASSIFICATION: 530
ATTONEY/AGENT INFORMATION:
NAME: MCGATTIGLE UT., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 31,395
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10FORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: MCGATYGIG Jr., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681.011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/08425876
Patent No. 6117422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: (510) 655-3542
TELEX: n/a
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.4%;
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amino acid
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Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-08-426-570-24
                               Emveryville
                                                                  California
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                                                                                                     RY: U.S.A. 94662-8097
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                                                                                                             COUNTRY:
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APPLICANT: LADNER, MARTHA B.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: COYNE, MAZIE YEE
APPLICANT: HALENBESCK, ROBERT F.
APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 3; Length 552; Pred. No. 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
CITY: Emveryville
STATE: California
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS
ADDRESSE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
CITY: Enveryville
STATE: California
CONTRY: U.S.A.
ZIP: 94662-8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                         SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 77;
2; Mismatches
                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 07/999,280
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Philip L.
REGISTATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681.007
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-401-632-22; Sequence 22, Application US/08401632; Patent No. 6204020; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNA.
TELEPHONE: (510,
TELEFAX: (510) 655-35**
TELEFAX: n/a
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
""PR: amino acids
""PR: amino acids
""PR: amino acids
""PR: amino acids
                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 49.4
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 PGNKSPHRDPAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-426-243-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 94662-8097
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                                                                                           Sequence 22, Application US/08426243

Patent No. 6146851
GENERAL INFORMATION.
APPLICANT: LADNER, MARTHA B.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KAMSAKI, ENGER A.
APPLICANT: KAMSAKI, ENGER S.
APPLICANT: KAMSAKI, ENGER F.
APPLICANT: KOTHE, MARTHY WEE
APPLICANT: KOTHE, KOTHE, KOBERT F.
APPLICANT: KOTHE, KRETON E.
TITLE OF INVENTION: MEW FORMS OF COLONY STIMULATING FACTOR-1
NUMBER OF SEQUENCES: 24
CORRESPONDENCE MUDICES.
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IIILE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.4%; Score 44; DB 3; Length 552; 58.3%; Pred. No. 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94662-8097

ZIP: 94662-8097

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/999,280
APPLICATION NUMBER: 07/999,280
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
RAME: MGGARTIGLE V., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0691.007
TELECHONE: (510) 601-2118
TELEPHONE: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24, Application US/08426243;
Patent No. 6146851;
GENERAL INFORMATION:
APPLICANT: LADJUER, MARTHA B.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
                                                                                                                                                                                                                                                                                                                                                                                   CHIRON CORPORATION
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amino acid
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Best Local Similarity 58.3-
Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 PASASPHQPPAP 213
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Emveryville STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 31
US-08-426-243-24
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                                                                  RESULT 30
US-08-426-243-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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Gaps

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NEGLOR 252-991A-26118

Sequence 26118, Application US/09252991A

Sequence 26119, Application US/09252991A

Sequence 26119, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE REFERENCE: 107196.136

CURRENT PRELATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26118

LENGTH: 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: MAIC J. Rubenfield et al.

APPLICANT: MAIC J. Rubenfield et al.

APPLICANT: MAIC J. RUBENFIC AND AND ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22814

LENGTH: 172
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  Length 552;
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1 Similarity 64.7%; Pred. No. 31;
11; Conservative 1; Mismatches
Query Match
49.4%; Score 44; DB 3;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 49.4%;
Best Local Similarity 53.8%;
Matches 7; Conservative 2
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                                                                                                                                               202 PASASPHOPPAP 213
                                                                                                    3 PGNKSPHRDPAP 14
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Matches 11; Conserv
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US-09-252-991A-22135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
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APPLICANT: NOBLE, JANELLE A.
APPLICANT: NARTIN, GEORGE A.
APPLICANT: KAWASAKI, ERREST S.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 3; Length 552;
Pred. No. 77;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSER: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
CITY: Buveryville
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/401,632
FILING DATE: 09-MAR-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/POCKET NUMBER: 0681.009
TELECOMMUNICATION INFORMATION:
                                     CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: McGARTIGLE C., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681.009
TELECOMUNICATION INFORMATION:
TELEFHONE: (510) 601-2718
TELEFAC: (510) 655-3542
TELEX: n/a
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP. 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24, Application US/08401632
Patent No. 6204020
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INFORMATION FOR SEQ ID NO: 24:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.4%;
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                    09-MAR-1995
                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 PASASPHOPPAP 213
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Matches 7, Conservative
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                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-401-632-22
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                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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US-08-401-632-24
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APPLICANT: Steller, Hermann
APPLICANT: Abrams, Othn M.
APPLICANT: Abrams, Othn M.
APPLICANT: Grether, Megan E.
APPLICANT: White, Kristin
TITLE OF INVENTION: Cell Death Genes of Drosophila
TITLE OF INVENTION: Melanogaster and Vertebrate Analogs
TITLE OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
CITY: Lexington
CONTRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.3%; Score 43; DB 1; Length 410; 63.6%; Pred. No. 79; 1.ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,343A
FILING DATE: 17-SEP-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/004,957
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                         MEDIUM TYPE: FIOPPY GIBN COMPUTER: FIOPPY GIBN COMPUTER: IBN PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Parentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/123,343A FILING DATE: 17-SEP-1993 CLASSIFICATION NUMBER: US 08/004,957 FILING DATE: 1-5EP-1993 ATTORNEY/AGENT INPORMATION: NAME: GRANDAL INPORMATION: NUMBER: 32,227 REFERENCE/DOCKET NUMBER: MIT-5907A TELEPRATION NUMBER: 32,227 REFERENCE/DOCKET NUMBER: MIT-5907A TELEPRATION NUMBER: 32,227 REFERENCE/DOCKET NUMBER: MIT-5907A TELEPRATION NUMBER: STORMETON: 618-61-6240 INPORMATION: 618-61-6240 INPORMATION SEQUENCE GHRANCTERISTICS: LENGTH: 410 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08123343A Patent No. 5593879
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 GNSSPHNHPLP 34
                                                                                            COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                    Lexington
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                                                      CITY: Lex:
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-123-343A-5
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Sequence 22135, Application US/0925291A
Patent No. 6551795
GENERAL INFORMATION:
HENDERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
PRIOR PERCENCE:
PRIOR APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PELING DATE: 1999-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MAIC J. Rubenfield et al.

APPLICANT: MAIC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26571

LENGTH: 356
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Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 4; Length 247; Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Cell Death Genes of Drosophila IIILE OF INVENTION: Melanogaster and Vertebrate Analogs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-123-343A-5; Sequence 5, Application US/08123343A; Patent No. 5593879; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Steller, Hermann
Abrams, John M.
Grether, Megan E.
White, Kristin
                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 53.33
Matches 8; Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 37
US-09-252-991A-26571
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APPLICANT:
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APPLICANT:
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Sequence 4, Application US/09431573

Patent No. 6235524

GENERAL INFORMATION:

APPLICANT: STELLER, HERMAN

APPLICANT: AGAPITE, JULIE

APPLICANT: MCALL, KINBERRIS

TITLE OF INVENTION: INHIBIT MAPK MEDIATED ANTI-APOPTOTIC SIGNALS

TITLE OF INVENTION: INHIBIT MAPK MEDIATED ANTI-APOPTOTIC SIGNALS

TITLE OF INVENTION INMERS: US/09/431,573

CURRENT FILING DATE: 1999-10-29

PRIOR PPLICATION NUMBER: 60/106,108

PRIOR FILING DATE: 1998-10-29

NUMBER OF SEQ ID NOS: 5

SEQ ID NO 4

LENGTH: 410
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Best Local Similarity 63.6%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 4; Indels
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Best Local Similarity 63.6%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 4; Indels
FILING DATE: 15-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: GRAINAIN, PATICIA

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: MIT-5907A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEPHONE: 617-861-6240

TELEPHONE: G17-861-6240

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 410 amino acids

TYPE: amino acid

STRANDENESS: unknown

MOLECULE TYPE: protein

WOLECULE TYPE: protein

US-08-123-343A-7
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US-09-431-573-4
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US-09-431-573-4
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Search completed: March 2, 2004, 16:09:02 Job time : 3.6875 secs

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ORGANISM: Homo sapiens
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Matches 16; Conserv
100.00
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US-09-901-938-33
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US-10-060-765-7
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Sequence 33, Appl
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                                                                                           2, 2004, 16:07:28; Search time 5.4 Seconds (without alignments) 625.639 Million cell updates/sec
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-755-695-2

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US-10-237-884-78

US-10-230-338-78

US-10-230-338-78

US-10-218-631-78

US-10-218-849-78

US-10-218-849-78

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Maximum Match 100%
Listing first 45 summaries
                                                                   OM protein - protein search, using sw model
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US-10-227-881-78

US-10-23-25-78

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US-10-23-25-78

US-10-23-225-78

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US-10-23-225-78
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Sequence 7, Application US/10060765 publication No. US20020164713A1 GENERAL INFORMATION: APPLICANT: Itch, No. US20020164713A1uyuki APPLICANT: Itch, No. US20020164713A1uyuki APPLICANT: Itch, No. US20020164713A1uyuki TITLE OF INVENTION: HUMAN FCP-21 GENE AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS FILE REFERENCE: PP-16758.001/201130.408 CURRENT APPLICATION NUMBER: US/09/715,805 PRIOR APPLICATION NUMBER: US/09/715,805 NUMBER OF SEQ ID NOS: 17 SOFTWARE: FASTERE for Windows Version 4.0 SEQ ID NO? SEQ ID NO?

Gaps ·. Length 16; Indels 100.0%; Score 86; DB 13; 100.0%; Pred. No. 4.8e-08; tive 0; Mismatches 0; 16; Conservative

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1 RORYLYTDDAOOTEAH 16 1 RORYLYTDDAQOTEAH Sequence 33, Application US/09901938
Patent No. US20020156001A1
GENERAL INFORMATION:
APPLICANT: ECONS, Michael
APPLICANT: WHITE, Kenneth

Gaps

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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Suith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
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APPLICANT: ACIDS ENCODING THE SAME
FILE REPREBRE: PS330PLT79
CURRENT APPLICATION NUMBER: US/10/227,884
CURRENT FILING DATE: 2002-08-26
                                                                                                                                                                                                        Length 208;
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                                                                                                                                                                                                        Query Match
100.0%; Score 86; DB 9; I
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 208
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PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-10-18
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PRIOR PILING DATE: 1997-10-31
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Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Baker, Kevin P. APPLICANT: Desnoyers, Luc APPLICANT: Gerritsen, Mary APPLICANT: Goddard, Audre)
                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-227-884-78
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Sequence 33, Application US/10379334

Publication No. US20030181379A1

GENERAL INFORMATION:

APPLICANT: BCOOK, Michael

APPLICANT: WHITE, Kenneth

APPLICANT: WHITE, Kenneth

APPLICANT: WHITE, Kenneth

APPLICANT: WHITE, Kenneth

APPLICANT: WHITE, Kenneth

APPLICANT: WHITE, Kenneth

APPLICANT: WHITE, Kenneth

CURRENT FILING INVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE

FILE REFERENCE: 053884-5001

CURRENT APPLICATION NUMBER: US/09/901,938

PRIOR APPLICATION NUMBER: 60/219,137

PRIOR APPLICATION NUMBER: 60/219,137

PRIOR APPLICATION NUMBER: 60/219,137

PRIOR PILING DATE: 2000-07-19

NUMBER OF SEQ ID NOS: 34

SEQ ID NO 33

LENGTH: 136

LENGTH: 136
         APPLICANT: STROM, Tim
APPLICANT: MEDITINGER, Thomas
APPLICANT: MEDITINGER, Thomas
TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
FILE REFERENCE: 053884-5001
CURRENT FILING DATE: 2001-07-10
PRIOR PILING DATE: 2001-07-19
PRIOR PLING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
SEQ ID NO 33
LENGTH: 136
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100.0%; Score 86; DB 9; I
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: NOVEL FGF HOMOLOG ZFGF11
FILE REPERENCE: 00-03
CURRENT APPLICATION NUMBER: US/09/755,695
CURRENT FILING DATE: 2001-05-11
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo Sapiens
US-09-901-938-33
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PRIOR APPLICATION NUMBER: 60/11329
PRIOR APPLICATION NUMBER: 60/11329
PRIOR PILING DATE: 1938-12-23
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APPLICANT: GULMALIA, O. CHINSTOPHER
APPLICANT: SEMPLA, VANCTORIA
APPLICANT: STAPLANT: SEMPLA, VANCTORIA
APPLICANT: STAPLANT: SEMPLANT: SEMPLANT: SEMPLANT: SEMPLANT: SEMPLANT: SEMPLANT: SEMPLANT: SEMPLANT: SEMPLANT: SEMPLANT: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: ACADAM: A
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Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels (
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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                                    FILING DATE: 1998-12-22
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APPLICATION NUMBER: 60/113296
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Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
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APPLICANT: Godowski, Paul 5,
APPLICANT: Godowski, Paul 6,
APPLICANT: Godowski, Paul 19,
APPLICANT: Godowski, Paul 19,
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Augustin L.
APPLICANT: Watanabe, Colin L.
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APPLICANT: Watanabe, Colin L.
APPLICANT: MANER: 105/10420
CURRENT APPLICATION NUMBER: 10/119,480
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Gerritsen, Mary
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Sequence 78, Application US/10230338; Publication No. US20030044934A1; GENERAL INFORMATION:
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Matches 16; Conservative
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                                                                                                          APPLICANT: Baker, Kevin P. APPLICANT: Desnoyers, Luc APPLICANT: Gerritsen, Mar
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CORGANISM: Homo Sapien
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PRIOR FILLING DATE: 1997-10-31
PRIOR PLICATION NUMBER: 60/069873
PRIOR PILLING DATE: 1997-12-17
PRIOR PLICATION NUMBER: 60/078910
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APPLICANT: Geritsen, Mary
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SCENETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P5530PLC6
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NUMBER OF SEQ ID NOS: 246
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100.0%; Score 86; DB 14;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0;
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CURRENT PEPLICATION NUMBER: US/10/216,159A
CURRENT FILING DATE: 2002-08-09
PRIOR PELING DATE: 1907-109-10
PRIOR PILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/0652B7
PRIOR APPLICATION NUMBER: 60/06387
PRIOR APPLICATION NUMBER: 60/06389
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06319
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
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PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/079294
PRIOR PILING DATE: 1998-03-25
PRIOR PILING DATE: 1998-03-26
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                                                 PPLICATION NUMBER: 60/064103
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PRIOR FILING DATE: 1997-10-28
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                           APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 2020-08-12
FILE REPERENT PLING DATE: 2002-08-12
FRICK APPLICATION NUMBER: 0/109/13
FRICK APPLICATION NUMBER: 60/06287
FRICK APPLICATION NUMBER: 60/06287
FRICK APPLICATION NUMBER: 60/06349
FRICK APPLICATION NUMBER: 60/06349
FRICK APPLICATION NUMBER: 60/06913
FRICK APPLICATION NUMBER: 60/06913
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FRICK APPLICATION NUMBER: 60/07924
FRICK FILING DATE: 1998-03-20
FRICK APPLICATION NUMBER: 60/07924
FRICK APPLICATION NUMBER: 60/07924
FRICK APPLICATION NUMBER: 60/07924
FRICK FILING DATE: 1998-03-25
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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimald, J. Christopher
APPLICANT: Grimald, J. Christopher
APPLICANT: Suphan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
CITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC98
CURRENT APPLICATION NUMBER: US/10/230,414
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
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NUMBER OF SEQ ID NOS: 246
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    Stephan, Jean-Philippe F.
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US-10-230-414-78
Sequence 78, Application US/10230414
Publication No. US20030050448A1
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PRIOR APPLICATION NUMBER: 60/062287
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PRIOR APPLICATION NUMBER: 60/063549
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PRIOR APPLICATION NUMBER: 60/0
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-631-78
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    APPLICANT:
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APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grinaldi, J. Christopher
APPLICANT: Grinaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PL11
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: US/10/218,849
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION THE NOS: 246
SEQ ID NOS: 246
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APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gromaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Mood, William I.
APPLICANT: Wood, William I.
APPLICANT: Mood, William I.
APPLICANT: Mood, Milliam I.
APPLICANT: Mood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC72
CURRENT APPLICATION NUMBER: US/10/227,873
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100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                           Query Match
100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels (
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Publication No. US20030073816A1
GENERAL INFORMATION:
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; Publication No. US20030073814A1
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                     1 RORYLYTDDAQQTEAH 16
                                                                                                                                                                                                                                                                                                                                          44 RORYLYTDDAQOTEAH 59
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Desnoyers, Luc
Gerritsen, Mary
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US-10-218-849-78
                                                        TYPE: PRT
CORGANISM: Homo Sapien
US-10-216-159A-78
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US-10-227-873-78
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US-10-218-849-78
SEQ ID NO 78
LENGTH: 208
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PRIOR APPLICATION NUMBER: 10/119,480
PRIOR PLING DATE: 2002-04-09
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
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PRIOR APPLICATION NUMBER: 60/099812
PRIOR FLING DATE: 1998-09-10
PRIOR FLING DATE: 1998-09-10
PRIOR PLICATION NUMBER: 60/10038
PRIOR PLING DATE: 1998-09-10
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APPLICATION NUMBER: 60/131270
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APPLICANT: Desnoyers, Inc.

APPLICANT: Gerriteen, Mary
APPLICANT: Gerriteen, Mary
APPLICANT: Gerriteen, Mary
APPLICANT: Gerriteen, Mary
APPLICANT: Godowski, Paul J.
APPLICANT: Granaldi, J. Christopher
APPLICANT: Granaldi, J. Christopher
APPLICANT: Smith, Victorial
APPLICANT: Smith, Victorial
APPLICANT: Matanabe, Colin L.
APPLICANT: Watanabe, Colin L.
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PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR APPLICATION NUMBER: 60/131445
PRIOR APPLICATION NUMBER: 60/13445
PRIOR APPLICATION NUMBER: 60/134487
PRIOR FILING DATE: 1999-04-28
PRIOR FILING DATE: 1999-06-22
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
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PRIOR APPLICATION NUMBER: 60/140723
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PRIOR APPLICATION NUMBER: 60/144758
PRIOR APPLICATION NUMBER: 60/144768
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146963
PRIOR PILING DATE: 1999-07-28
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NUMBER: 60/06354; 1997-10-28 1997-10-31 1997-10-31 NUMBER: 60/06987; 1998-03-20 NUMBER: 60/07891, 1998-03-20 1998-03-20 NUMBER: 60/07959 1998-03-26 NUMBER: 60/07955 1998-03-26	NUMBER 1998 (NUMBER 1998 60/09614 1998-08-10 1998-08-11 1998-08-12 1998-08-12 1998-08-13 1998-08-26 NUMBER: 60/09989 1998-09-09 1098-09-09 1098-09-09 1098-09-09 1098-09-09 1098-09-09 1098-09-09 1098-09-10 1098-09-10 1098-09-10 1098-09-10 1098-09-10 1098-09-10 1098-09-10 NUMBER: 60/09981 11998-09-10 NUMBER: 60/09981 11998-09-10 NUMBER: 60/09981 11998-09-10 NUMBER: 60/09981 11998-09-10 NUMBER: 60/09981	
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PRIOR APPLICATION NUMBERS: 60/10147
PRIOR PILING DATE: 1998-09-23
PRIOR APPLICATION NUMBERS: 60/101738
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APPLICANT: Gulth, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERRENCE: P3530PLG2
CURRENT FILING DATE: 2002-04-09
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-10-31
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PRIOR APPLICATION WUBBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 86; DB 14; Length 208; 100.0%; Pred. No. 8.3e-07;
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Gerritsen, Marry
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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APPLICATION NUMBER: 60/082804
FILING DATE: 1998-04-22
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FILING DATE: 1998-05-06
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Best Local Similarity 100.03
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                TYPE: PRT

ORGANISM: Homo Sapien

US-10-219-076-78
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APPLICANT:
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APPLICANT: Goddward, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, Justin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SCEERED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR PLILING DATE: 2002-04-09
PRIOR PLILING DATE: 3002-04-09
PRIOR PLILING DATE: 1997-09-17
PRIOR PLILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR PLILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR PLILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06913
PRIOR APPLICATION NUMBER: 60/06913
PRIOR PLILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/069873
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PRIOR APPLICATION NUMBER: 60/140650
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PRIOR PAPLICATION NUMBER: 60/141037
PRIOR PELLING DATE: 1999-06-23
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PRIOR PELING DATE: 1999-07-26
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Gerritsen, Mary
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NUMBER: 60/085323 1998-05-13 NUMBER: 60/085579 1998-05-15 1998-05-12 1998-05-22 1998-06-17 NUMBER: 60/089532 1998-06-17 NUMBER: 60/089538 1998-06-18 NUMBER: 60/08905 1998-06-18 NUMBER: 60/080472 NUMBER: 60/080472 NUMBER: 60/080472 NUMBER: 60/080472 NUMBER: 60/080472 NUMBER: 60/080472 NUMBER: 60/080472	6-25 60/09069 60/09069 60/09530 8-04 60/09531 8-10 60/09531 8-10 60/0954 8-10 60/0959 8-17 8-10 60/09959 8-17 8-10 60/09959 8-3 60/09959 8-3 60/09959	9-10 60/09981- 9-10 9-10 9-10 9-10 9-11 60/10039 9-15 60/10084 9-16 60/10081 9-17 9
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PRIOR FILING DATE: 1998-10-28

RRIOR APPLICATION WUMBER: 60/106464

PRIOR PILING DATE: 1998-10-29

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R FILING DATE: 1998-06-17

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R APPLICATION NUMBER: 60/095318

R FILING DATE: 1998-08-04

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R FILING DATE: 1998-08-10

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R APPLICATION NUMBER: 60/096146

R FILING DATE: 1998-08-11

R APPLICATION NUMBER: 60/096791

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RR FILING DATE: 1998-09-16
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RR APPLICATION NUMBER: 60/100417
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DR FILING DATE: 1998-09-24

DR APPLICATION NUMBER: 60/101741

DR FILING DATE: 1998-09-24

DR APPLICATION NUMBER: 60/101741

DR FILING DATE: 1998-09-25

DR APPLICATION NUMBER: 60/101916

DR APPLICATION NUMBER: 60/10192

DR FILING DATE: 1998-09-24

DR APPLICATION NUMBER: 60/106178

DR FILING DATE: 1998-09-24

DR APPLICATION NUMBER: 60/106178

DR FILING DATE: 1998-10-29

DR APPLICATION NUMBER: 60/10648

DR APPLICATION NUMBER: 60/10648

DR FILING DATE: 1998-10-29

DR APPLICATION NUMBER: 60/106464

DR FILING DATE: 1998-10-29

DR APPLICATION NUMBER: 60/106905

DR FILING DATE: 1998-11-30
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FILING DATE: 1998-09-15
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100.0%; Score 86; DB 14;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FLING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR PEPLICATION NUMBER: 60/169495
PRIOR PILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835
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APPLICANT: Goddard, Audrey
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrein.
APPLICANT: Gurnal, J. Christopher
APPLICANT: Gurnal, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
CURRENT APPLICANTON NUMBER: US/10/19, AB
FILE REPERBNCE: P3530PLG1
CURRENT FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR PRIOR DATE: 1997-10-28
PRIOR PLING DATE: 1997-10-31
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Length 208;
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Query Match
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                           US-10-219-075-78

"Sequence 78, Application US/10219075
; Publication No. US20030088064A1
; GENREAL INFORMATION:
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Best Local Similarity 100.
Matches 16; Conservative
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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; ORGANISM: Homo Sapien
US-10-219-075-78
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US-10-219-464-78
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                                                                                                                                                  APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watchabe, Colin L.
APPLICANT: Watchabe, Colin L.
APPLICANT: Watchabe, Colin L.
APPLICANT: ALIDIAM ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 1933-091-10,
FRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-31
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Publication No. US2030088066A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Geritleen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Stephan, Jean-Philippe F.

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PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
LENGTH: 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-464-78
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US-10-219-466-78
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APPLICANT: Gerriceen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Scphan, Jean-Philippe F.
APPLICANT: Scphan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Mood, William I.
TILLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLG3
CURRENT APPLICATION NUMBER: US/10/19,480
FRIOR APPLICATION NUMBER: 60/65287
FRIOR FILING DATE: 1997-04-09
PRIOR FILING DATE: 1997-017
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/663849
PRIOR APPLICATION NUMBER: 60/66387
PRIOR FILING DATE: 1997-10-21
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/669873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910

    See File Wrapper or PALM.

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PRIOR PELILAGO NUMBER: 10/119,480
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PELICATION NUMBER: 60/063549
PRIOR PELICATION NUMBER: 60/063549
PRIOR PELING DATE: 1997-10-28
PRIOR PELING DATE: 1997-10-28
PRIOR PELING DATE: 1997-10-31
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Best Local Similarity 100.
Matches 16; Conservative
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US-10-219-466-78
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FILE OF INVENIOUS: P3530PLC28
CURRENT FILING DATE: 2002-08-13
PRIOR PEPLICATION NUMBER: US/10/219,481
PRIOR PELICATION NUMBER: 0/059113
PRIOR PELICATION NUMBER: 60/06213
PRIOR FILING DATE: 1997-09-17
PRIOR PELICATION NUMBER: 60/06354
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PRIOR PLICATION NUMBER: 60/06973
PRIOR FILING DATE: 1997-12-17
PRIOR PLICATION NUMBER: 60/079294
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APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
LENGTH: 208
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Godowski, Paul J.
Grimaldi, J. Christopher
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No. US20030088068A1
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Best Local Similarity 100.0
Matches 16; Conservative
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Gerritsen, Mary
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ORGANISM: Homo Sapien
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; ORGANISM: Homo Sapien
US-10-219-479-78
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Publication No.
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Query Match

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APPLICANT: Geddadd, Audrey
APPLICANT: Geddadd, Audrey
APPLICANT: Geddadd, Audrey
APPLICANT: Geddadd, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: WALES ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: 10/119,480
FRIOR PELING DATE: 1907-04-09
FRIOR PELING DATE: 1997-09-17
FRIOR APPLICATION NUMBER: 60/06287
FRIOR PELING DATE: 1997-10-21
FRIOR APPLICATION NUMBER: 60/063549
FRIOR PILING DATE: 1997-10-21
FRIOR PELING DATE: 1997-10-21
FRIOR APPLICATION NUMBER: 60/063549
FRIOR PILING DATE: 1997-10-21
FRIOR APPLICATION NUMBER: 60/063549
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FRIOR APPLICATION NUMBER: 60/063549
FRIOR PILING DATE: 1997-10-21
FRIOR APPLICATION NUMBER: 60/063549
FRIOR PILING DATE: 1997-03-20
FRIOR PILING DATE: 1998-03-26
FRIOR PILING DATE: 1998-03-26
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                            Gaps
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NUMBER OF SEQ ID NOS: 246
LENGTH: 208
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  Pred. No. 8.3e-07;
                            Mismatches
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Publication No. US20030088071A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                               Sequence 78, Application US/10230260 Publication No. US20030088070A1 GENERAL INFORMATION:
Best Local Similarity 100.0%; P. Matches 16; Conservative 0;
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                                                                              1 RORYLYTDDAQQTEAH 16
                                                                                                                                 44 RORYLYTDDAQQTEAH 59
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                         16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Baker, Kevin P. APPLICANT: Desnoyers, Luc
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CORGANISM: Homo Sapien
US-10-230-260-78
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Matches 16; Conserv
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; Sequence 78, Application US/10216165; Publication No. US20030092886A1; GENERAL INFORMATION:
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FILING DATE: 1998-03-25
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US-10-232-233-78
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Matches
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                                                                        APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Collin L.
APPLICANT: Wood, Milliam I.
APPLICANT: Wood, Milliam I.
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APPLICANT: Wood, Milliam I.
APPLICANT: Wood, Milliam I.
APPLICANT: ACTION NUMBER: US/10/232,231
CURRENT FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062397
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06349
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
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APPLICANT: Goddowal, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Surney, Austin L.
APPLICANT: Shith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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SEQ ID NO 78
LENGTH: 208
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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US-10-232-231-78
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Best Local Similarity
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APPLICANT: BeaRer, Audre,
APPLICANT: Gerriteen, Mary
APPLICANT: Gerriteen, Mary
APPLICANT: Gedard, Audre,
APPLICANT: Goddard, Audre,
APPLICANT: Goddard, Audre,
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin I.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Schan, Jean-Philippe F.
APPLICANT: Smith, Victoria
APPLICANT: Schan, Jean-Philippe F.
APPLICANT: Schan, Jean-Philippe F.
APPLICANT: Schan, Jean-Philippe F.
APPLICANT: Schan, Jean-Philippe F.
APPLICANT: Schan, Jean-Philippe F.
APPLICANT: ACIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P5530PLO;
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: 10910PLO;
FRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 1997-0-17
PRIOR FILING DATE: 1997-0-17
PRIOR FILING DATE: 1997-0-17
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/06973
PRIOR APPLICATION NUMBER: 60/06973
PRIOR APPLICATION NUMBER: 60/073000
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PELING DATE: 1997-09-17
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Goddweki, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guine, Vaustin L.
APPLICANT: Smith, Vatoria
APPLICANT: Smith, Vatoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENITON: ACIDE ENCODING THE SAME
FILE REFERENCE: P3530PLC15
CURRENT APPLICATION NUMBER: US/10/218,956
CURRENT APPLICATION NUMBER: 10/119,480
PRIOR PILING DATE: 2002-08-12
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
LENGTH: 208
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FILING DATE: 1998-03-26
APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/081819
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PRIOR FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/08441
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APPLICATION NUMBER: 60/085323
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Gerritsen, Mary
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Best Local Similarity 100.
Matches 16; Conservative
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US-10-216-165-78
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APPLICATION NUMBER: 60/106248
FILING DATE: 1998-10-29
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APPLICATION NUMBER: 60/095302
FILING DATE: 1998-08-04
APPLICATION NUMBER: 60/095318
FILING DATE: 1998-08-04
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PPLICATION NUMBER: 60/099596
TILING DATE: 1998-09-09
PPLICATION NUMBER: 60/099598
TILING DATE: 1998-09-09
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FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099816
FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/100038
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APPLICATION NUMBER: 60/100848
FILING DATE: 1998-09-18
APPLICATION NUMBER: 60/100919
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FILING DATE: 1998-08-11
APPLICATION NUMBER: 60/096791
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FILING DATE: 1998-09-15
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APPLICATION NUMBER: 60/101477
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APPLICATION NUMBER: 60/101738
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FILING DATE: 1998-09-24
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FILING DATE: 1998-09-25
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APPLICATION NUMBER: 60/101922
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APPLICATION NUMBER: 60/086392
FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/089532
                                                          FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/091982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/095916
FILING DATE: 1998-08-10
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APPLICATION NUMBER: 60/097986
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FILING DATE: 1998-09-10
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LING DATE: 1998-09-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/100627
                                                                                                                                       APPLICATION NUMBER: 60/089905
                                                                                                                                                             FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/090472
                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
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                                                                 100.0%; Score 86; DB 14; Length 208; 100.0%; Pred. No. 8.3e-07;
                                                                                          Indels
                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                      Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Stephan, Jean-Philippe F.
Watanabe, Colin L.
Wood, William I.
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION WUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835
                                                                                                                                                                                                           ; Sequence 78, Application US/10219468; Publication No. US20030092888A1; GENERAL INFORMATION:
                                                                                                                     1 RORYLYTDDAQQTEAH 16
                                                                                                                                              44 RORYLYTDDAQQTEAH 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RORYLYTDDAQQTEAH 16
                                                                                                                                                                                                                                                 APPLICANT: Baker, Kevin P.
APPLICANT: Bernoyers, Luc
APPLICANT: Geritlen, Mary
APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Grimaldi, J. Chr.
APPLICANT: Smith, Victoria
APPLICANT: Swith, Victoria
APPLICANT: Watenabe, Colin:
APPLICANT: Watenabe, Colin:
APPLICANT: Watenabe, Colin:
APPLICANT: Wood, William I.
                                                       Query Match
Best Local Similarity 100.0
.....hes 16; Conservative
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Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Conservative
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ORGANISM: Homo Sapien
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Best Local Similarity
Matches 16; Conserv
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RESULT 28

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P3530PLG7

TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P3530PLG7

CURRENT APPLICATION NUMBER: US/10/219,536

CURRENT FILING DATE: 2002-08-14

PRIOR FILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-09-17

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PRIOR PILING DATE: 1998-03-26

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NUMBER OF SEQ ID NOS: 246
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APPLICANT: Desnoyers, Inc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Gramaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 78, Application US/10233205
Publication No. US20030096362A1
GENERAL INFORMATION:
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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APPLICANT: Goddard, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: ACTUB SENCODING THE SAME
FILE REFERENCE: P3530PLCON.
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CURRENT PELLING DATE: 2002-08-13
PRIOR PELLING DATE: 2002-08-13
PRIOR PILING DATE: 2002-04-09
PRIOR PILING DATE: 2002-04-09
PRIOR PILING DATE: 1997-09-17
PRIOR PELLOGATION NUMBER: 60/062287
PRIOR PELLOGATION NUMBER: 60/062287
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063649
PRIOR PILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/079294
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PRIOR APPLICATION NUMBER: 60/07928
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Publication No. US20030092890A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Gerriteen, Mary
APPLICANT: Geodard, Audrey,
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stephan, Jean-Philippe F.
Watanabe, Colin L.
Wood, William I.
                                                Sequence 78, Application US/10219478
Publication No. US20030092889A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
Matches 16; Conservative
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ORGANISM: Homo Sapien
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; ORGANISM: Homo Sapien
US-10-219-072-78
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ANT: Debrayers, Luc
ANT: Gerrites, Mary

JANT: Gerrites, Mary

CANT: Gerrites, Mary

CANT: Gerrites, Mary

CANT: Gerrites, Mary

CANT: Gerrites, Mary

LICAN: Granaldi, J. Christopher

JICAN: Gurney, Autoria

LICAN: Gurney, Autoria

LICAN: Stephan, Debrith Paul J.

LITER OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

LITER OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

LITER OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

UNREAR PAPLICATION SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

UNREAR PAPLICATION NUMBER: 05/10/219,072

PRIOR FILING DATE: 2002-004-19

PRIOR FILING DATE: 2002-004-19

PRIOR PLING DATE: 2002-004-19

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PRIOR PLING DATE: 2002-004-19

PRIOR PLING DATE: 3002-004-19

PRIOR PLING DATE: 3002-004-18

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PRIOR APPLICATION NUMBER: 60/069973
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-25
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PRIOR PILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR PRICH DATE: 1998-03-27
PRIOR SEQ ID NOS: 246
SEQ ID NO 78
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Publication No. US20030096959A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Conservative
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; ORGANISM: Homo Sapien
US-10-233-205-78
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Best Local Similarity
Matches 16; Conserv
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APPLICANT: Goddwaff, Madry
APPLICANT: Goddwaff, Audrey
APPLICANT: Goddwaff, Audrey
APPLICANT: Goddwaff, Audrey
APPLICANT: Goddwaff, Austin J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SCRETED ENCODING THE SAME
FILE REFERENCE: P3530PLG3
CURRENT APPLICATION NUMBER: US/10/19, 470
CURRENT FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-20
PRIOR PLING DATE: 1997-10-20
PRIOR PLING DATE: 1997-10-20
PRIOR FILING DATE: 1997-10-31
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100.0%; Score 86; DB 14; Length 208; 100.0%; Pred. No. 8.3e-07;
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                                                                             0; Mismatches
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US-10-219-474-78
; Sequence 78, Application US/10219474
                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 78, Application US/10219470; Publication No. US20030096960A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08;
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                                                                                                                                                   1 RORYLYTDDAQQTEAH 16
                                                                                                                                                                                                                  44 RORYLYTDDAGOTEAH 59
                                                                             16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desnoyers, Luc
Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo Sapien
   Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                             RESULT 32
US-10-219-470-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-219-470-78
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TYPE: PRT
CORGANISM: Homo Sapien
US-10-219-524-78
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LENGTH: 208
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                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P$330PTC36
CURRENT APPLICATION NUMBER: U6/10/219,474
CURRENT RILING DATE: 2002-08-13
PRIOR FILING DATE: 1997-10-17
PRIOR PRILING DATE: 1997-10-17
PRIOR PRILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-31
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PRIOR FILING DATE: 1997-10-31
PRIOR PLILING DATE: 1997-12-17
PRIOR PLILING DATE: 1998-03-20
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APPLICANT: Besnoyers, Luc
APPLICANT: Besnoyers, Luc
APPLICANT: Gerriteen, Mary
APPLICANT: Godowski, Audrey
APPLICANT: Godowski, Peul J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watunion: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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100.0%; Score 86; DE
Best Local Similarity 100.0%; Pred. No. 8.3
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                     Godowski, Paul<sup>J</sup>J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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Publication No. US20030096962A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RORYLYTDDAQOTEAH 16
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Publication No. US20030096961A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                           Desnoyers, Luc
Gerritsen, Mary
                                                                                                                                                                                                Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-474-78
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APPLICANT: Besnoyers, Inc.
APPLICANT: Gerriteen, Mary
APPLICANT: Geddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Sathan, Jean-Philippe F.
APPLICANT: Sathan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SACIDE ENCODING THE SAME
FILE REFERENCE: P3530F1C68
CURRENT FILING DATE: 2002-08-14
RIOR APPLICATION NUMBER: 60/06213
RRIOR APPLICATION NUMBER: 60/06349
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06349
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/06349
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-110-31
CURRENT PAPPLICATION NUMBER: US/10/219,524

CURRENT PEPPLICATION NUMBER: US/10/219,524

CURRENT PEPPLICATION NUMBER: US/10/119,480

PRIOR FILING DATE: 2002-04-09

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-10-17

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Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 78, Application US/10219528
Publication No. US20330096963A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RORYLYTDDAQOTEAH 16
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PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/10019
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-09-24
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PRIOR PLING DATE: 1998-09-25
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PRIOR PLING DATE: 1999-01-27

FILING DATE: 1998-09-15
APPLICATION NUMBER: 60/100627
FILING DATE: 1998-09-16
APPLICATION NUMBER: 60/100848

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REPLICATION NUMBER: 60/08441

RAPPLICATION NUMBER: 60/08441

RAPLICATION NUMBER: 60/085323

RETLING DATE: 1998-05-05

RETLING DATE: 1998-05-13

RETLING DATE: 1998-05-13

RETLING DATE: 1998-05-15

RAPLICATION NUMBER: 60/08532

RAPLICATION NUMBER: 60/08532

RAPLICATION NUMBER: 60/089532

RETLING DATE: 1998-06-17

RETLING DATE: 1998-06-17

RETLING DATE: 1998-06-17

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RETLING DATE: 1998-06-17

RETLING DATE: 1998-06-18

RETLING DATE: 1998-06-24

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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/091982
APPLICATION NUMBER: 60/091982
APPLICATION NUMBER: 60/095302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/098544
FILING DATE: 1998-08-31
APPLICATION NUMBER: 60/099596
APPLICATION NUMBER: 60/099598
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APPLICATION NUMBER: 60/099811
FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099812
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APPLICATION NUMBER: 60/099816
FILING DATE: 1998-09-10
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APPLICATION NUMBER: 60/100385
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APPLICATION NUMBER: 60/101738
FILING DATE: 1998-09-24
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APPLICATION NUMBER: 60/095916
FILING DATE: 1998-08-10
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FILING DATE: 1998-08-11
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APPLICATION NUMBER: 60/099803
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APPLICATION NUMBER: 60/100627
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APPLICATION NUMBER: 60/097986
APPLICATION NUMBER: 60/081955
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082804
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APPLICANT: Gurmald, J. Christopher
APPLICANT: Saith, Victoria
APPLICANT: Saith, Victoria
APPLICANT: Saith, Victoria
APPLICANT: Saith, Victoria
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3530PLC74
CURRENT APPLICATION NUMBER: US/10/22, 880
CURRENT PILING DATE: 2002-04-09
PRIOR PILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1998-03-20
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                                                                              PRIOR APPLICATION UNDER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR FILING DATE: 1999-08-03
PRIOR FILING DATE: 1999-08-03
PRIOR PILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/14930
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-11-09
PRIOR PELING DATE: 1999-11-09
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PRIOR APPLICATION NUMBER: 60/16416
PRIOR APPLICATION NUMBER: 60/164416
PRIOR PELING DATE: 1999-11-05
PRIOR PELING DATE: 1999-11-07
PRIOR APPLICATION NUMBER: 60/16945
PRIOR PELING DATE: 1999-12-07
PRIOR PELING DATE: 1999-12-07
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                                                         PRILING DATE: 1999-07-20

REPLING DATE: 1999-07-20

REPLING DATE: 1999-07-26

RAPPLICATION NUMBER: 60/14598

RAPLICATION NUMBER: 60/14622

RAPLICATION NUMBER: 60/14653

RELING DATE: 1999-08-03

RELING DATE: 1999-08-03

RELING DATE: 1999-08-17

RAPLICATION NUMBER: 60/149320

RELING DATE: 1999-08-17

RAPLICATION NUMBER: 60/149418

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Godowski, Paul J.
Grimaldi, J. Christopher
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FILING DATE: 1998-03-25
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FILING DATE: 1998-03-26
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No. US20030096964A1
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Best Local Similarity 100.0
Matches 16; Conservative
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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Publication No. US20
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/10176
PRIOR FILING DATE: 1998-09-24
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PRIOR PELICATION NUMBER: 60/10196
PRIOR FILING DATE: 1998-09-25
PRIOR PELICATION NUMBER: 60/10192
PRIOR PELING DATE: 1998-09-25
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APPLICANT: Godowski, Paul J.
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APPLICANT: Godowski, Paul J.
APPLICANT: Gothard, Austin, Christopher
APPLICANT: Gurney, Austin, Christopher
APPLICANT: Suth, Widtoria
APPLICANT: Watanbe, Colin L.
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PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
PRIOR PLING DATE: 1999-08-17
PRIOR APLICATION NUMBER: 60/149638
PRIOR PILING DATE: 1999-08-17
PRIOR PEDLICATION NUMBER: 60/151733
PRIOR PELING DATE: 1999-08-31
PRIOR PELING DATE: 1999-08-31
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Publication No. US2030096965A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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Gerritsen, Mary
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Best Local Similarity 100.
Matches 16; Conservative
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PRIOR FILING DATE: 1998-09-24

PRIOR APPLICATION NUMBER: 60/10648

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APPLICANT: Baker, Kevin P.
APPLICANT: Gerriter, Luc
APPLICANT: Gerriter, Luc
APPLICANT: Gerriter, Luc
APPLICANT: Gerriter, Audrey
APPLICANT: Gerriter, Audrey
APPLICANT: Godowski, Audrey
APPLICANT: Godowski, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Colin L.
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APPLICANT: Watanabe, J. Colin L.
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100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels (
                 PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-16
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/16945
PRIOR FILING DATE: 1999-12-07
PRIOR PELING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
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FILING DATE: 1998-05-15
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R APPLICATION NUMBER: 60/108801
R FILING DATE: 1998-11-17
R APPLICATION NUMBER: 60/108849
R FILING DATE: 1998-11-18
R APPLICATION NUMBER: 60/112422
R FILING DATE: 1998-12-15
R APPLICATION NUMBER: 60/113296
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APPLICATION NUMBER: 60/169445
FILING DATE: 1999-12-07
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APPLICATION NUMBER: 60/145698
FILING DATE: 1999-07-26
APPLICATION NUMBER: 60/146222
FILING DATE: 1999-07-28
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FILING DATE: 1999-08-03
APPLICATION NUMBER: 60/149320
FILING DATE: 1999-08-17
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APPLICATION NUMBER: 60/149638
FILING DATE: 1999-08-17
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APPLICATION NUMBER: 60/164418
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APPLICATION NUMBER: 60/166361
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APPLICATION NUMBER: 60/169495
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APPLICATION NUMBER: 60/131022
FILING DATE: 1999-04-26
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APPLICATION NUMBER: 60/131445
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FILING DATE: 1999-06-23
APPLICATION NUMBER: 60/144758
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FILING DATE: 1999-01-12
APPLICATION NUMBER: 60/115565
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FILING DATE: 1999-01-12
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APPLICATION NUMBER: 60/127887
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PLICATION NUMBER: 60/134287
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APPLICATION NUMBER: 60/113605
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APPLICATION NUMBER: 60/113621
FILING DATE: 1998-12-23
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FILING DATE: 1998-11-03
APPLICATION NUMBER: 60/108787
FILING DATE: 1998-11-17
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CURRENT PAPPLICATION NUMBER: US/10/230,436

CURRENT PAPPLICATION NUMBER: 10/119,480

PRIOR PILING DATE: 2002-08-28

PRIOR FILING DATE: 2002-04-09

PRIOR FILING DATE: 1997-09-17

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Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels (
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100.0%; Pred. No. 8.3e-07;
tive 0; Mismatches 0;
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APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
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US-10-232-223-78
; Sequence 78, Application US/10232223
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835
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Publication No. US20030096568A1
GREEAL INFORMATION:
APPLICANT: Baker, Vevin P.
APPLICANT: Beneroyers, Luc
APPLICANT: Genitalen, Mary
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APPLICANT: Genitalen, Mary
APPLICANT: Genitalen, Mary
APPLICANT: Genitalen, Mary
APPLICANT: Genitalen, Mary
APPLICANT: Genitalen, March
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wood william I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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- protein search, using sw model OM protein 2, 2004, 15:50:07; Search time 9.6 Seconds (without alignments) 470:913 Million cell updates/sec March Run on:

US-10-060-765-7 86 Perfect score: Title:

1 RQRYLYTDDAQQTEAH 16 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched: 1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:* Database :

geneseqp1980s:*
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SUMMARIES		Description		Abb81312	9 Aab73069	Aau00965	Aae05078	Aau83630	Abg32358	Aae17601	7 Abu80777	3 Abo33743		Abp96156	Abj72266	Abj72394		Ada37038	Abj72096	Adb83568	Adb80674	Adb73215	Adb78297	Adb84945	051 Adb78051 Novel	117 Adb87117 Human	699 Adb84699 Human
SU		a ID	1 AAB68418	5 ABB81312	4 AAB7306	4 AAU00965		5 AAU83630	5 ABG32358	5 AAE17601	5 ABU8077		6 ABU82086	6 ABP96156					7 ABJ72096				7 ADB78297	7 ADB84945	7 ADB78051	7 ADB87117	
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ALIGNMENTS

Fibroblast growth factor-21; FGF-21; cell growth; cell differentiation; hepatic cell; cirrhosis; infertility; impotence; testicular cancer; leukemia; lymphoma; autoimmune disease; thymus proliferative disorder. Epitope-bearing portion of human fibroblast growth factor-21 (FGF-21). AAB68418 standard; peptide; 16 AA. 23-JUL-2001 (first entry) AAB68418; RESULT 1 AAB68418

Homo sapiens.

WO200136640-A2

25-MAY-2001.

16-NOV-2000; 2000WO-US031745.

18-NOV-1999; 99US-0166540P. 11-MAY-2000; 2000US-0203633P.

(CHIR) CHIRON CORP. (KYOU) UNIV KYOTO.

Itoh N, Kavanaugh WM;

WPI; 2001-343823/36.

New nucleic acid molecule useful for treating disease, e.g. infertility, impotence, or testicular cancer.

Claim 17; Page 39; 61pp; English.

The present sequence represents an epitope-bearing portion of human fibroblast growth factor-21 (FGF-21). FGF proteins regulate growth and differentiation of a variety of cell types. FGF-21 mucleic acids and polypeptides are useful for treating diseases and disorders characterised by inadequate numbers of hepatic cells, preferably cirrhosis of the liver. They may also be used in the treatment of infertility, impotence, and testicular cancer, as well as leukemia, lymphoma, autoimmune disease, or proliferative disorders of the thymus

Sequence 16 AA;

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Indels

2.5e-07;

Pred. No. 2.5 Mismatches

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Best Local Similarity Matches 16; Conserv

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The present invention describes an active variant (1) of a fibroblast growth factor (FGF) having at least one mutation in the beta-8-beta-9 loop, having enhanced specificity for one receptor subtype compared to the corresponding wild type FGF, by decreasing the biological activity mediated by at least one receptor subtype while retaining the activity conscipation another receptor subtype. (1) has cytostatic, vulnerary, consteppathic and antiatritric activities. (1) can be used as a regulator of vasculogenesis or angiogenesis. (1) is useful for preparing a medicament and for treating a disease or disorder related to normal or medicament and for treating a disease or disorder related to normal or commance bone fracture healing or bone growth processes and wound healing processes. (1) is useful in detection and treatment of various FGFR related disorders including skeletal disorders e.g. achondroplasia, or processes (1) is useful in detection and treatment of various FGFR related disorders including skeletal disorders e.g. achondroplasia, or processes (1) is useful in detection and cartilage defects, multiple myeloma, epithelial cancers such as transitional cell carcinoma of the bladder and cervical carcinoma. The novel mutants are useful in high companies in various disorders such as skeletal disorders and sarve as template for the formation of improved agonists and an earner cannon cannon and an analysis and mits and the serve as template for the formation of improved agonists and carries and manner cannon and the cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon cannon can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fibroblast growth factor 9; FGF-9; cytostatic; vulnerary; osteopathic; antiarthritic; vasculogenesis; angiogenesis; FGFR; skeletal disorder; fibroblast growth factor receptor; cancer; bone fracture healing; bone growth; wound healing; achondroplasia; hypochondroplasia; osteoporosis; cartilage defect; multiple myeloma.
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                 Length 16;
                                                               0; Indels
                 Score 86; DB 4; I
Pred. No. 2.4e-08;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human FGF21 core structure amino acid sequence.
                                                                                                                                                                                                                                                                                          ABB81312 standard; protein; 124 AA.
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cancer. The present sequence represents a FGF core structure amino acid sequence which is given in the exemplification of the present invention

DB 5; Length 124;

100.0%; Score 86;

Sequence 124 AA;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes the protein and coding sequences of thuman fibroblast growth factor (FGF) 19 homologue FGF19%, the former which is shown here. The sequences can be used in the prognosis and treatment of proliferative diseases such as cancer, restenosis, psoriasis, rheumatoid arthritis and Dupuytren's contracture, as well to stimulate cell growth for treating neurological disorders such as Alzheimer's disease
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                                                                                                  Human; fibroblast growth factor 19; FGF19X; embryonic development; proliferative disorder; cancer; restenosis; psoriasis; rheumatoid arthritis; Dupuytren's contracture.
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                                                                             Human fibroblast growth factor 19 homologue FGF19X.
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Herrmann JL;
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Rastelli L,
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AAB73069 standard; protein; 153 AA.
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19-JUL-2000; 2000US-00619251.
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                                                     (first entry)
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                        Vernet C,
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N-PSDB; AAF76715.
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                                                     17-MAY-2001
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(first entry)

24-MAY-2001

neurodegenerative disease, haematopoietic cell reconstitution, cachexia, chemotherapy; corneal epithelium damage; retinal tissue damage; myopathy; multiple sclerosis; short stature; delayed maturation; excessive growth, acromegaly; premature maturation; alopecia; bronchopulmonary dysplasia; androgen target organ abnormality; respiratory distress syndrome; stroke; cancer; atherosclerosis; hypercholesterolaemia; osteoporosis; baldness; osteoarthritis, muscle arrophy; sarcopenia; wrinkles; increased fatigue; decreased stamina; decreased cardiac function; immune system dysfunction; Parkinson's disease; Alzheimer's disease; decreased cognitive function; treatment; cirrhosis; mucositis; diabetes; Fibroblast Growth Factor; FGF; treatment; cirrhosis; mucositis; diabetes inflammatory bowel disease; Crohn's disease; obesity; tubular necrosis; renal tubule damage; gastrointestinal abnormality; wasting syndrome; Human Fibroblast Growth Factor-like (FGF-like) polypeptide fragment senile dementia; human

Homo sapiens.

WO200118172-A2.

05-SEP-2000; 2000WO-US024373.

07-SEP-1999; 99US-00391861. 23-AUG-2000; 2000US-00644052. 07-SEP-1999;

(AMGE-) AMGEN INC.

Thomason AR, Liu B;

WPI; 2001-226743/23

Novel isolated fibroblast growth factor-like polypeptide useful for treating, preventing or ameliorating cirrhosis, inflammatory bowel disease, mucositis, Crohn's disease, diabetes, obesity, stroke and

Claim 14; Page 116-117; 138pp; English

The sequence represents a fragment of a fibroblast growth factor-like (FGF-like) polypeptide. FGF-like protein and its associated nucleic acid play a role in modulating body growth, maturation or life-span. They are also useful for treating, preventing or ameliotating disorders such as cirrhosis, inflammatory bowel disease, mucositis, Crohn's disease, diseases, damage to renal tubules as a result of acute tubular necrosis, haematopoietic cell reconstitution following chemotherapy, wasting syndromes (e.g., cancer associated cachexia), damage to the corneal of premature maturation, alopecia, abnormalities of androgen target organs, cather element dissues, androgen target organs, bronchopilmonary dysplasia, acute respiratory distress syndrome, tumours of the eye or other tissues, atherosolerosis, hypercholesterolemia, stroke, osteoporosis, osteoarthritis, muscle atrophy, sarcopenia, baldness, wrinkles, increased fatigue, decreased stamina, decreased baldness, wrinkles, increased fatigue, decreased stamina, decreased cardiac function, immune system dysfunction, cancer, Parkinson's disease, senile dementia, Alzheimer's disease, and decreased cognitive function

Sequence 181 AA;

Gaps ö 100.0%; Score 86; DB 4; Length 181; 100.0%; Pred. No. 3.8e-07; Indels . Mismatches 0; Local Similarity 100. Query Match Best Loca Matches

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ROKYLYTDDAOOTEAH 32 1 RQRYLYTDDAQQTEAH 16

AAE05078 standard; protein; 208 AA. AAE05078

AAE05078;

(first entry) 18-SEP-2001 Human fibroblast growth factor (FGF) homologue, zFGF11 protein.

proliferation, messenchymal cell, osteoblastic lineage cell, osteoporosis; chromosomal disorder; chondrosarcoma atherosclerosis; obesity; fracture; bone formation; diabetes mellitus; neural cell development; angiogenesis; amyotrophic lateral sclerosis; cerebrovascular stroke; neuropathy; ulcer; congenital disorder; wound healing; cardiac function; glomerulonephritis; surfactant production; anorectic; ischaemia; neogenesis; hyperplasia; hypertension; cytostatic; vasotropic; therapy. fibroblast growth factor; FGF; zFGF11; chromosome 19; restenosis;

Homo sapiens

. .27 /label= Signal_peptide Location/Qualifiers Binding-site Protein Peptide

WO200149849-A1

12-JUL-2001

05-JAN-2001; 2001WO-US000324.

05-JAN-2000; 2000US-00477886.

(ZYMO) ZYMOGENETICS INC.

Conklin DC, Chen Z;

WPI; 2001-441880/47. N-PSDB; AAD09151. Novel rFGF11 polypeptide and polynucleotide, a member of fibroblast growth factor family, for stimulating proliferation of mesenchymal, osteoblastic lineage cells and treating diabetes, obesity, osteoporosis,

Claim 1; Page 63; 69pp; English.

The present sequence is human fibroblast growth factor (FGF) homologue, CC zFGF11 protein. zFGF11 game is located on chromosome 19. zFGF11 is useful for stimulating proliferation of mesenchymal cells, osteoblastic lineage cells. zFGF11 is useful for identifying chromosomal disorders associated with abnormal expression of zFGF11 protein. zFGF11 is also useful for stimulation, inhibition or proliferation of myocytes, smooth muscle cells adipocytes, chondrocytes, neural tube-derived stem cells, neural cells and neuronal progenitors, pancreatic cells, prostate-derived cells and neuronal progenitors, pancreatic cells, prostate-cesus resences, restenced sand obseity. Stimulation of osteoblasts catheroscierosis, restenced and obseity. Stimulation of osteoblasts catheroscis and other deficiencies in bone structure and formation. zFGF11 is useful for treating disorders associated with diabetes costeoprosas and other deficiencies in bone structure and formation. ZFGF11 is useful for treating disorders associated with diabetes costeoprosis, cerebrovascular stroke, neuropathy associated with lack of maintenance of neuronal differentiation and congenital disorders of the companies of neuronal development, promoting angiogenesis and wound healing, for revascularisation in eye, complications related to poor circulation such as diabetic food ulcers, improving cardiac correduce damage to the tissue caused by isohemia or ischaemia-reperfusion events, particularly in the heart or brain and for inducing skeletal muscle neogenesis and/or hyperplasia, kidney regeneration and/or for

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treating of systemic and pulmonary hypertension. Antagonists of zFGF11 are useful for inhibiting disorders associated with kidney epithelium such as glomerulonephritis
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Watanabe CK, W
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Smith V, Stephan JF,
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2000WO-US030873.
2000US-0253646P.
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25-JUL-2000; 2000US-0220624P.
25-JUL-2000; 2000US-0220638P.
25-JUL-2000; 2000US-0220664P.
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                                                                                                                                                                                                     16; Conservative
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10-NOV-2000;
28-NOV-2000;
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22-AUG-2000;
23-AUG-2000;
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10-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU83630;
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The invention relates to one hundred and twenty two nucleic acids canceding PRO polypeptides. The sequences of the 122 PRO polymucleotides encoding PRO polypeptides. The PRO nucleic acids, polypeptides, and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in periorte cells, for simulating the proliferation or differentiation of chondrocyte cells, for simulating the release of tumour necrosis factor-alpha from human blood, for stimulating the release of tumour necrosis factor-alpha from human blood, fibroblast cells. The PRO polypeptide may also be used as molecular of fibroblast cells. The PRO polypeptide may also be used as molecular applications in molecular biology, including use as hybridisation probes, and in chromesome and gene mapping. Au033592-AAU83713 represent human PRO protein sequences of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Mature fibroblast growth factor homologue, zFGF11. This sequence is specifically claimed in claim 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth factor; FGF; zFGF11; mesenchymal cell; FGFRIIIc;
             related disorder and for diagnosing tumors such
useful for treating a PRO related disorder and for diagnosing tumors such as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or liver tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, fibroblast growth factor, FGF; zFGF11; mesenchymal cell; FGFRII: osteoblastic lineage cell; diabetes mellitus; neuropathy; neural development; amyotrophic lateral sclerosis; cerebrovascular stroke; neuronal differentiation; congenital disorder; nervous system disorder; cardiac function; wound healing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human fibroblast growth factor (FGF) homologue, zFGF11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 86; DB 5; ]
100.0%; Pred. No. 4.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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/label= Signal_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG32358 standard; protein; 208 AA.
                                                                                     Claim 11; Fig 78; 359pp; English.
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-626540/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 208 AA;
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N-PSDB; ABK91310.

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Nguyen DB, Walia N, Gandhi AR, Azimzai Y;
Lu Y, Baughn MR, Duggan BM, Lee S, Hafalia A;
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23-JUN-2000; 2000US-0213465P.
14-NOV-2000; 2000US-0249019P.
                                                                                                                                                                                   Claim 4; Fig 1; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-2001; 2001WO-US018476.
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O, Tang YT, L
                                                                                                                                 cerebrovascular stroke.
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Best Local Similarity
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Policky JL;
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The present invention relates to new extracellular messenger polypeptides and polymucleotides encoding them. XMES is useful in the diagnosis, and polymucleotides encoding them. XMES is useful in the diagnosis, are treatment and prevention of neurological disorders (e.g. epilepsy, extroke, or Alzheimer's disease), autoimmune/inflammatory disorders (e.g. acquired immune deficiency syndrome, AIDS, Addison's disease, or allergies), developmental disorders (e.g. renal tubular acidosis, anaemia or Cushing's syndrome), endocrine disorders (e.g. hypophysectomy, or cushing's syndrome), and call proliferative disorders (e.g. cancer), and in the assessment of the effects of exogenous or compounds on the expression of nucleic acid and amino acid sequences of compounds on the expression of nucleic acid and amino acid sequences of viral, bacterial, fungal, parasitic, processal and helminthic infections, trauma, disorders associated with hypopituitarism, continually the infections, trauma, disorders associated with hypopituitarism, continually parasitic disorders such as type II diabetes mellitus. The xMES may be used for somatic or germline gene therapy. The present
                                                                                                                    New extracellular messenger polypeptides and polynucleotides encoding them, useful for diagnosing, treating or preventing e.g. neurological, autoimmune, inflammatory, developmental and endocrine disorders.
                                                                                                                                                                                                                                                                            claim 1; Page 111; 123pp; English.
                           WPI; 2002-154573/20.
N-PSDB; AAD28493.
The invention relates to an isolated human polypeptide (1) for zFGF11 (a fibroblast growth factor), and the encoding polynucleotide (II). (I) and (II) are used in methods of the invention stimulating proliferation of mesenchymal cells, detecting the presence of zFGF11 in a biological sample, detecting the presence of zFGF11 in a biological sample, detecting the presence of sFGF11 in a biological sample, stimulating proliferation of osteoblastic lineage cells. The polypeptides, nucleic acid and/or antibodies of the invention may be used in treatment of disorders associated with diabetes mellitus, neural cell development or degeneration, anyotrophic lateral sclerosis, development or degeneration, anyotrophic lateral sclerosis, cerebrovascular stroke, neuropathy associated with lack of maintenance of cerebrovascular stroke, neuropathy associated with lack of maintenance of cerebrovascular stroke, neuropathy associated with lack of maintenance of cerebrovascular development. Molecules of the invention may also be useful for improving cardiac function and for promoting wound healing of the epidezmis. The present sequence represents the amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                      Isolated polypeptide for zFGFI1 (fibroblast growth factor) useful in treatment of disorders associated with diabetes mellitus, neural cell development or degeneration, amyotrophic lateral sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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100.0%; Pred. No. 4.4e-07;
Live 0; Mismatches 0; Indels
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Human; PRO polypeptide; secreted and transmembrane protein; anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
                         100.0%; Score 86; DB 5; Length 208; 100.0%; Pred. No. 4.4e-07; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                            ABU80777 standard; protein; 208 AA.
                                     Query Match
100.0%; Some Seat Local Similarity 100.0%; P. Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUL-2000; 2000US-0220638P.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-2002; 2002US-00230163.
                                                                                                                                              59
                                                                                                          1 RORYLYTDDAQQTEAH 16
                                                                                                                                                                                                                                                                                                                     23-JUN-2003 (first entry)
                                                                                                                                              44 RORYLYTDDAOOTEAH
                                                                                                                                                                                                                                                                                                                                                           Human PRO polypeptide #39
Sequence 208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2003036635-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                  ABU80777;
                                                                                                                                                                                                                           ABU80777
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                                                                                                                                                                                                                                                                                                                                       Human; extracellular messenger; neurological disorder; epilepsy; XMES-3; Alzheimer's disease; autoimmune disorder; renal tubular acidosis; stroke; acquired immune deficiency syndrome; ALDS; Addison's disease; cytostatic; developmental disorder; anaemia; Cushing's syndrome; endocrine disorder; vascular malformation; cell proliferative disorder; gene therapy; cancer; neuroprotective; trauma; hypopiunitarism; hypothyroidism; antihelminthic; hyperthyroidism; gonadal steroid hormone; pancreatic disorder; nootropic, diabetes mellitus; immunosuppressive; anti-inflammatory; antibacterial; antiviral; antifungal; parasitic; protozoal; allergy.
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Goddard A, Godowski PJ; phan JF, Watanabe CK, Wood WI;

Gerritsen ME, Goddard Smith V, Stephan JF,

Baker KP, Desnoyers L, Grimaldi JC, Gurney AL, (GETH) GENENTECH INC.

WPI; 2003-342045/32

N-PSDB; ACA66879

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Gaps

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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the diagnostis and treatment of tumoure. Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ABUS0739-ABUB0860 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the
One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                      USPTO web site at segdata.uspto.gov/psipsDIDEntry.html
                                                                                                           Claim 11; Fig 78; 314pp; English
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Score 86; DB 6; Length 208; Pred. No. 4.4e-07; Mismatches 0; 100.0%; 1 RORYLYTDDAQQTEAH 16 44 ROKYLYTDDAQQTEAH 59 Query Match
Best Local Similarity 100." g

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Gaps · 0

0; Indels

ABO33743 standard; protein; 208 AA. (first entry 17-SEP-2003 ABO33743; RESULT 10 AB033743

Human; secreted and transmembrane protein; PRO; cytostatic; antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha; chondrocyte stimulator; fibrobiast modulator; paramaceutical; diagnostic; biosensor; bloreactor; tumour; lung tumour; oolon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; bone disorder; cartilage disorder; sports injury; Novel human secreted and transmembrane protein PRO10196. arthritis; wound

Homo sapiens.

US2003045687-A1

12-AUG-2002; 2002US-00218631. 06-MAR-2003

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Desnoyers L, C, Gurney AL, WPI; 2003-512315/48. Grimaldi JC, Baker KP,

N-PSDB; ACD68631.

New genes, and its encoded secreted and transmembrane polypeptides, useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or pericyte proliferation, especially for treating lung tumors, arthritis or wounds in a mammal

Claim 11; Fig 78; 314pp; English.

Godowski PJ;

Gerritsen ME, Goddard A,

Desnoyers L,

Baker KP,

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The invention describes an isolated mucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 122 PRO (secreted and transmembrane) polypeptides whose sequences are fully defined in the specification; or (b) any of 122 nucleotide cilloation; or the full length coding sequence of any these 122 mucleotide sequences. The PRO polypeptides or polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour, or liver tumour, prostate tumour, rectal tumour, or liver tumour, or liver tumour, or simulating the proliferation or differentiation of chondrocyte cells, for stimulating proliferation of pericyte cells, or for modulating configuration of pericyte cells, or for modulating colypeptides are useful in drug screening, particularly as targets or cartilage disorders (e.g. sports injuries or arthritis), or wounds. The PRO polypeptides are useful in drug screening, particularly as targets or the transperior of the presence of these diseases. The PRO polypeptides are useful as molecular weight markers, or for chromosome conference of these diseases. The PRO polypeptides are useful as molecular weight markers, or for chromosome conference of these diseases. The PRO polypeptides are useful as molecular weight markers, or for chromosome conference of these diseases. The PRO polypeptides are useful as molecular weight markers, or for chromosome conference of these diseases. The PRO genes may gereening libraries of human cDNA, genond cDNA or mRNA. The PRO genes may exceening libraries are useful as novel human secreted and conservation and sequence of a novel human secreted and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, secreted and transmembrane protein, PRO, cardiant, cytostatic, antiangiogenic, hypotensive, vulnenry, antiarteriosclerotic, gene therapy, cardiovascular disorder, endothelial disorder; anglogenic disorder; cardiac hypertrophy; trauma; cancer;
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100.0%; Pred. No. 4.4e-07;
tive 0; Mismatches 0;
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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Best Local Similarity 100.
Matches 16; Conservative
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Wood WI;

Watanabe CK,

Stephan JF,

Smith V,

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Treating a mammal exhibiting Type 2 diabetes or Type 1 diabetes or obesity, by administering composition comprising fibroblast growth factor
                                                                                                                                                                                              encoding movel human secreted and transmembrane (PRO) polypeptides. The produing novel human secreted and transmembrane (PRO) polypeptides. The pRO nucleic acids, polypeptides, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, agerelated macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromesome and gene mapping. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; fibroblast growth factor 21; FGF-21; chromosome 19; 19q13.1-qter; diabetes; obesity; antidiabetic; anorectic; type 2 diabetes;
                                                                            One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                     The invention describes one hundred and eighty seven nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human fibroblast growth factor 21 protein SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 86; DB 6; I
100.0%; Pred. No. 4.4e-07;
:ive 0; Mismatches 0;
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Gurney AL,
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                                  WPI: 2003-393229/37.
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Best Local Similarity
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                                                    N-PSDB; ACA68535
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Grimaldi JC,
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59

Shiyanova TL;

Claim 3; Fig 1; 32pp; English

Gaps

0;

Length 208; Indele

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The present sequence represents human fibroblast growth factor 21 (FGF-21). FGF-21 is located to chromosome 19, more specifically to 19q13.1—CG qter. The present invention describes a method for treating a mammal exhibiting type 2 diabetes or type 1 diabetes, or treating a mammal combisition type 2 diabetes or type 1 diabetes, or treating a mammal for obesity which comprises administering to the mammal a composition comprising FGF-21 which has at least 95% amino acid sequence identity to the 208 amino acid sequence given in ABP96156. Also described: (1) administering FGF-21 to induce an increase in glucose uptake in adipocyte cells by administering FGF-21 to induce an increase in glucose uptake, and (2) administering a medicament for treating type 1 diabetes, type 2 diabetes or obesity in a mammal using FGF-21 having 95% amino acid sequence identity to ABP96156. FGF-21 has antidiabetic and anorectic activities. The method is useful for treating a mammal for obesity. The method is preferably useful for treating twee 1 or type 2 diabetes, and for treating domestic animals for obesity. The method is preferably the animals for obesity the method is preferably the animals for obesity the method is preferably the animals for obesity the method is preferably the animals for obesity the method is preferably the animals for obesity the method is preferably the animals for obesity the method is preferably the animals for obesity the method is preferably the animals for obesity the method is preferably the treating domestic animals for obesity the method is preferably the method is preferably the method is preferably the method and preferably the method is preferably the method is preferably the method is preferably the method is preferably the method is preferably the preferably the method is preferably the preferably the method is preferably the method is preferably the method is preferably the method is preferably the method is preferably the preferably the preferably the preferably the preferably the preferably the pr
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Wood WI;
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Smith V, Stephan JF, Watanabe CK,
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100.0%; Pred. No. 4.4e-07;
ive 0; Mismatches 0;
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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Best Local Similarity
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Grimaldi JC,
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proliferation and the detection of the presence of a tumour within a mammal. Furthermore, the nucleic acid may be useful for the manufacture of a medicament for diagnosing or treating a tumour within a mammal or for measuring or detecting the expression of an associated gene, as well as during gene therapy. The current sequence is that of the human PRO protein of the invention
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Sequence 208 AA;

100.0%; Score 86; DB 6; Length 208; 100.0%; Pred. No. 4.4e-07; 0; Indels 0; Mismatches 1 RORYLYTDDAQQTEAH 16 44 RORYLYTDDAQQTEAH 59 Query Match Best Local Similarity 100." Matches 16; Conservative à

0

Gaps 0;

ABJ72394 standard; protein; 208 AA.

ABJ72394;

06-NOV-2003 (first entry)

PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte; tumour necrosis factor; proliferation; differentiation; gene therapy; dermal fibroblast. Human PRO10196 protein

Homo sapiens.

US2003027988-A1.

06-FEB-2003

26-AUG-2002; 2002US-00227884.

01-JUN-2001; 2001MO-US017800. 29-JUN-2001; 2001MO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Goddard A, Godowski PJ; ephan JF, Watanabe CK, Wood WI; Gerritsen ME, Goddard Smith V, Stephan JF, Desnoyers L, Grimaldi JC, Baker KP,

WPI; 2003-503301/47. N-PSDB; ABT44547.

New PRO protein encoding nucleic acid, useful for preparing PRO polypeptides and anti-PRO antibodies for detecting the presence of a tumor in a mammal

The invention relates to an isolated nucleic acid encoding a PRO polypeptide. Nucleic acids that encode PRO can be used to generate either transgenic animals or knock-out animals useful in developing and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy for replacing defective gene, in chromosome identification, as chromosome markers, or in generating probes to isolate thil length PRO cDNA. The PRO polypeptides are useful for chondrocyte stimulation, TNF-alpha stimulation, human dermal fibroblasts stimulation and for detecting the presence of tumour in an mammal. The PRO colypeptides are useful as molecular markers for protein electrophoresis and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO antibodies are useful in diagnostic assays for pro an affinity purification of PRO from recombinant cell culture or natural sources. The present sequence represents the amino acid sequence of a human secreted/transmembrane PRO polypeptide

Claim 19; Fig 78; 315pp; English.

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Gaps

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Length 208;

100.0%; Score 86; DB 6; Length 20 100.0%; Pred. No. 4.4e-07; .ive 0; Mismatches 0; Indels

1 RORYLYTDDAOOTEAH 16

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16; Conservative

Local Similarity

Query Match Best Loca Matches

Sequence 208 AA;

59

44 RORYLYTDDAOOTEAH

Claim 11; Fig 78; 324pp; English

The invention relates to a novel isolated PRO protein encoding nucleic acid. The nucleic acid of the invention may be useful for preparing PRO polypeptides and anti-PRO antibodies for detecting the presence of a tumour in a mammal. Furthermore, the molecules of the invention may be useful for stimulating proliferation or gene expression in pericyte cells, the release of tumour necrosis factor (TNF)-alpha from human blood, the proliferation or differentiation of chondrocyte cells and for inhibiting the proliferation of normal human dermal fibroblast cells. Finally, the molecules may be utilised during gene therapy. The current sequence is that of the human PRO protein of the invention

Sequence 208 AA;

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Score 86; DB 6; Length 208; Pred. No. 4.4e-07;
    100.08;
    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                     Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
Gaps
                                                                                                                                                             Human, chondrocyte stimulation; TNF-alpha stimulation; gene therapy;
human dermal fibroblast stimulation; tumour; tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                            New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, or in generating probes.
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Indels
                                                                                                                                            Human secreted/transmembrane polypeptide PRO 10196.
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Mismatches
                                                                                    ABO34289 standard; protein; 208 AA.
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                         (first entry)
                   1 RORYLYTDDAQQTEAH
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Grimaldi JC, Gurney AL,
16; Conservative
                                                                                                                                                                                affinity purification.
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1 RORYLYTDDAQQTEAH 16

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Disclosure; Page 15-16; 22pp; English.
       ADA37038 standard; protein; 208 AA.
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                                                                                                         15-JAN-2002; 2002US-0348890P
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                     (first entry)
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                                                                            Homo sapiens
                     20-NOV-2003
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              ADA37038;
RESULT 16
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Human membrane bound receptor/protein PRO10196 amino acid sequence.
                                                                                                                ABJ72096 standard; protein; 208 AA.
44 RORYLYTDDAOOTEAH
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                                                                                                                                                               ABJ72096;
                                                                       RESULT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method for the reduction of mortality and morbidity in critically ill patients, which involves the and morbidity in critically ill patients, which involves the daministration of fibroblast growth factor 21 (FGF-21) (I). (I) has critically independent immunosuppressive, continifiammatory, antibacterial, immunosuppressive, vasotropic, haemostatic and aphrotropic activities, and can be used as a glucose level regulator, a glucose uptake stimulator, and an insulin continity enhancer. (I) can be used in the manufacture of a medicament of for the reduction of morbidity and mortality in critically ill patients suffering from systemic inflammatory response syndrome (SIRS), confering from systemic inflammatory response syndrome (SIRS), confering from systemic inflammatory sepais and chronic obstructive pulmonary disease (e.g. emphysema and chronic broncitie).

The SIRS includes pancreatitis, ischaemia, multiple trauma and tissue (failure. FGF-12 regulates Shock, immune-mediated organ injury, shock and renal calidestion; affects the overall metabolic state and counter-acts negative side effects that occur during the body's stress response to sepsis; reduces morbidity and mortality that occurs in critically ill patients; and stimulates glucose uptake and enhances insulin sensitivity. The present sequence represents the human FGF-21 amino acid sequence, which is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of fibroblast growth factor 21 for reduction of mortality and morbidity in parients suffering from e.g. systemic inflammatory response syndrome and acute respiratory distress syndrome.
                                                                                                                                                                                                                             mortality; morbidity; fibroblast growth factor 21; FGF-21; antiinflammatory; respiratory; antibacterial; immunosuppressive; vasotropic; haemostatic; nephrotropic; glucose level regulator; glucose uptake stimulator; insulin sensitivity enhancer; systemic inflammatory response syndrome; respiratory distress; acute lung injury; acute respiratory distress syndrome; multiple organ dysfunction syndrome; sepsis; chronic bronchitis; chronic obstructive pulmonary disease; emphysema; chronic bronchitis; pancreatitis; ischaemia; multiple trauma; tissue injury; haemorrhagic shock; immune-mediated organ injury; shock; renal failure.
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                                                                                                                                                                                              Human fibroblast growth factor 21 SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 208 AA;
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process. Income succession by the control of the control of the pharmaceutical and diagnostic agents, such as in the blocking of receptor sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the mammal. In addition, they may be useful for measuring or detecting the expression of a tumour in a manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is the amino acid sequence of a human PRO protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating
Human, PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; oytotoxic factor fadifferentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2000; 2000WO-US005841.
01-UUN-2001; 2001WO-US01900.
29-UUN-2001; 2001WO-US021.066.
09-APR-2002; 2002US-00119480.
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24-FEB-2000; 2000WO-US005004.
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Gaps ; 0

Conservative

Local Similarity les 16; Conserva

Matches

Query Match

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LINGHIGH OIL URBGILDER AN INDUATED KNO (SECTEFEG AND ITABIREMEDIZABLE)

DOLYPEPTIGE (II) PRO982, PRO1160, PRO1187 PRO1239 polypeptide are
useful for stimulating the proliferation of or gene expression in
perioque cells. PRO357, PRO329, PRO1272 or PRO4405 polypeptide are useful
for stimulating the proliferation of differentiation of chondrocyte
cells. PRO231, PRO357, PRO752, PRO1185, PRO1180 or PRO1419 polypeptide
are useful for stimulating the release of tumour necrosis factor (INF)-
alpha from human blood. PRO982, PRO531, PRO155, PRO136, PRO1419, PRO1149,
PRO137, PRO126, PRO1166, PRO1167, PRO1077, PRO1411, PRO1411,
PRO159, PRO1181, PRO1166, PRO1197, PRO1197, PRO1411, PRO1412,
PRO1266, PRO1370, PRO347, PRO1166, PRO1373, PRO1379, PRO1374, PRO13139,
PRO1867, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1160, PRO1387,
PRO1867, PRO1368, PRO1387, PRO1409, PRO1474, PRO1917, PRO1461, PRO1367,
PRO1867, PRO6363, PRO1801, PRO1404, PRO4333, PRO5444, PRO6322,
PRO9404, PRO6393 or PRO10056 polypeptide are useful for
stimulating the proliferation of normal human dermal fibroblasts cells.
PRO181, PRO229, PRO188, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New PRO polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard A, Godowski PJ;
phan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                               release;
                                                                                                                                                                                                                                                                                                                                                                              human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release, (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; prosette tumour; prosette tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                          Gaps
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100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07;
                                     Indels
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                                       Mismatches
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                                     0;
                                                                                                                                                                                                                        ADB83568 standard; protein; 208
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                               1 RORYLYTDDAQQTEAH 16
                                                                                                               44 RORYLYTDDAQQTEAH 59
                                                                                                                                                                                                                                                                                                      (first entry)
                                       16; Conservative
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C, Gurney AL,
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N-PSDB; ADB83567.
                     Local Similarity
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                                       Matches
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pro5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides involves comparing the level of expression of the above PRO polypeptides of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polyuncleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful corremanting useful for treating bone and/or cartilage disorders (e.g., arthritis, sueful for treating bone and equence of a human secreted and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted and transmembrane protein; PRO; cytostatic; vulnexary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; prostate tumour; lung tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
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Smith V, Stephan JF, Watanabe CK, Wo
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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Grimaldi JC, Gurney AL,
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es 16; Conservative
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N-PSDB; ADB80673.
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invention describes an isolated PRO (secreted and transmembrane)

Claim 11; Fig 78; 305pp; English

The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (1). PRO982, PRO116) PRO1187 or PRO1329 polypeptide are
useful for stimulating the proliferation of or gene expression in

CC for stimulating the proliferation of dindrocyte

cells. PRO231, PRO125, PRO1305 or PRO4405 polypeptide are useful

CC for stimulating the proliferation or differentiation of chondrocyte

cells. PRO337, PRO525, PRO1305 or PRO1499 polypeptide

are useful for stimulating the release of tumour necrosis factor (TMF)
are useful for stimulating the release of tumour necrosis factor (TMF)
calpha from human blood. PRO982, PRO3131, PRO1905, PRO1130,

PRO132, PRO134, PRO136, PRO1065, PRO1093, PRO9141, PRO1411,

PRO126, PRO130, PRO136, PRO1905, PRO1909, PRO1141, PRO1309,

CC PRO133, PRO137, PRO1906, PRO1909, PRO1411, PRO1309,

CC PRO1867, PRO1928, PRO1906, PRO1901, PRO1917, PRO1917, PRO1901,

PRO1987, PRO1928, PRO1981, PRO1901, PRO1917, PRO1901, PRO4913,

CC PRO1987, PRO1928, PRO1981, PRO1901, PRO1917, PRO1901, PRO1901,

CC STIMULATING the proliferation of normal human dermal fibroblast cells.

CC PRO1985, PRO1986, PRO1994, PRO1994, PRO1986, PRO4902, PRO4904,

CC Estimulating the proliferation of normal human dermal fibroblast cells.

CC PRO1985, PRO1986, PRO1994, PRO1997, PRO9996, PRO4902, PRO4904,

CC PRO1986, PRO1986, PRO1994, PRO1997, PRO9996, PRO4903, PRO4904,

CC PRO1986, PRO1986, PRO1998, PRO1997, PRO9996, PRO4905, PRO9996,

CC Inhibiting the proliferation of normal human dermal fibroblast cells. PRO

CC C polypeptides such as PRO6004, PRO4998, PRO9996,

CC C polypeptides such as PRO6004, PRO9998, PRO9996,

CC Involves comparing the level of expression of the above PRO polypeptides

CC Thromal cells of the same cell type, where a higher level of expression of the prosence of tumour in a mammal, and a centrol sample of colls the presence of tumour in a mammal, and a centrol sample of the presence of tumour in a mammal which mammal cells of the presence of tumour in a mammal which mammal cells of the presence

transmembrane PRO polypeptide. Sequence 208 AA;

44 RORYLYTDDAQOTEAH 59 1 RORYLYTDDAQQTEAH 16 Query Match Best Local Similarity 100. Matches 16; Conservative

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Gaps

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Indels

; 0

0; Mismatches

Score 86; DB 7; Length 208; Pred. No. 4.4e-07;

100.0%; 100.0%;

ADB73215 standard; protein; 208 AA RESULT 20

04-DEC-2003 (first entry) ADB73215;

Novel human secreted and transmembrane protein PRO10196.

chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; qene therapy

US2003096968-A1.

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The invention describes an isolated RPO (secreted and transmentally polypeptide are polypeptide (I). PRO982, PRO1167 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in the proliferation of differentiation of chondrocyte (I). PRO357, PRO229, PRO1305 or PRO4405 polypeptide are useful for stimulating the proliferation of differentiation of chondrocyte (I). PRO317, PRO725, PRO1305 or PRO1419, polypeptide are useful for stimulating the release of tumour necrosis factor (TMP). The release of tumour necrosis factor (TMP). The release of tumour necrosis factor (TMP). PRO1305, PRO1305, PRO1305, PRO1306, PRO1419, PRO1309, PRO1305, PRO1305, PRO1306, PRO1305, PRO1306, PRO1305, PRO1306, PRO1306, PRO1305, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1307, PRO1306, PRO1306, PRO1306, PRO1307, PRO1306, PRO1306, PRO1307, PRO1306, PRO1306, PRO1307, PRO1306, PRO1307, PRO1306, PRO1307, PRO1306, PRO1307, PRO1306, PRO1306, PRO1306, PRO1307, PRO1306, PRO1307, PRO1306, PRO1307, PRO1306, PRO1307, PRO1306, PRO1307, PRO1307, PRO1306, PRO1307, PRO1306, PRO1307, PRO1307, PRO1306, PRO1307, PRO1307, PRO1306, PRO1307, PRO1306, PRO1307, PRO1307, PRO1306, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307, PRO1307
                                                                                                                                                                                                                                        Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes an isolated PRO (secreted and transmembrane)
                                                                                                                                                                                                                                                                                                                                                                        New isolated PRO polypeptides useful as molecular weight markers in protein electrophoresis, useful for tissue typing, and for treating arthritis and tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Fig 78; 308pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ransmembrane PRO polypeptide.
                                                                                                         01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                29-AUG-2002; 2002US-00232223
                                                                                                                                                                                                                                                  Desnoyers L,
                                                                                                                                                                                                         (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADB73214.
                                                                                                                                                                                                                                                                          Grimaldi JC,
                     22-MAY-2003.
                                                                                                                                                                                                                                                       Baker KP,
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100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07; Indels 0; Mismatches ADB78297 standard; protein; 208 AA. 1 RORYLYTDDAQQTEAH 16 44 RORYLYTDDAOOTEAH 59 16; Conservative Query Match Best Local Similarity Matches RESULT 21 ADB78297 ID ADB7 ð

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Gaps

0

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Baker
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2003-730024/69.
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                                                                                                                                               Sequence 208 AA;
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01-JUN-2001; 2
29-JUN-2001; 2
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                                                                                                                                                                                            Query Match
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Complepetide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

consecul for stimulating the proliferation of or gene expression in

pericyte cells. PRO237, PRO225, PRO1132, PRO4405 polypeptide are useful

for stimulating the proliferation or differentiation of chondrocyte

cells. PRO231, PRO357, PRO125, PRO1155, PRO1196 or PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TMF)-

alpha from human blood. PRO982, PRO357, PRO125, PRO1306, PRO1419, PRO1414,

PRO1134, PRO3137, PRO526, PRO1363, PRO183, PRO1419, PRO1419, PRO1416,

CR PRO1478, PRO1134, PRO1365, PRO1305, PRO1191, PRO1411, PRO1411,

CR PRO1478, PRO1376, PRO1365, PRO1305, PRO1474, PRO1411, PRO1411,

CR PRO1478, PRO1376, PRO1305, PRO1405, PRO1474, PRO1311, PRO13138,

CR PRO1478, PRO1376, PRO1305, PRO1405, PRO1474, PRO1311, PRO13138,

CR PRO1478, PRO1376, PRO1409, PRO1474, PRO1917, PRO1411, PRO13138,

CR PRO1478, PRO1376, PRO1409, PRO1474, PRO1917, PRO1444, PRO1326,

CR PRO1478, PRO1376, PRO1409, PRO1474, PRO1317, PRO1444, PRO1326,

CR PRO1487, PRO1376, PRO1409, PRO1474, PRO1417, PRO1444, PRO4322,

CR PRO1487, PRO528, PRO4341, PRO1409, PRO1474, PRO1417, PRO1444, PRO4322,

CR C Stimulating the proliferation of normal human dermal fibroblasts cells.

CR PRO529, PRO7184, or PRO7455 polypeptide are useful for detecting the presence of tumour in a mammal which in a test sample of cells taken from the mammal, and a control sample of normal cells of the presence of tumour in the mammal, and a control sample of tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or tumour, or as theramantic prostate tumour, in the mammal or the properior of tumour, prostate tumour, rectal tumour or the properior of tumour prostate tumour, in the mammal or the properior of tumour prostate tumour, in the properior of tumour or the properior of tumour prostate tumour, in the properior of tumour or tumour or tumour or tumour or the properior of the properior
                                                                                                                                                                  Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; chondrocyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated PRO polypeptide useful for tissue typing, gene therapy, a molecular weight markers in protein electrophoresis, and for treating arthritis and tumors.
                                                                                                                     Novel human secreted and transmembrane protein PRO10196.
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-2002; 2002US-00219478
                                                                      04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Desnoyers L,
I, Gurney AL,
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N-PSDB; ADB78296.
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                       ADB78297;
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for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polynucleotides encoding them. The PRO polypeptides and polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TMF)-alpha from human blood, for stimulating the proliferation of chondrocyte cells, for stimulating the proliferation of or gene chondrocyte cells of for stimulating the proliferation of or gene normal human dermal fibroblasts. The PRO nucleic acids are useful as hybridisation probes, in chromsome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New PRO polypeptides and nucleic acids encoding the polypeptides, useful e.g. in gene therapy, disease diagnosis, chromosome identification and
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Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; darmal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                     Length 208;
                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                     100.0%; Score 86; DB 7; I 100.0%; Pred. No. 4.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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2001WO-US017800.
2001WO-US021066.
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technology, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents, in gene therapy, in chromosome identification, as chromosome markers and in generating probes. The PRO polypeptides, or anti-PRO antibodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.
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Sequence 208 AA;

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                            Gaps
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0
100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07;
                          0; Indels
                          0; Mismatches
                             16; Conservative
    Query Match
Best Local Similarity
                               Matches
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RESULT 23

ADB78051 standard; protein; 208 AA.

(first entry) 04-DEC-2003 ADB78051;

Noyel human secreted and transmembrane protein PRO10196.

Human, secreted and transmembrane protein, PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation, chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF) - alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; gene therapy

ното варіенв

US2003092886-Al.

15-MAY-2003

09-AUG-2002; 2002US-00216165.

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 25-JUL-2000; 2000US-0220607P.

(GETH) GENENTECH INC

09-APR-2002; 2002US-00119480.

Gerritsen ME, Goddard A, Godowski F Smith V, Stephan JF, Watanabe CK, Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

WPI; 2003-765494/72.

N-PSDB; ADB78050.

PJ; Wood WI;

Claim 11; Fig 78; 308pp; English.

Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as molecular weight markers in protein electrophoresis, for treating arthritis, tumor.

The invention describes an isolated PRO (secreted and transmembrane) polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in

pericyte cells. PRO357, PRO1229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO357, PRO355, PRO1355, PRO1365 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TMF) calpha from human blood. PRO982, PRO357, PRO3136, PRO1319, PRO1341, PRO1316, PRO1319, PRO1365, PRO1305, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1307, PRO1306, PRO1306, PRO1307, transmembrane PRO polypeptide.

Sequence 208 AA;

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0
Query Match
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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1 RORYLYTDDAQOTEAH 16 44 RORYLYTDDAQQTEAH 59 원 ð

RESULT 24

ADB87117 standard; protein; 208 AA.

04-DEC-2003 (first entry) ADB87117;

Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; break; prostate; rectum; liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic. Human PRO polypeptide #39.

Homo sapiens

US2003088067-A1.

08-MAY-2003.

L3-AUG-2002; 2002US-00219479.

01-JUN-2001; 2001MO-US017800. 29-JUN-2001; 2001MO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Wood WI;

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, W

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Human, PRO, secreted polypeptide, transmembrane polypeptide, tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                  ADB84699 standard; protein; 208 AA.
                                                                               Claim 11; Fig 78; 314pp; English.
                                                                                                                                                                                                                                                                                                                                 1 RORYLYTDDAOOTEAH 16
                                                                                                                                                                                                                                                                                                                                               44 RORYLYTDDAQQTEAH 59
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                                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO polypeptide #39
                                                                                                                                                                                                                                                                                                         Local Similarity 100.
       Desnoyers L,
                            2003-657981/62
                                     N-PSDB; ADB87116
                                                                                                                                                                                                                                                                                      Sequence 208 AA;
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              Grimaldi JC,
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       Baker KP,
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Matches
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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polynuclectides encoding them. The PRO polypeptides and polynuclectides are useful as pharmaceuticals, diagnostics, bioseness or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene cormal human dermal fibroblasts. The PRO nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, in generating technology, in generating transgenic animals which may be used in the development and screening of therapeutically useful reagents, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents, in gene therapy, in chromosome identification, as chromosome matibodies, are useful for preparing medicament for treating a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated PRO polypeptides, useful for tissue typing, gene therapy, molecular weight markers in protein electrophoresis, and for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Fig 78; 308pp; English.
28-JUL-1999; 99US-0146222P.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
01-JUN-2001; 2001WO-US01060.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                   Grimaldi JC,
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                The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polypeptides encoding them.

Transmembrane polypeptides) and the PRO polynucleotides encoding them. CC transmembrane polypeptides and polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumour, rectal tumour or liver tumour, breast tumour, rectal tumour or liver tumour, in a mammal, for stimulating the release of tumour necrosis factor (TNF) alpha from human constituting the proliferation of or gene chondrocyte cells, for stimulating the proliferation of or gene expression in perioyte cells or for stimulating the proliferation of or gene chondrocyte calls, for stimulating the proliferation of or gene choracyte cells in chromosome and gene mapping, in generating probes, in chromosome and gene mapping, in generating transgenic animals or knock-out animals which reagents, in gene therapy, in chromosome and gene mapping, in generating probes. The PRO polypeptides, or anti-PRO markers and in generating probes. The PRO polypeptides, or anti-PRO antibodies, such as perioyte-casociated tumours and bone and/or cartilage condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as perioyte-casociated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the recondition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as perioyte-casociated tumours and bone and/or cartilage consociated an encourar markers from condition because else and in tissue typing. This conditions and howers for protein electrophoresis, and in tissue typing. This conditions the properties of the invention.
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                    Godowski PJ;
rk Wood WI;
                                                                                                                                                                                                                                      One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
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                          Goddard A, Goucaco
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                                              Gerritsen ME, Goddard Smith V, Stephan JF,
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disorders (e.g. arthritis, sports injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             numan; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
                                                                                                                                                                                      Gaps
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                                                                                                                                        100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                            ADB83814 standard; protein; 208 AA.
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                                                                                                                                                                                                                               1 RORYLYTDDAQQTEAH 16
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                                                                                                                                                                                                                                                              44 RORYLYTDDAQQTEAH
                                                                                                                                                                                          16; Conservative
                                                                                                                                                                  Local Similarity
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14-AUG-2002; 2002US-00219536.

transmembrane PRO polypeptide.

New isolated polypeptides designated PRO polypeptides including polypeptides useful for stimulating the proliferation or differentiation of specific cell types, and for diagnosing cancer. Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; Claim 11; Fig 78; 314pp; English 25-JUL-2000; 2000US-0220607P. 01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480. 09-AUG-2002; 2002US-00216159. Baker KP, Desnoyers L, Grimaldi JC, Gurney AL, (GETH) GENENTECH INC. WPI; 2003-657584/62. N-PSDB; ADB83813. JS2003069397-A1 Homo sapiens gene therapy LO-APR-2003.

Sequence 208 AA;

ö Gaps ; 100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0
Matches 16; Conservative

The invention describes an isolated PRO (secreted and transmembrane)

CD polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
co useful for stimulating the pro229, PRO1272 or PRO4405 polypeptide are useful
co stimulating the pro11feration or differentiation of chondrocyte
colls. PRO321, PRO325, PRO1255, PRO1365, PRO1419 polypeptide
cals. PRO331, PRO365, PRO982, PRO357, PRO1256 or PRO1419 polypeptide
are useful for stimulating the release of tumour necrosis factor (INR)calpha from human blood. PRO982, PRO357, PRO126, PRO1419, PRO1419,
CD PRO137, PRO326, PRO363, PRO357, PRO1206, PRO1419, PRO1419,
CD PRO125, PRO1134, PRO126, PRO1186, PRO1192, PRO1274, PRO1314,
CD PRO1343, PRO1376, PRO1367, PRO1379, PRO1274, PRO1314, PRO1338,
CD PRO1343, PRO1376, PRO1409, PRO1419, PRO1419, PRO1419, PRO1419,
CD PRO1481, PRO1286, PRO1401, PRO1403, PRO1444, PRO1317, PRO1411, FRO432,
CD PRO3481, PRO229, PRO798, PRO1194, PRO1372, PRO1488, PRO4322,
CD PRO181, PRO229, PRO798, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
CD PRO5181, PRO225, PRO7184, Or PRO7428, PRO1488, PRO525, PRO7184, PRO1184, PRO1272, PRO1488, PRO525, PRO5184, PRO1184, PRO1374, PRO1481, PRO525, PRO5184, PRO1

Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as molecular weight markers, for treating arthritis, tumor.

Claim 11; Fig 78; 308pp; English.

inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal while involves comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of

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Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                  human, secreted and transmembrane protein, PRO; cytostatic; vulnerary; antiarthritic, pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF) alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
                                                                                                                                                                                                                    colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                                                                                                                 Novel human secreted and transmembrane protein PRO10196.
                                                                     ADB72969 standard; protein; 208 AA.
                                                                                                                                                                                                                                                                                                                              12-AUG-2002; 2002US-00218956.
                                                                                                                                                                                                                                                                                                                                                   29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
1 RORYLYTDDAQQTEAH 16
                                                                                                               (first entry)
                   44 RORYLYTDDAQQTEAH
                                                                                                                                                                                                                                                                                                                                                                                                      Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                     JS2003092887-A1.
                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                               04-DEC-2003
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the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour. The timour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polymucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polymptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmembrane polypeptides) and the PRO polynucleotides encoding them. The PRO polypeptides and polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation or differentiation of
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                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-alpha; TMY-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerritsen ME, Goddard A, Godowski ÞJ;
Smith V, Stephan JF, Watanabe CK, Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, or for preparing a medicament for treating
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                                                                                                                                                                                                                                                                    Length 208;
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                                                                                                                                                                                                                                                                    100.0%; Score 86; DB 7; I 100.0%; Pred. No. 4.4e-07;
                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC36807 standard; protein; 208 AA.
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                                                                                                                                                                                               transmembrane PRO polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                                 1 RORYLYTDDAQQTEAH 16
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                                                                                                                                                                                                                                                                                                                                                                                     44 RORYLYTDDAGOTEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PRO polypeptide #39.
                                                                                                                                                                                                                                                                                                              Conservative
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C, Gurney AL,
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N-PSDB; ADC36806.
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Les 16; Conserv
                                                                                                                                                                                                                                     Sequence 208 AA;
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                                                                                                                                                                                                                                                                        Query Match
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chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells or for stimulating the proliferation of cormal human dermal fibroblasts. The PRO nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant cethmology, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents, in gene therapy, in chromosome identification, as chromosome antibodies, are useful for preparing a medicament for treating a mithodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartiage disorders (e.g. arthritis, sports injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                          Length 208;
                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                          100.0%; Score 86; DB 7; 100.0%; Pred. No. 4.4e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC21797 standard; protein; 208 AA.
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25-JUL-2000; 2000US-0220666P.
26-JUL-2000; 2000US-0220893P.
01-AUG-2000; 2000US-022425P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0220585P.
2000US-0220605P.
2000US-0220607P.
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20-JUN-2000; 2000US-0212901P.
22-JUN-2000; 2000US-0213807P.
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25-JUL-2000; 2000US-0220585P
25-JUL-2000; 2000US-0220605P
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25-JUL-2000; 2000US-0220624P.
25-JUL-2000; 2000US-0220638P.
25-JUL-2000; 2000US-0220664P.
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2000WO-US030873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 RORYLYTDDAQQTEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO polypeptide #39
                                                                                                                                                                                                                                                                                                                                                                               16; Conservative
                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                           Sequence 208 AA;
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24-AUG-2000;
10-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 29
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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polynucleotides encoding them. The PRO polypeptides and polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour nerosis factor (TMF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene cormal human dermal fibroblasts. The PRO nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, in generating the chnology, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents, in generating probes. The PRO polypeptides, or anti-PRO antibodies, are useful for preparing a medicament for treating a medicament for treating a medicament for treating a medicament for treating a medicament for treating a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-properting and the properties or anti-properties or anti-properting and the properties or anti-properties                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibodies, such as periorte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated PRO polypeptide useful for tissue typing, as molecular weight markers in protein electrophoresis, for treating arthritis, tumor.
                                                                                                                                                                                                                                       Godowski PJ;
~~ Wood WI;
                                                                                                                                                                                                                                                             Gerritsen ME, Goddard A, Godowski P
Smith V, Stephan JF, Watanabe CK,
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                           2001WO-US006520.
2001WO-US017092.
2001WO-US017800.
                                                                                                                  2001WO-US021066.
2002US-00119480.
2000WO-US034956
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nes 16; Conservative
                                                                                                                                                                                                                                                                   Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-765526/72.
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                                                          25-MAY-2001;
01-JUN-2001;
                                                                                                                  29-JUN-2001;
09-APR-2002;
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Best Local S:
Matches 16
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0; Gaps 6 Length 208; 1 RORYLYTDDAQQTEAH 16

44 RORYLYTDDAQQTEAH 59

ADC49828 standard; protein; 208 AA. RESULT 30 ADC49828

(first entry) 18-DEC-2003

ADC49828;

Novel human secreted and transmembrane protein PRO10196.

human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; chondrocyte cell proliferation; tumour necrosis factor alpha release; (TNF) -alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;

The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

cuseful for stimulating the proliferation of or gene expression in

periopte cells. PRO357, PRO229, PRO1272 or PRO445 polypeptide are useful

cor stimulating the proliferation of differentiation of chondrocyte

cells. PRO231, PRO357, PRO7155, PRO1306 or PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TNRF)
cells. PRO331, PRO356, PRO951, PRO3156, PRO1306, PRO1419, PRO1416,

RRO1478, PRO1134, PRO526, PRO5105, PRO1909, PRO1101, PRO1410, PRO1406,

RRO1478, PRO1134, PRO1266, PRO1105, PRO1909, PRO1174, PRO11306,

RRO1478, PRO1137, PRO1307, PRO1401, PRO1401, PRO1412,

RRO1266, PRO1330, PRO1377, RRO1409, PRO1473, PRO1411, PRO1412,

RRO1867, PRO1326, PRO1401, PRO1406, PRO1409, PRO1404, PRO1409,

RRO1867, PRO1326, PRO1401, PRO1401, PRO1401, PRO1401,

RRO1867, PRO1526, PRO1401, PRO1401, PRO1401, PRO1401,

RRO1867, PRO1529, PRO1468, PRO11009, PRO1401, PRO1401, PRO1401,

RRO1867, PRO1529, PRO1468, PRO1109, PRO1401, PRO1401, PRO1401,

RRO1867, PRO1529, PRO1468, PRO1109, PRO1401, PRO1401, PRO1401,

RRO1867, PRO1401, PRO16164, Or PRO14027, PRO1408, PRO4408, PRO1409,

CC RRO1861, PRO16164, Or PRO1405, PRO1404, PRO1406, PRO1408,

CC RRO1861, PRO16164, Or PRO1405, PRO1406, PRO1408,

CC RRO1861, PRO1406, PRO16164, OR PRO16164, PRO1406, PRO1408,

CC RRO1867, PRO1406, PRO16164, OR PRO16164, PRO16164, PRO16164,

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CC RRO1867, PRO16164, OR PRO16164, PRO16164,

CC RRO1867, PRO16164, OR PRO16164, PRO16164,

CC RRO1867, PRO16164, PR Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; New secreted and transmembrane PRO polypeptide useful for preparing medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody, e.g. cancer. liver tumour; tissue typing; chromosome mapping; gene mapping; Claim 11; SEQ ID NO 78; 314pp; English 25-JUL-2000; 2000US-0220605P. 01-JUN-2001; 2001WO-US017B00. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-001194B0. 14-AUG-2002; 2002US-00219075. Desnoyers L, (GETH) GENENTECH INC. WPI; 2003-801154/75. N-PSDB; ADC49827 US2003088064-A1 gene therapy. Grimaldi JC, Homo sapiens 08-MAY-2003 Baker KP,

Gaps 0: Query Match 100.0%; Score 86; DB 7; Length 208; Best Local Similarity 100.0%; Pred. No. 4.4e-07; Matches 16; Conservative 0; Mismatches 0; Indels Sequence 208 AA;

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transmembrane PRO polypeptide.

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44. RQRYLYTDDAQQTEAH 59

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The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
useful for stimulating the proliferation of or gene expression in

pericyte cells. PRO327, PRO229, PRO1272 or PRO4405 polypeptide are useful

for stimulating the proliferation or differentiation of chondrocyte

cells. PRO231, PRO357, PRO225, PRO1155, PRO1306 or PRO1419 polypeptide

care useful for stimulating the release of tumour necrosis factor (TNP)-

alpha from human blood. PRO982, PRO357, PRO1306, PRO1419, PRO214,

PRO247, PRO337, PRO526, PRO363, PRO537, PRO1035, PRO4419, PRO1419,

CRO247, PRO330, PRO1367, PRO1065, PRO8199, PRO1011, PRO1301,

PRO1286, PRO1380, PRO1387, PRO1106, PRO1192, PRO1274, PRO1314,

PRO1286, PRO1380, PRO3431, PRO1409, PRO1474, PRO1279, PRO1341, PRO1322,

CRO387, PRO5029, PRO988, PRO1801, PRO4333, PRO3444, PRO4322,

CRO388, PRO5025, PRO7184, or PRO1005 polypeptide are useful for

stimulating the proliferation of normal human dermal fibroblast cells. PRO509, PRO523, PRO7184, or PRO4225, PRO1489, PRO4322, PRO432, PRO5725, PRO7184, or PRO4225, PRO4981, PRO4225, PRO4981, or PRO5723, PRO4408,

CRO PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO5723, PRO5725, PRO7164, or PRO5725, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO4981, PRO49881, PRO49881, PRO49881, PRO49881, PRO49881, PRO49881, PRO49881, PRO49881, PRO49881, PRO49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New PRO polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                       human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation influbior; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                            Novel human secreted and transmembrane protein PRO10196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; SEQ ID NO 78; 315pp; English
                                           ADC49027 standard; protein; 208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001; 2001MO-US017800.
29-JUN-2001; 2001MO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                 18-DEC-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
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N-PSDB; ADC49026.
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                                                                                              ADC49027;
RESULT 31
                        ADC4902
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the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour is lung liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polymoleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New PRO polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        release;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard A, Godowski PJ;
phan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic, pericyte cell proliferation; pericyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes an isolated PRO (secreted and transmembrane) polymeptide (1). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in
                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                             100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human secreted and transmembrane protein PRO10196.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; SEQ ID NO 78; 315pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC49544 standard; protein; 208 AA
                                                                                                                                                                                          sport injuries). This is the a
transmembrane PRO polypeptide.
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-AUG-2002; 2002US-00232231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                                                                         16; Conservative
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                                                                                                                                                                                                                                                                                                        Best Local Similarity
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N-PSDB; ADC49543.
                                                                                                                                                                                                                                                  Sequence 208 AA;
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pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful cor stimulating the proliferation or differentiation of chondrocyte cells. PRO357, PRO355, PRO3155, PRO3165 or PRO1419 prolypeptide are useful for stimulating the release of tumour necrosis factor (TMF) alpha from human blood. PRO982, PRO357, PRO325, PRO1306, PRO1419, PRO1419, PRO141, PRO1419, PRO1414, PRO1411, PRO1411, PRO1411, PRO1411, PRO1412, PRO1424, PRO1424, PRO1427, PRO1330, PRO1340, PRO1340, PRO1340, PRO1340, PRO1340, PRO1340, PRO1340, PRO1340, PRO1340, PRO1340, PRO1340, PRO1340, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO
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The invention describes an isolated PRO (secreted and transmembrane)

CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

useful for stimulating the proliferation of or gene expression in

Dericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful

for stimulating the proliferation of differentiation of chondrocyte

cells. PRO357, PRO355, PRO135, PRO1306 or PRO1419 polypeptide

cells. PRO351, PRO555, PRO185, PRO1306 or PRO1419 polypeptide

cells. PRO317, PRO556, PRO351, PRO1525, PRO1306, PRO1419, PRO1419,

CC RRO1478, PRO1134, PRO826, PRO351, PRO1031, PRO1411, PRO1309,

RRO1478, PRO1134, PRO126, PRO1305, PRO1927, PRO1411, PRO1309,

CC RRO1478, PRO1314, PRO1347, PRO1305, PRO1917, PRO1411, PRO1309,

CC RRO187, PRO1329, PRO788, PRO1909, PRO1474, PRO1414, PRO1327,

CC RRO187, PRO529, PRO788, PRO1909, PRO1474, PRO1917, PRO19140, PRO1326,

CC RRO1897, PRO529, PRO788, PRO11096, PRO1927, PRO1917, PRO19184,

CC RRO1897, PRO529, PRO788, PRO11096, PRO1488, PRO332, PRO4408,

CC RRO1897, PRO529, PRO788, PRO1194, PRO1272, PRO488, PRO432, PRO4408,

CC RRO1897, PRO529, PRO788, PRO1194, PRO1272, PRO488, PRO432, PRO4408,

CC RRO1897, PRO529, PRO788, PRO1194, PRO1272, PRO488, PRO432, PRO4408,

CC RRO1897, PRO529, PRO788, PRO1194, PRO1272, PRO488, PRO432, PRO4408,

CC RRO1897, PRO529, PRO788, PRO1194, PRO1272, PRO5718, PRO432, etc.,

CRO529, PRO572, PRO578, PRO1194, PRO5729, PRO5778, PRO432, etc.,

CRO529, PRO572, PRO578, PRO1194, PRO5729, PRO5778, PRO5732, etc.,

CRO572, PRO572, PRO572, PRO5729, PRO5729, PRO5732, etc.,

CRO572, PRO572, PRO572, PRO5729, PRO5729, PRO5732, etc.,

CRO572, PRO572, PRO572, PRO5729, PRO5723, PRO5732, etc.,

CRO572, PRO572, PRO5729, PRO5729, PRO5729, PRO5723, etc.,

CRO572, PRO572, PRO5729, PRO5729, PRO5729, PRO5729, PRO5729, PRO5729, PRO5729, PRO5729, PRO5729, PRO5729, PRO5729, PRO5729, PRO5729, PRO5729, PRO5729, PRO5729, PRO5720, PRO5729, PRO5720, PRO5720, PRO5720, PRO5720, PRO5720, PRO5720, PRO5720, PRO5720, PRO5720, PRO5720, PRO5720, PRO5720, PRO5720, PRO5720, PRO5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and
                                                                                                                                                    Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                             New PRO polypeptide for use as molecular weight markers for protein electrophoresis purposes and for detecting the presence of tumor in
                                                                                                                               Goddard A, Godowski PJ;
shan JF, Watanabe CK, Wo
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                                                                                                                                    Gerritsen ME, Goddard
Smith V, Stephan JF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADC47150 standard; protein; 208 AA.
                                                                                                                                                                                                                                                                                                                                                         Claim 11; Fig 78; 314pp; English.
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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Matches 16; Conservative
                                                                                                                                      Desnoyers L,
                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                     WPI; 2003-801157/75.
N-PSDB; ADC47404.
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                                                                                                                                    Baker KP, De
Grimaldi JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC47150;
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transmembrane PRO polypeptide.

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gene therapy
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Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; chondrocyte cell proliferation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
Novel human secreted and transmembrane protein PRO10196,
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Homo sapiens

US2003105288-A1.

05-JUN-2003

13-AUG-2002; 2002US-00219070,

25-JUL-2000; 2000US-0220666P. 01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

WPI; 2003-801246/75. N-PSDB; ADC47149. New isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO), for use in recombinantly producing a PRO polypeptide, as a hybridization probe, and in gene therapy.

Claim 11; Fig 78; 308pp; English.

The invention describes an isolated PRO (secreted and transmembrane)

COUNTY The PROSEZ, PRO1160, PRO1137 or PRO1329 polypeptide are

COUNTY THE INCOMENTATION PRO1292, PRO1272 or PRO1329 polypeptide are

COUNTY PRO1292, PRO1292, PRO1292 or PRO4405 polypeptide are useful

COUNTY PRO1292, PRO1292, PRO1292 or PRO4405 polypeptide

COUNTY PRO1292, PRO1292, PRO1292, PRO1306 or PRO1419 polypeptide

COUNTY PRO1292, PRO1292, PRO1903, PRO1909, PRO1419, PRO1419,

COUNTY PRO1301, PRO1262, PRO1005, PRO1909, PRO1419, PRO1419,

COUNTY PRO1301, PRO1262, PRO1005, PRO1909, PRO1904, PRO100192,

COUNTY PRO1301, PRO1302, PRO1005, PRO1903, PRO1904, PRO1904,

COUNTY PRO1301, PRO1303, PRO1304, PRO1904, PRO1904, PRO1904,

COUNTY PRO1303, PRO1304, PRO1005, PRO1903, PRO1904, PRO1904,

COUNTY PRO19083 or PRO1005, PRO1904, PRO1904, PRO1904,

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COUNTY COUNTY PRO1908

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The invention describes an isolated PRO (secreted and transmembrane)

CD1ypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

CD2 polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

CD3 seeful for stimulating the pro11feration of or gene expression in

CD2 pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful

CD3 stimulating the pro11feration or differentiation of chondrocyte

CD3 seculs. PRO357, PRO357, PRO1185, PRO1190 or PRO1419 polypeptide

CD3 alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO140,

CD3 seculs. PRO3137, PRO526, PRO363, PRO537, PRO1244, PRO1141, PRO11309,

CD3 PRO1025, PRO1134, PRO1126, PRO1105, PRO1192, PRO1244, PRO1274, PRO1412,

CD3 PRO1025, PRO1330, PRO1347, PRO1306, PRO1131, PRO1339,

CD3 PRO1343, PRO338, PRO4341, PRO1409, PRO1414, PRO1317, PRO1326,

CD3 PRO1987, PRO338, PRO4341, PRO1801, PRO4331, PRO3444, PRO1327,

CD3 PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNR) - alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; colon tumour; breast tumour; prostate tumour; rectal tumour; ling tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated PRO polypeptide useful for tissue typing, gene therapy, molecular weight markers, for treating arthritis and tumor.
                                                                                                        Gaps
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0
                                                                   100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                  Novel human secreted and transmembrane protein PRO10196.
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                                                                                                        Mismatches
                                                                                                                                                                                                                                                                         ADC78025 standard; protein; 208 AA.
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                                                                       100.08; Ft.
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                             1 RORYLYTDDAQOTEAH 16
                                                                                                                                                                      44 RORYLYTDDAQOTEAH 59
                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Grimaldi JC, Gurney AL,
                                                                                                          16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-765529/72.
N-PSDB; ADC78024.
                                                                       Query Match
Best Local Similarity
                                    Sequence 208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003096972-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy
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                                                                                                                                                                                                                                                                                                                                                 01-JAN-2004
                                                                                                                                                                                                                                                                                                              ADC78025;
                                                                                                                                                                                                                                      RESULT 35
ADC78025
                                                                                                            Matches
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stimulating the proliferation of normal human dermal fibroblasts cells. PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408, PRO5233, PRO5725, PRO7154, or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO54332, etc., are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour colon timour in the properties. tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO255, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide. 8888888888888888888888888888

Sequence 208 AA;

Indels 100.0%; Score 86; DB 7; L. 100.0%; Pred. No. 4.4e-07; 0; Mismatches 1 RORYLYTDDAQQTEAH 16 Query Match Best Local Similarity 100.0 Matches 16; Conservative ò

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Gарв

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Length 208;

44 RORYLYTDDAQQTEAH 59

Novel human secreted and transmembrane protein PRO10196. ADD06260 standard; protein; 208 AA. 01-JAN-2004 ADD06260; ADD06260 TX Y X L X X B X B X B X X B

(first entry)

human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; epericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;

Ношо варіепв

gene therapy

US2003073816-A1.

17-APR-2003

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

26-AUG-2002; 2002US-00227873.

(GETH) GENENTECH INC

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

WPI; 2003-644807/61. N-PSDB; ADD06259 New PRO polypeptides and nucleic acids encoding the polypeptides, useful

The invention describes an isolated PRO (secreted and transmembrane)

COUNTED TO STRONGO, PROLISO, PROLISO, PROLISO PROLISO; PROLISO P in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping. Claim 11; SEQ ID NO 78; 314pp; English. transmembrane PRO polypeptide.

Sequence 208 AA;

ö Gaps ö 100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07; Live 0; Mismatches 0; Indels Query Match Best Local Similarity 100. Matches 16; Conservative

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ADC77779 standard; protein; 208 AA. RESULT 37

01-JAN-2004 (first entry)

ADC77779;

Novel human secreted and transmembrane protein PRO10196.

Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; tumour; chondrocyte cell differentiation; tumour necrosis factor alpha (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation;

colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; gene therapy

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01-JUN-2001; 2001WO-US017800
29-JUN-2001; 2001WO-US021066
09-APR-2002; 2002US-00119480.
                                                                                    13-AUG-2002; 2002US-00219466
                                                                                                                                                                                                                                                              Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                WPI; 2003-657980/62.
                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADC77778
US2003088066-A1.
                                           08-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e.g. cancer.
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Goddard A, Godowski PJ; phan JF, Watanabe CK, Wood WI;

Gerritsen ME, Goddard / Smith V, Stephan JF,

One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, or for preparing a medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody,

Claim 11; Fig 78; 314pp; English.

The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

to useful for stimulating the proliferation of or gene expression in

pericyte cells. PRO325, PRO225, PRO1272 or PRO4405 polypeptide are useful

cells. PRO331, PRO357, PRO225, PRO1355, PRO1366 or PRO1419 polypeptide

cells. PRO331, PRO355, PRO155, PRO1355, PRO1366 or PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TMF)
alpha from human blood. PRO982, PRO351, PRO125, PRO1306, PRO1139,

PRO137, PRO337, PRO826, PRO1005, PRO195, PRO1304, PRO1411, PRO1140,

PRO1025, PRO1134, PRO136, PRO1305, PRO1174, PRO1311, PRO1411, PRO1309,

PRO1286, PRO1330, PRO1341, PRO1404, PRO1373, PRO1274, PRO1311,

PRO1887, PRO1376, PRO1387, PRO1409, PRO11474, PRO1374, PRO1316,

PRO1887, PRO1389, PRO4380, PRO1404, PRO1373, PRO1367,

PRO1887, PRO529, PRO788, PRO1184, PRO1174, PRO1367, PRO1867,

PRO1891, PRO5225, PRO7184, or PRO1405 polypeptide are useful for

comparing the proliferation of normal human dermal fibroblast cells. PRO189,

PRO5723, PRO5725, PRO7184, or PRO7425 polypeptide are useful for

comparing the proliferation of normal human dermal fibroblast cells. PRO180,

PRO5723, PRO5725, PRO7184, or PRO7425 polypeptide are useful for

comparing the proliferation of normal human dermal fibroblast cells.

colypeptides such as PRO6004, PRO4981, PRO7778, PRO4322,

PRO5723, PRO5725, PRO786, PRO6004, PRO4981, PRO7778, PRO4322,

are useful for detecting the presence of tumour in a mammal which

convolves comparing the level of expression of the above PRO polypeptides

involves comparing the test sample as command to endrol sample

control sample

control sample

control sample

control sample

control sample

control sample

control sample

control sample

control sample tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.

Sequence 208 AA;

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100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07;
                        Indels
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         100.0%; Pred. w. ....ive 0; Mismatches
                           16; Conservative
             Best_Local Similarity
Matches 16; Conserv
 Query Match
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ADD50742 standard; protein; 208 AA.
ADD50742
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ADD50742;

15-JAN-2004

(first entry)

Novel human secreted and transmembrane protein PRO10196.

release; Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;

gene therapy

US2003105291-A1.

Homo sapiens.

05-JUN-2003.

26-AUG-2002; 2002US-00227877.

29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC

PJ; Wood WI; Goddard A, Godowski P phan JF, Watanabe CK, Gerritsen ME, Goddard P. Smith V, Stephan JF, Ā, Desnoyers Grimaldi JC, Baker KP,

2003-829361/77. N-PSDB; ADD50741.

New isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO), for use in recombinantly producing a PRO polypeptide, as a hybridization probe, and in gene therapy.

Claim 11; Fig 78; 308pp; English.

The invertion describes an isolated PVO Secreted and Laismenbrane CC polypeptide (1). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in periotyce cells. PRO357, PRO1259, PRO1250 or PRO4405 polypeptide are useful for stimulating the proliferation of or gene expression in for stimulating the proliferation or differentiation of chondrocyte cells. PRO351, PRO357, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TMF)-alpha from human blood. PRO982, PRO357, PRO1081, PRO1306, PRO1419, PRO1419, PRO1414, PRO1314, PRO526, PRO357, PRO1081, PRO1080, PRO1086, PRO1414, PRO1367, PRO1085, PRO1181, PRO1367, PRO1086, PRO1377, PRO1180, PRO1377, PRO1180, PRO1378, PRO1377, PRO1180, PRO1378, PRO1377, PRO1379, PRO1379, PRO1387, PRO1387, PRO1379, PRO1379, PRO1387, PRO1387, PRO1387, PRO1387, PRO1387, PRO1387, PRO1387, PRO1387, PRO1387, PRO1387, PRO1881, PRO1387, PRO1388, PRO1387, PRO1388, The invention describes an isolated PRO (secreted and transmembrane)

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typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful tor chromosome and gene mapping or gene therapy. (II) is useful tor generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                      0
                                                                                                                                                                                                 Length 208;
                                                                                                                                                                         100.0%; Score 86; DB 7; Length 20:
100.0%; Pred. No. 4.4e-07;
wiematches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 ADD50988 standard; protein; 208 AA
                                                                                                                      transmembrane PRO polypeptide.
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                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                    Similarity
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                                                                                                                                                             Sequence 208
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                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                             RESULT 39
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Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; periotte cell proliferation; periotte cell proliferation; chondrocyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping; Novel human secreted and transmembrane protein PRO10196. gene therapy

(first entry)

15-JAN-2004

29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480. 13-AUG-2002; 2002US-00219527. 01-JUN-2001; 2001WO-US017800. US2003105290-A1. Homo sapiens 05-JUN-2003

PJ; Wood WI; Gerritsen ME, Goddard A, Godowski F Smith V, Stephan JF, Watanabe CK, Desnoyers L, C, Gurney AL, WPI; 2003-829360/77. N-PSDB; ADD50987. Grimaldi JC, Baker KP,

(GETH) GENENTECH INC.

New isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO), for use in recombinantly producing a PRO polypeptide, as a hybridization probe, and in gene therapy.

polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO231, PRO357, PRO1155, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214, The invention describes an isolated PRO (secreted and transmembrane) Claim 11; Fig 78; 309pp; English.

WPI; 2003-765528/72

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PRO147, PRO137, PRO526, PRO163, PRO531, PRO1083, PRO840, PRO1080,
PRO1476, PRO1134, PRO826, PRO1005, PRO809, PRO171, PRO1411, PRO1130,
PRO1286, PRO1134, PRO1126, PRO1106, PRO1917, PRO1214, PRO1121,
PRO1286, PRO11376, PRO1186, PRO1192, PRO1279, PRO1214, PRO1121,
PRO1286, PRO1376, PRO1387, PRO1409, PRO1917, PRO1240, PRO1326,
PRO1843, PRO1376, PRO1387, PRO1409, PRO1917, PRO1576, PRO1326,
PRO1841, PRO1292, PRO341, PRO1801, PRO4313, PRO3444, PRO4322,
PRO940, PRO56079, PRO9886 or PRO1096 polypeptide are useful for
Exposed to the proliferation of normal human dermal fibroblasts cells.
PRO5723, PRO5725, PRO7154, or PRO4425, PRO1742, PRO1480, PRO4408,
PRO5723, PRO5725, PRO7164, PRO1272, PRO1488, PRO4322, PRO5726, PRO5725, PRO5726, PRO4981, PRO1774, PRO5778, PRO4408,
PRO5723, PRO5725, PRO7164, or PRO4425, pro196ptide are useful for detecting the presence of tumour in a mammal which
involves comparing the level of expression of the above PRO polypeptides
involves comparing the level of expression of the above PRO polypeptides
involves comparing the presence of tumour in the test sample as compared to the control sample
is indicative of the presence of tumour in the mammal. The tumour or
tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
liver tumour. (1) is useful as molecular weight markers, for tissue
typing, or as therapeutic agents. A polynucleotide (11) encoding (1) is
useful for chromosome and gene mapping or gene therapy. (II) is useful
for generating transgenic animals or knock-out animals which are useful
screening useful reagents. PRO357, PRO229, PRO1405 polypeptide
is useful for treating bone and/or cartilage disorders (e.g., arthritis,
property injuries). This is the amino acid sequence of a human secreted and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Stephan JF, Watanabe CK, Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-aipha; TNR-aipha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.
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Smith V, St
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29-JUN-2001; 2001MO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO polypeptide #39.
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C, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 208 AA;
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Grimaldi JC,
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N-PSDB; ADD50468.

Novel isolated PRO polypeptide useful for tissue typing, as molecular weight markers in protein electrophoresis, for treating arthritis, tumor.

Claim 11; Fig 78; 308pp; English.

The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polymucleotides encoding them. The PRO polypeptides and polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, colon tumour, breast tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TNF) alpha from human blood, for stimulating the proliferation of or gene conditoryte cells, for stimulating the proliferation of or gene expression in perioyte cells or for stimulating the proliferation of conditoring probes, in chromosome and gene mapping, in generating contains the development and screening of therapeutically useful rechnology, in generating transgenic animals or knock-out animals which reagents, in gene therapy, and screening of therapeutically useful reagents, in gene therapy, in chromosome identification, as chromosome condition which is responsive to the PRO polypeptides, or anti-PRO antibodies, such as perioyre-associated tumours and bone and/or cartiage condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as perioyre-associated tumours and bone and/or cartiage disorders (e.g. arthritis, sports injuries), involving inducing the re-condition of chondrocyte-associated tumours and bone and/or cartiage disorders (e.g. arthritis, sports injuries), involving inducing the re-condition of chondrocytes. The PRO polypeptides are useful as molecular markers a human PRO polypeptide of the invention.

Sequence 208 AA;

Gaps .; 0 Query Match
100.0%; Score 86; DB 7; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels

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2, 2004, 16:04:51

Search completed: March Job time : 10.6 secs

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PRELIMINARY;
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Q8vi80 rattus norv
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Q65610 kairi virus
Q8ibcl plasmodium
045881 caenorhabdi
P71428 lactobacill
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064868 oryza sativ
Q7xmq2 oryza sativ
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Ojeyun3 caenorhabdi
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(without alignments)
757.244 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                              1017041 seqs, 315518202 residues
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Listing first 45 summaries
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46.5	46.5	46.5	46.5	46.5	46.5	46.5	46.5	46.5	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	44.2	44.2			44.2	44.2	44.2
40	40	40	40	40	40	40	40	40	33	39	33	39	39	33	39	39	39	39	39	39	39	38	38	38	38	38	38	38
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2003 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 21.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9666;
[1]
SEQUENCE RROM N.A.
TISSUB-Lung;
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349 AA; 38724 MW; 8836B8DF2AAE2AF7 CRC64;
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Best Local Similarity 53.3%;
Matches 8; Conservative
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                      1 RORYLYTDDAQQTEA 15
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Best Local Similarity
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Kairi virus.
   SQ SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE=CV. Columbia;
MEDLINE=2 COlumbia;
MEDLINE=2 COLUMBIA;
MEDLINE=2 COLUMBIA;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldhuwn T.V.,
Fulii C.Y., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., Vanken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lin X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AC002392; AAD12024.1; -.
PIR; T00526; T00526.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR001087; Lipase_GDSL.
Pfan; PF00657; Lipase_GDSL.
Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                 "Ruttus norvegicus FGF21.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB078901; BAB84229-1;
GO, GO:0008083; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok III_like.
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
   Q8VIB0;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 21.
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PRINTS, PRODGES; ILLHBGF.
PRODOM; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
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                                                                                                                                                                                                Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
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NCBI_TaxID=80939;
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                                    Gaps
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Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL844507; CAD51085.1; -.
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Score 46; DB 10; Length 349;
Pred. No. 8.6;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%; Score 43; DB 12; Length 233; 50.0%; Pred. No. 19; ive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%; Score 43; DB 5; Length 1916; 42.9%; Pred. No. 2.1e+02; ive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 1916 AA; 230013 MW; 68FF914BBA3519BD CRC64;
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Last annotation update)
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Last annotation update)
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Gen. Genet. 200:193-198(1985)
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Best Local Similarity
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064468;
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Rhabditidae; Peloderinae; Caenorhabditis.
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L. Science 282:2012-2018(1998).

E. Science 282:2015-2018(1998).

E. Science 282:2015 (1998).

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E. Science 282:2015 (1998).

E. Science 2016:1998 (1998).

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STRAIN=Group B: TRANSPOSON=ISL1;
STRAIN=Group B: TRANSPOSON=1SL1;
Shimizu-Radota M.; Kiwaki M.; Hirokawa H.; Tsuchida N.;
"ISL1: a new transposable element in Lactobacillus casei.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 5; Length 2225;
Pred. No. 2.5e+02;
3; Mismatches 3; Indels
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PROSITE; PS50279; BPTI KUNITZ 2; 10.
PROSITE; PS00484; THYRGGLOBULIN 1; 1.
PROCEASE inhibitor: Serine procease inhibitor.
SEQUENCE 2225 AA; 242198 MW; ASDDBABSDDZA7B02A CRC64;
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01-FEE-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Transposable element ISL1.
Lactobacillus casei.
                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                             WOIF3.3 protein. WOIF3.3.
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01-JUN-1998 (
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SEQUENCE FROM N.A.
SEQUENCE CO. Columbia;
MEDLINE=20083487; PubMed=10617197;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley G.D., Shea
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, magnoliids, Piperales, Saururaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ito M., Imafuku M., Tanabe Y., Aoki S., Hasebe M.;
"MADS-box genes needed for determining petal identity express in petal-like bracts of Houttuynia cordata (Saururaceae).";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB089157; BAC80253.1; -
SRQUENCE 243 AA; 27728 MW; 7B34DBER4609D8B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                          Length 93;
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SEQUENCE FROM N.A.
STRAIN=Group B; TRANSPOSON=ISL1;
STRAIN=Group B; TRANSPOSON=ISL1;
Shintian-Kadota M.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X02734; CAA26516.1; -.
PIR; S28726; S28726.
Interprise; IPROSS14; Transposase_8.
Interprise; IPROSS14; Transposase_8; 1.
SEQUENCE 93 AA; 10745 MM; 62584573F7F83DCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-07T-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
MADS-box transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                          2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 AA
                                                                                                                                                                                                                                                                          DB
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                          47.7%; Score 41;
61.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houttuynia cordata (Chameleon plant).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Putative GDSL-motif lipase/hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 ŘRŘLĽQLĎĎGSQŤNPH 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RORYLYTDDAQQTEAH 16
                                                                                                                                                                                                                                                                                                                                                                                     1 RORYLYTDDAQQT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                           43 RWRKLYTEDGKÖT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                   Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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2 QRYLYTDDAQQTEA 15
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                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                        OSJNBb0059K02.9 protein.
                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactobacillus casei.
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hes 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4530;
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                                                                                                                                                                     01-OCT-2003
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Q48525;
                                                                            07XMQ2
                                                                                                                               Q7XMQ2
        RESULT 11
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                                              Q7XMQ2
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Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.B., Umayam L., Tallon L.J., Gill J.B., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.7%; Score 41; DB 10; Length 349; 46.7%; Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AC002392; AAD12023.1; -. PIR; T00525; T00525. GO; GO:0016787; F:hydrolase activity; IEA. InterPro; IPR001087; Lipase_GDSL. Pfam; PF00057; Lipase_GDSL. Hydrolase. 349 AA; 38577 MW; OSDAC363EA5F3D2A CRC64; SEQUENCE 349 AA; 38577 MW; OSDAC363EA5F3D2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
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Submitted (BEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; A1442007. CAC09353.1; -.
Gramene; Q9FSS1; -.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
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InterPro; IPR001092; HLH basic.
InterPro; IPR001087; Lipase_GDSL.
Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS00038; HLH_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RORYLYTDDAQQTEA 15
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                                                                                                                                                                                                                                                                                        Nature 402:761-768(1999)
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                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
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Matches
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Han B., Fend C., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.C., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y. Li J., Li J., Zhang Y.J., Lu Y. Li J., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y., Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y., Zhang Y., Lu G., Lin W., Gu W.D., Zhang C.Y., Shao C.Y., Shang X.L., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu W. Hang G.F., Thoung G.F., Shang X.L., Zhang W., Wang L.J., Ding G.W., Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.; ENBLY ALGOGOSO2, CARO4499.1; SRQUENCE 355 AA, 39680 MW, CPDEBEADCCD52650 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                           Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Shimizu-Kadota M., Kiwaki M., Hirokawa H., Tsuchida N.;
"ISLJ: a new transposable element in Lactobacillus casei.";
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Lactobacillus.
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SEQUENCE FROM N.A.
STRAIN=Group B; TRANSPOSON=ISL1;
Shimizu-Kadota M.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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Pfam; PF01527; Transposase 8; 1.
SROUENCE 385 AA; 44659 WW; D905D7AC279D8FF7 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                              01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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50.0%; Pred. No. 69;
tive 2; Mismatches 5;
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355 AA
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61.5%; Pred. No.
                                                                  Created)
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STRAIN=Group B; TRANSPOSON=ISL1;
                                                              (TrEMBLrel. 25,
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STRAIN=VF5;
MEDLINE=98196666; PubMed=9537320;
EMBL; AF308468; AAG42467.1; -.
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Matches 7; Conser
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MEDLINE-22294977; PubMed=12381787;

MEDLINE-22294977; PubMed=12381787;

MEDLINE-22294977; PubMed=12381787;

MEDLINE-22294977; Parmirantzou M., Snel B., Vilanova D., Berger B.,

MEDLINE-22294977; Pergerial M., Snel B., Vilanova D., Berger B.,

MEDLINE-22294977; Pergerial M., Snel B., Medline M.,

MEDLINE-22294977; Pergerial Tolding; Medline M.,

MEDLINE-22294977; Pergerial Folding; Med.

MEDLINE-22294977; Pergerial Folding; Med.

MEDLINE-22294977; Pergerial Folding; Med.

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Enterobacteriaceae, Klebsiella.
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NCBI_TaxID=216816;
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O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Alkaline phosphatase isozyme conversion protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kolko M.M., Kapetanovich L.A., Lawrence J.G.;
"Alternative pathways for sixoheme synthesis in Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.7%; Score 41; DB 16; Length 10
61.5%; Pred. No. 2.3e+02;
tive 2; Mismatches 3; Indels
     Indels
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Narrowly conserved hypothetical protein.
     3,
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Selficion T.A., Lawrence J.G.;
"Methionine recycling in Klebsiella aerogenes.";
J. Bacteriol. 0:0-0(2001).
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     2; Mismatches
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MEDLINE=20566700; PubMed=11114933;
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                                          1 RORYLYTDDAGOT 13
                                                                             43 RWRKLYTEDGKOT 55
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     8; Conservative
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Bifidobacterium longum.
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Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Q8G5K2
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Rhabditidae; Peloderinae; Caenorhabditis.
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
InterPro; IPR003003; 7TM_chemrecept2.
InterPro; IPR0010169; Nm7TM_chemrecept2.
Pfam; PF01604; 7tm_5; 1.
SEQUENCE 332 AA; 38162 MW; 5D903258D5357D9F CRC64;
                                                                                         Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Genome sequence of the nematode C.elegans: A platform for
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NCBI_TaxID=63363;
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Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
MERCPE, M28.005; -.
NON TER 174 174 AA; 19047 MW; 1F3869202E11437B CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein AQ_985.
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Last sequence update)
Last annotation update)
                                                                                         46.5%; Score 40; DB 2; 50.0%; Pred. No. 46;
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                                                                                                                                    2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z81593; CAB04743.1; -.
PIK; T25023; T25023.
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8 RIDYIHTADFQQTVLH
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Matches 8; Conservative
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Caenorhabditis elegans.
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Ephydroidea; Drosophilidae; Drosophila.
                                   NCBI_TaxID=7227;
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MEDLINE_21950561; PubMed=11953381;

Li M., Shimada T., Morris J.G. Jr., Sulakvelidze A., Sozhamannan S.;

Li M., Shimada T., Morris J.G. Jr., Sulakvelidze A., Sozhamannan S.;

Li M., Shimada T., Morris J.G. Jr., Sulakvelidze A., Sozhamannan S.;

Evzians with pathogenic potential by exchange of O-antigen

blosynthesis regions.;

Linfect. Immun. 70:2441-253 (2002).

EMBL; AF390577; F.DA Dinding; IEA.

GO; GO:0005377; F.DA Dinding; IEA.

GO; GO:0005310; P.DNA recombination; IEA.

InterPro; IPR007102; IS408 HTH.
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Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Shead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; Inthe complete genome of the hyperthermophilic bacterium Aquifex
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                               46.5%; Score 40; DB 16; Length 403; 37.5%; Pred. No. 1.2e+02; cive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio cholerae 037.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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BMBL; AB000717, AAC07076.1; -.

PIR,; C70385, C70385.

InterPro; IPR055017; Toluene_X.

Pfam, PF03349; Toluene X, 1.

Hypothetical protein; Complete proteome.

SEQUENCE 403 AA; 45861 MW; 04B04382A9F76D03 CRC64;
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SEQUENCE 506 AA; 58610 MW; 06887234D0D27131 CRC64;
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01-UNN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Best Local Similarity 63.6
Matches 7; Conservative
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SU(DX) OR CG4244.
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REMEMBER OF SURVENCE FROM N.A.

Addama M.D. Celnikers S.E., Holf R.A., Evans C.A., Gocayne J.D.,

RADAMA M.D. Celnikers S.E., Hill R.A., Hoskins R.A., Galle R.F.,

RADAMA M. Celnikers S.E., Richards S., Ashburner M., Henderson S.N.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RADAMA M. C., Rogers Y.H., Blazej R.G., Champe M., Pfesifer B.D.,

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RADAMA M. C., Rogers Y., Bernan B.P., Bandari D., Bolahakov S.,

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RADAMA M. Cawley S., Dahlke C., Davenport L.B., Evetier P. B.,

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Alali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,

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A Brans C.A., Gocayre J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Besson K.Y., Busam D.A.,
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A McIncosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
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Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
                                           STRAIN=Berkeley; Strain P., Hong L., Agbayani A., Carlson J., Stapleton M., Broketein P., Hong L., Farfan D., Frise E., George R., Gonzalez M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacles S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
SEQUENCE FROM N.A.
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7; Conservative
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Best Local Similarity
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  Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Calang M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Krommiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.W.J., Smith E., Shu S., Smutniak F., Whitfield E., Shu S., Smutniak F., Whitfield E., "Ambhurner M., Gelbart W.M., Rubin G.M., Mingall C.J., Lewis S.E., "Amnotation of Drosophila melanogaster genome."; submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                       SEQUENCE FROM N.A.
Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.5%; Score 40; DB 5; Length 518; 57.1%; Pred. No. 1.6e+02; ive 1; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AX068406; AAL39551.1, --
EMBL, AX06846; AAL13951.1, --
FlyBase; FBGN0003557; Su(dx).
FlyBase; FBGN003557; Su(dx).
GO; GO:0007219; P:N signaling pathway; IGI.
GO; GO:0008587; P:wing margin morphogenesis; IGI.
GO; GO:0008586; P:wing wein morphogenesis; IGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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GO; GO:0004556; F:alpha-amylase activity; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR006047; Alpha amyl_cat.

InterPro; IPR006589; Alp amyl_cat_sub.

Pfam; PF00128; alpha-amylase; 1.

SMART; SM00642; Aamy; 1.

SMART; SM00642; Aamy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR0012059; HECT_domain.
InterPro; IPR001202; WW_RSP5_WWP.
Pfam; PF006397; WW; 2.
SWART; SM00456; WW; 2.
PROSITE; PS00237; HECT; 1.
PROSITE; PS002037; HECT; 1.
SROSITE; PS002037; HECT; 1.
SROSITE; PS002037; HECT; 1.
SROSITE; PS002037; HECT; 1.
SROSITE; PS00203; WW DOMAIN 1; 2.
SROUENCE 518 AA; 61579 MW; 394540BB5695B56D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biogci, Biotechnol, Biochem. 62:1093-1102(1998)
EMBL; AB003697; BAB18518.1; -.
PIR; JE0181; JE0181.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 10-0CT-2003 (TrEMBLrel. 25, 01:90-1, 6-glucosidase. Bacillus flavocaldarius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 QRYLYTDDAQQTEA 15
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Best Local Similarity
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Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Johnston M., Hillier L., Riles L., Dubois E., Dusterhoft A., Enten W., Bruckner M., Goffeau A., Hebling U., Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Kotter P., Louis E.J., Messenguy F., Mewes H.W., Miosga T., Mostl D., Muller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M., Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M., Schafers B., Schorens B., Schoper C., Schwarz S., Underwood A.P., Urrestaracu L.A., Vandenbol M., Verhasselt P., Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
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                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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Nashiru O., Lee S.Y., Lee D.S.;
"Thermostable alpha-glucosidase gene from Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caldophilus GRZ4.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF095282; AAD50603.1;
HSSP; P21332; P10K.
GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR006589; Alpha amyl_cat.
InterPro; IPR006647; Alpha amyl_cat.
FMART; SM00128; Alpha-amylase; 1.
SMART; SM00642; Amy; 1.
SEQUENCE 529 AA; 61383 MW; 9C036EICIF5118AA CRC64;
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46.5%; Score 40; DB 2; Length 529
Best Local Similarity 43.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 4; Mismatches 5; Indels
                                             Indels
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UJUN-2003 (TrEMBLrel. 24, Last annotation update)
Chromosome XII COSMID 9931.
VPS36 OR L9931.3 OR YLR417W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9RA62;
U-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
43.8%; Pred. No. 1.6e+02;
tive 4; Mismatches 5;
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227 RHEHLYTEDQPETYAY 242
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us-10-060-765-7.rspt

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Mus musculus (Mouse)
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es 8; Conserva
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                                                                                  Q8CED4
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                                           RESULT 23
                                                               Q8CED4
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GO; GO:0016299; F:regulator of G-protein signaling activity; IMP.
GO; GO:0016299; F:regulator of G-protein signaling activity; IMP.
GO; GO:0045014; P:negative regulation of transcription by glu. . .; IMP.
GO; GO:0046053; P:protein-Golgi retention; IMP.
InterPro; IPR007261; Vp836.
InterPro; IPR007261; Vp836.
InterPro; IPR007261; Vp836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=YR-1;
Ushijima H., Morikawa S., Mukoyama A., Nishio O.;
"Characterization of VP4 and VP7 of a murine rotavirus (YR-1) isolated
Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII."; Nature 387:0-0(0).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.5%; Score 40; DB 3; Length 566; 53.8%; Pred. No. 1.8e+02; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                     Cherry J.M.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, 20162; AAB67493.1; -.
PIR; SS9382; SS9382.
SGD; S0004409; VPS36.
                                                                                                                              Favello A.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                   Waterston R.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases
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Jpn. J. Med. Sci. Biol. 48:237-247(1996).
EMBL; D45215; BAA00147.1; -.
GQ; GO:0019028; C:vial capaid; IEA.
InterPro; IPR000416; Cap VP4.
InterPro; IPR008985; Conalike_lec_gl.
Pfam; PF00426; VP4; 1.
SEQUENCE 775 AA; 86306 MW; 4E4B90E49FCFDC97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfan; PF04132; Vps36; 1.
SMART; SM00547; ZnF RBZ; 2.
SEQUENCE 566 AA; 64017 MW; 60DDD4EA3A620409 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Dest Local Similarity 42.3",
Best Local Similarity 6; Conservative
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301 QYVYTRDGEEVTAH 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
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                                                                                                                                                                                                             STRAIN-S288C;
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STRAIN=22354683; TUSSUE=Skin;
MEDLINE=22354683; PubMed=12466851;
The FANTOM CONSORTIUM,
the RIKEN Genome Exploration Research Group Phase I & II Team;
MABLINESSIS of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X., Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
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                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mature 420:563-573 (2002).

EMBL; ARCOSSOO; BAC25981.1; -.

MGI; MGI:99174; Zfp27.

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0003676; F:mucleic acid binding; IEA.

GO; GO:0003676; F:mucleic acid binding; IEA.

GO; GO:000357; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR007097; Znf_C2H2.

Pfam; PF01352; KRAB; 1.

Pfam; PF01096; ZfC2H2; 21.

SMART; SM00349; KRAB; 1.

SMART; SM00355; ZnF_C2H2; 21.
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Su(dx) protein.
Su(dx) protein.
Drosophila melanogaster (Fruit fly),
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 819;
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Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50805; KRAB; 1.
PROSITE; PS00028; ZINC FINGER C2H2 1; 21.
SROSIE; PS50157; ZINC FINGER C2H2 2; 22.
SROUBNCE 819 AA, 92920 MW; C6782ECCOC379C4B CRC64;
                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.5%; Score 40; DB 11;
53.3%; Pred. No. 2.7e+02;
tive 2; Mismatches 5;
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                                                                 Created)
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MEDLINE=20196006; PubMed=10731132;
                             Q8CED4;
01-WAR-2003 (TrEMBLrel. 23,
01-WAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                             Zinc finger protein 27
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RESULT 25

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Abril J.F., Agbayani A., An H.-J., Andrews-Pfaunkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beason K.Y., Bence P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brostein P., Brottier P., Brottier P., Buttis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Charler A., Chandra I., Actery J.M., Cawley S., Dahlke C., Davenport L.B., Downes W., Dougan-Rocha S., Dunkov B.C., Dunn P., Borbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., R. Ponler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K., Anteris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Anteris N.L., Harvey D., Heiman T.J., Wernandez J.R., Houck J., Anteris N.L., Harvey D., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Alalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Mcherson D., Lei Y., Lei Y., Lei Y., Lei Y., Lei Y., Moharry C., Morris J., Moshrefi A., Rakako P., Lei Y., Levitsky A.A., Li J., J., Lei Y., Lei Y., Levitsky A.A., Li J., J., Lei Y., Lei Y., Rahingorn K., Nabaerry C., Morris J., Moshrefi A., Rahington K., Saunders R.D.C., Scheelber F., Shan H., Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rese M.G., Rahner K., Teckingon M., Strong R., Sun E., Strading A.C., Stapleton M., Strong R., Sun E., Stan H., Wang Z.Y., Wassarman D.A., Weinstock M., Wang A.H., Wang S., Yao Q.A., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., A Zhong X.H., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Rang Zhong X., Zhou S., Zhu S., Zhu X., Smith H.O., Shong Z., Zaveri W., Woodage T., Worley K.D., Wenter J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01159; WW DOMAIN 1; 3.
PROSITE; PS50020; WW DOMAIN 2; 2.
SEQUENCE 949 AA; 107966 Ww; 74B17A8B05AC6E6B CRC64;
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GO; GO:0008587; P:wing margin morphogenesis; IGI.
GO; GO:0008586; P:wing vein morphogenesis; IGI.
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-!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
EMBL; AE003584; AAF51312.1; -.
HSSP; Q13526; AAD38975.1; -.
HSSP; Q13526; IPIN.
FlyBase; FBGI0003557; Su(dx).
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InterPro; IPR008973; C2.
InterPro; IPR000569; HBCT domain.
InterPro; IPR001202; WW.REp5_WWP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 287:2185-2195(2000).
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SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 3.
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Pfam; PF00632; HECT; 1.
Pfam; PF00397; WW; 4.
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Best Local Similarity
Matches 8; Conserv
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                               SO DE REAL PROPERTIES DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DEL CARTA DE LA CARTA DEL CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DEL CARTA DEL CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE LA CARTA DE L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of Lactobacillus plantarum WCFS1.";
Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
EMBL. AL995254; CAD63387.1; -
InterProc. IPRO01999; Gram pos anchor.
Pfam; PF00746; Gram pos anchor; 1.
PROSITE; PS50847; GRAM POS_ANCHORING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cameron C., Hoca-Mitchell S., Chen L., Barrett J., Cao J.-X., Macaulay C., Willer D., Evans D., McFadden G.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFI/0726, AAFI4973.1, -
EMBL, RF000086; NUDIX hydrolase.
InterPro, IPR003301; Viral_VD10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X., Macanlay C., Willer D., Evans D., McPadden G.; "The complete DNA sequence of myxoma virus."; virology 264:298-318(1999).
                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2139 AA; 226353 MW; 71C8B7CDB8EC5838 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                           OBBYG6;
01-UJN-2003 (TrEMBLrel. 24, Created)
01-UJN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                     PRT; 2139 AA
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MEDLINE=20032073; PubMed=10562494;
                                                                                                                                                                                                                                                                        Cell surface protein precursor.
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PROSITE; PS00893; NUDIX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-NCIMB 8826 / WCFS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                         Lactobacillus plantarum.
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SEQUENCE 2139 AA
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M085R.
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DBBYG6
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MEDINE=22608415; PubMed=12721630;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Kapatrau V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N., Eden G., Bacillus cereus and comparative analysis with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                 / Match 45.3%; Score 39; DB 3; Length 327; Local Similarity 66.7%; Pred. No. 1.4e+02; nes 6; Conservative 2; Mismatches 1; Indels
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Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                           DC4F253E0B1ABD76 CRC64;
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Last annotation update)
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Last annotation update)
GO; GO:0009225; P:nucleotide-sugar metabolism; IEA InterPro; IPR001509; Epimerase_Dh. PF01370; Epimerase; 1.
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EMBL, AE0.1706; AAP09683.1; -.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR001861; Beta_lactamase_A.
Pfam; PF00144; beta-lactamase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                               327 AA; 37099 MW;
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01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penicillin-binding protein.
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                                                                                                                                                                                                                                                 Query Match
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RA MADIAN=AICC 35092 / DSM 1617 / P2;

RA MADIAN=AICC 35092 / DSM 1617 / P2;

RA MADIANE=21332266; PubMed=11427726;

RA MADIANE=21332266; PubMed=11427726;

RA MADIANE=21332266; PubMed=11427726;

RA MADIANE=21332266; PubMed=11427726;

RA MADIANE=21332266; PubMed=11427726;

RA MADIANE=21332266; PubMed=11427726;

RA MADIANE=21332266; PubMed=11427726;

RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Charlebois R.L., Doolittle M.F., Theriault C., Tolstrup N.,

RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Osst J.;

RT Complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

RI Proc. NAL! Acad. Sci. U.S.A. 98:7835-7840(2001).

BEMBI, AE006752; AAK41614.1; -.

DR FING, G90294; G90294.

KW Hypothetical protein; Complete proteome.

SEQUENCE 263 AA; 31204 MW; CE8B2E3919CEB7F7 CRC64;

SEQUENCE 263 AA; 31204 MW; CE8B2E3919CEB7F7 CRC64;
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Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Sulfolobus.
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NCBI_TaxID=4952;
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"Molecular cloning of the YlTGD1 gene in Yarrowia lipolytica.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AM77226-1;
GO; GO:0008460; F:ITDP-glucose 4,6-dehydratase activity; IEA.
GO; GO:0016829; F:lyase activity; IEA.
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                                                                                     45.3%; Score 39; DB 12; Length 259; 58.3%; Pred. No. 1.1e+02;
                                                                                                                                                                   3; Indels
        259 AA; 30411 MW; 2E1C254DC626848D CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Putative dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein SS01380.
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                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yarrowia lipolytica (Candida lipolytica).
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                SEQUENCE
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative sugar uptake ABC transporter periplasmic solute-binding
                                                                                                                                                                                                                                          Plasmid pSymb (megaplasmid 2).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                             protein.
RB0682 OR SMB21103.
Rhizobium meliloti (Sinorhizobium meliloti).
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152 QKSLYQDEAKKTE 164
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                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=382;
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01-MAR-2003 (
01-JUN-2003 (
CG7795-PB.
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"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0005481; Emitochondrial inner membrane; IEA.

GO; GO:0005481; Fibinding; IEA.

GO; GO:0006812; Fication transporter activity; IEA.

GO; GO:0006812; Fication transport; IEA.

R GO; GO:0006812; Fication transport; IEA.

InterPro; IPR000644; GBS domain.

InterPro; IPR001993; Mitoch_carrier.

R Ffam; PF00571; GBS; 2.

R Ffam; PF00571; GBS; 2.

R Ffam; PF00571; GBS; 2.
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NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.3%; Score 39; DB 16; Length 430; 63.6%; Pred. No. 1.9e+02; ive 2; Mismatches 2; Indels
                                                                                                                 "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.3%; Score 39; DB 5; Length 369; 70.0%; Pred. No. 1.6e+02; cive 1; Mismatches 2; Indels
                                                                                                                                      Investigating bloody: "Science 282:2012-2018(1998).

EMBL; Z79596; CABD1858.3; -.

EMBL; Z79596; CABD1858.3; -.

PIR; T18857; T18859.

WormPep; C02C6.3; CE29169.

InterPro; IPR001611; LRR.

InterPro; IPR001611; LRR.

Fam; PP00560; LRR; 4.

Pfam; PP01463; LRRCT; 1.

SMART; SM00081; LRRCT; 1.

SEQUENCE 369 AA; 42639 MW; CFB127DC68B96D3A CRC64;
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1-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
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          SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
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Matches 7; Conserv
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QBNRC7
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Q926H4 Q926H4;

Q926H4 ID Q9 AC Q9

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MEDLINE-20196006; PubMed=10731132;

MEDLINE-20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Ini P.M., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
M. M.K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Gabor G.L.,
Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Banu A., Baxendale J., Bayaktaroglu L., Beasley E.M.,
Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Colding B., Puehler A., The complete sequence of the 1,683-kb psymB megaplasmid from the NZ-fixing endosymbion Sincrhizobium meliloti.";

Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
45.3%; Score 39; DB 16; Length 439;
Best Local Similarity 53.8%; Pred. No. 2e+02;
Matches 7; Conservative 4; Mismatches 2; Indels
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PROSTITE; PS00013; PROKR LIPOPROTEIN; 1.
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 439 AA: 47505 MW; 274E8BDC80BF57D6 CRC64;
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                    PIR; B95927; B95927.

GO; GO:0046821; C:extrachromosomal DNA; IEA.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:0006810; P:transport; IEA.

InterPro; IPR000437; Prok lipoprot_S.

InterPro; IPR000699; SBP_bac_1.
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SEQUENCE FROM N.A.
Mistra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
Mistra S., Crosby W.A., Matthews B.B., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Galbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A.

Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A. FlyBase;

Length 598; 45.3%; Score 39; DB 5; Length 598 46.7%; Pred. No. 2.8e+02; tive 5; Mismatches 1; IndelB Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AB003620; AAN11163.1; -. FlyBase; PSR003620; CG7795. SEQUENCE E998 AA; 67370 MM; 2B9CA0BE22421CC9 CRC64; Local Similarity Query Match

|||| :|::|: | 428 YLYTMIEDSEETQRH 442 4 YLYT--DDAQQTEAH 16 ð

7; Conservative

Best Loca Matches

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Gaps

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Gaps Ctapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B., George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Parragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., 5, Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endoptera; Anthropoda; Hexapoda; Insecta; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. Score 39; DB 5; Length 604; Pred. No. 2.9e+02; 5; Mismatches 1; Indels Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AY118966; AAM50826.1; -. Flybase; FORD032019; CG7795. SEQUENCE 604 AA; 68182 MW; D8B168E7BFBA07FF CRC64; Created) Last sequence update) Last annotation update) 604 AA. Drosophila melanogaster (Fruit fly). PRT; 45.3%; |||| :|::|: | 428 YLYTMIEDSEETQRH 442 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23, 4 YLYT--DDAQQTEAH 16 Similarity 46.7 7; Conservative PRELIMINARY; SEQUENCE FROM N.A. STRAIN=Berkeley; Patel S., Phy Celniker S.; LD44821p. Query Match Best Local 28MSAB; QBMSAB RESULT 34 Q8MSA8 Matches q ò

PRT; PRELIMINARY; Q9VLP4; Q9VLP4 Q9VLP4

RESULT 35

Drosophila melanogaster (Fruit fly). Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update) CG7795 protein.

SEQUENCE FROM N.A.

MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E., Lib W., Hoskins R.A., Galle R.F.,
Adamatides P.G., Richards S.P., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champpe M., Pfelifer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Banco P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottiar P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dalke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dalke C., Davenport L.B., Davies P.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Burbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Rosler C., Gabriellian A.B., Garg N.S., Gelbart W.M., Glasser K.,
A Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., STRAIN-Berkeley; ID DTT ID

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766 AA;
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AC O61851;
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Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kalmael B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
McKhilov G., Milahina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Nelson D.R., Saden-Kiman G.S., Pan S., Polland J., Pacleb J.M.,
Reinert K., Remington K., Saungeon M., Skupski M.P., Smith T.,
Spier B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
Nussearman D.A., Weinstock G.M., Weissenbach J.,
Milliams S.M., Woodage T., Worley K.C., Wun D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao G.,
Zheng X.H., Zhong F.W., Rubin G.M., Venter J.C.;
Scheng Z.H., Morse B.W., Rubin G.M., Venter J.C.;
Milliams S.M., Morse B.W., Rubin G.M., Venter J.C.;
M. The genome sequence of Drosophila melanogaster.";
BMBL, Absolsto; Asservator.
BMBL, Absolsto; Asservator.
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Horinouchi S., Sone Y., Mori H., Sakai F., Hayashi T.;
Horinouchi S., Sone Y., Mori H., Sakai F., Hayashi T.;
Grontrol of expression by the cellulose synthase (bcsA) promoter
region from Acetobacter xylinum BPR 2001.";
Gene 213:93-100(1998).
EMBL; AB003689; BAA23555.1;
EMBL; AB003689; BAA31467.1;
PIR, JC5869, JC58869.
GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tonouchi N., Tahara N., Kojima Y., Nakai T., Sakai F., Hayashi T., Tsuchida T., Yoshinaga F., Isachida T., Yoshinaga F., "A beta glucosidase gene downstream of the cellulose synthase operon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Acetobacteraceae; Gluconacetobacter.
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       643 AA; 72867 MW; 94FFB937EE9CBB12 CRC64;
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Last annotation update)
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Biosci. Biotechnol. Biochem. 61:1789-1790(1997)
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MEDLINE=98296257; PubMed=9630539;
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01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 YLYT--DDAQQTEAH 16
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BETA-GLU.
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STRAIN=cv. B73;
Bergstrom D., Springer N.M., Schmitt L.T., Guthrie B., Sidorenko L.,
Kaeppler S.M., Cone K.C.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF545813; AAN41253.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                 Length 735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. B73;
Chandler V.L., Kaeppler S.M., Kaeppler H.F., Cone K.C.;
"Sequences from the Plant Chromatin Consortium.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83842 MW; D2778799EFB9E4BB CRC64;
                                                                                                                                                78223 MW; 463DB8116F1C55E1 CRC64;
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OHAR-2003 (TrEMBLrel. 23, Created)

O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)

O1-UN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                              45.3%; Score 39; DB 2; 1
70.0%; Pred. No. 3.6e+02;
GO; GO:0005975; P:carbohydrate metabolism; IEA. InterPro; IPR002772; Glyco_hydro_3C. InterPro; IPR001764; Glyco_hydro_3N. Pfam; PP00933; Glyco_hydro_3; 1. Pfam; PP01915; Glyco_hydro_3; 2; 1. Pfam; PP01915; GLHYDRLASE3. SEQUENCE 735 AA; 78223 MW; 463DB8116F1C55E1
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InterPro; IPR003516; PoetSET.
InterPro; IPR007728; Pre-SET.
InterPro; IPR001214; SET.
InterPro; IPR003606; Zn2-binding.
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PROSITE; PS50867; PRE SET; 1.
PROSITE; PS50280; SET; 1.
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Pfam; PF00856; SBT; 1.
Pfam; PF02182; YDG SRA; 1.
SMART; SM00468; PFESET; 1.
SMART; SW00317; SET; 1.
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SDG113.
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Genome sequence of the nematode C. elegans: a platform for
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251 AA;
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SIGNAL
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Rhabditidae; Peloderinae; Caenorhabditis.
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Rhabditidae, Peloderinae, Caenorhabditis.
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL, AF06/761, AAC17540.2;
R PIR, T33163;
R WormPep; F55F10.1; CE30377.
R GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000166; F:ATP binding; IEA.
GO; GO:000166; F:MClectide binding; IEA.
GO; GO:000166; F:Wc-component signal transduction system (p. .;
InterPro; IPR002393; AAA ATPASE.
R InterPro; IPR002393; AAA ATPASE.
R InterPro; IPR002098; Sig34 interact.
InterPro; IPR002098; Sig34 interact.
R InterPro; IPR002098; Sig44 interact.
R SMART; SM00327; VWF.A.
R SMART; SM00327; VWA; 1.
R RPROSITE; PS00675; SIGMA54 INTERACT_1; 1.
R PROSITE; PS00675; SIGMA54 INTERACT_1; 1.
R HYDOCHETICAL DIOCTERN; GCE6A78E56A57969 CRC64;
SEQUENCE 4368 AA; 492651 MW; 6CE6A78E56A57969 CRC64;
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Local Similarity 60.0%; Pred. No. 2.8e+03;
les 9; Conservative 1; Mismatches 5; Indels
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Pauley A., Gattung S., Scheet P.;
"The sequence of C. elegans cosmid F55F10.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
01-AUG-1998 (TrEMBLrel. 07, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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MEDLINE=99069613; PubMed=9851916;
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Science 282:2012-2018(1998).
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                                                                                                                     Aypothetical protein.
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SEQUENCE FROM N.A.
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Programmer Fron N. N.

MEDLINE=20456722; PubMed=11003389;

Vitved L., Holmskov U., Koch C., Teisner B., Hansen S., Skjodt K.;

Nitved L., Holmskov U., Koch C., Teisner B., Hansen S., Skjodt K.;

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterggii, Neopterggii, Teleostei, Ostariophysi, Cypriniformes;
Cyprinidae; Danio.

NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.2%; Score 38; DB 5; Length 235
50.0%; Pred. No. 1.5e+02;
tive 1; Mismatches 7; Indels
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                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Blanchard M., Bradshaw H.;
Blanchard M., Dradshaw H.;
submitted of C. elegans cosmid WOLAll.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston R.;
"Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL; U64852; AAB04972.1;
PIR; T33962; T33962.
PIR; T3962 T33962.
Hypochetical protein.
SEQUENCE 235 AA; 26776 MW; C087F352ED5F9874 CRC64;
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K -> N.
12D0ABD06B6E3B11 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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nes 8; Conservative
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Query Match
44.2%; Score 38; DB 13; Length 251;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps

0;

2 QRYLYTDDAQQT 13 |:| ||| ::| 135 QKYYVTDDVEET 146

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Db 135 QKYYVIDDVEET 146

Search completed: March 2, 2004, 16:07:19 Job time : 8.66667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                    OM protein - protein search, using sw model
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March 2, 2004, 15:51:17 ; Search time 1.53333 Seconds
 (without alignments)
543.341 Million cell updates/sec Run on:

US-10-060-765-7 86 1 RQRYLYTDDAQQTEAH 16 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched: 141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Q9nsal homo sapien										-	-					human r	simian	simian	bovine	bovine	simian 11	simian 1		xylella	xenopus	. ,	N.	vaccinia	372	_	Q9spe5 arabidopsis	P73655 synechocyst
SUMMARIES		QI	FGFL HUMAN	FGFL MOUSE	HEM1 NEIGO	DPOL_ADEG1	ZN08 HUMAN	VP4_ROTPY	SURZ CAEEL	IF4E_APLCA	2AD2_SCHPO	VP4_ROTH6	CUSC ECOLI	CUSC_ECO57	CUSC ECOL6	SYR STAEP	VP4_NCDV						VP4	•			OSTA		RPOA_LELV	AFA	VEO	VEO	VEO	SNA	SYW SYNY3
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SIP2_YEAST	STE3_YEAST SYR STAAM	SYR_STAAN SYR_STAAW	DSBD VIBVU UBP2 HUMAN	MUTA_STRCM PFEA_PSEAE	VP4 ROTHJ VP4 ROTHQ
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37	37	37	37	37	37
34	36.	80 01	4 4	42	4 4 3 4 73

ALIGNMENTS

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Matches
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STRAIN=CSTBL/64); TISSUE=PANCTEAS;

KAMAIN=CSTBL/64); TISSUE=PANCTEAS;

KAMAINE=21085660; PubMed=11217851;

KAMAINE=21085660; PubMed=11217851;

KAWAIN T., HARA A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fubunishi Y., Komoo B., Yamanaka I.,

Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Zamanaka I.,

Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Kohenbach C., Seya T., Shibata Y., Storch K.-F.,

Nymbaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hanseli V., Schoenbach C., Rawaji H., Kohtsuki S.,

Nymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: Secreted (Potential).
-1- TISSUE SPECIFICITY: Most abundantly expressed in the liver, also expressed in the thymus at lower levels.
-1- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-20461777; PubMed-10858549; Nishimura T., Nakatake Y., Konishi M., Itoh N.; "Identification of a novel FGF, FGF-21, preferentially expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                             Score 86; DB 1; Length 209;
Pred. No. 3.6e-08;
; Mismatches 0; Indels
                                                                                                                                                                                      FIBROBLAST GROWTH FACTOR-21.
                                                                                                                                                                                                               ISSING (IN REF. 2).
27925C52A0023823 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-21 precursor (FGF-21)
                                                                                                                                                                                                                 MISSING (IN REF
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                                                                                                                                                                    POTENTIAL.
                        Pfam; PF00167; FGF; 1.
PRINTS; PR00262; ILLHBGF.
ProDom, PD000083; ILL HBGF; 1.
SMART; SN00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; FALSE_NBG.
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                                                                                                                                                                                                                                        209 AA; 22300 MW;
    InterPro; IPR002348; IL1_HBGF.
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                                                                                                                                                                                                                                                                                                                                    16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                  209
                                                                                                                                           Growth factor; Signal.
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                                                                                                                                                                                                                                                                                                              Best Local Similarity
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Q9JJN1;
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MEDLINE=99030330; PubMed=9811666;

MEDLINE=99030330; PubMed=9811666;

MEDLINE=99030330; PubMed=9811666;

"Transport of intact porphyrin by HpuAB, the hemoglobin-haptoglobin utilization system of Neisseria meningitidis.";

J. Bacteriol. 180:6043-6047(1998).

-: CATALYTIC ACTIVITY: Glutamyl-tRNA(Glu) + NADFH = glutamate-1-semialdehyde + NADP(+) + tRNA(Glu).

-: PATHWAY: Porphyrin blosynthesis by the C5 pathway; first step.
-: SIMILARITY: Belongs to the glutamyl-tRNA reductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria gonorrhoeae.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 28 POTENTIAL.
29 210 FIBROBLAST GROWTH FACTOR-21.
210 AA; 23237 MW; AE02AABA6477E6F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.2%; Score 75; DB 1; I
87.5%; Pred. No. 3.4e-06;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
36-EBB-2003 (Rel. 41, Last annotation update)
Glutamyl-tRNA reductase (EC 1.2.1.-) (GluTR).
                                                                                                                                                                                                 HSSP, P03968; IBAR.
MGD; MGI:1861377; F9f21.
InterPro; IPR008996; Cytok_III_like.
InterPro; IPR002348; ILI_HBGF.
Pfam; PF00167; FGF; I.
PRINTS; PR00262; ILIHBGF.
PRODOM; PD000831; ILI_HBGF.
PROSITE; SW00442; FGF; I.
PROSITE; PS00247; HBGF_FGF; PALSE_NEG.
Growth factor; Signal.
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InterPro; IPR000343; GlutR.
Pfam; PF00745; GlutR dimer; 1.
Pfam; PF05201; GlutR N; 1.
TIGMFAMS; TIGRO1035; hemA; 1.
PROSITE; PS00747; GLUTR; 1.
                                                                                                                                            EMBL; AB025718; BAA99416.1; -. EMBL; AK007574; BAB25115.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF067426; AAC79428.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RORYLYTDDAQQTEAH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 kokvivrodoporeah 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q42843; 1B29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEMI NEIGO
ID HEMI NEIGO
AC Q9ZHDG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                   adenovirus CELO.";
J. Virol. 70:2939-2949(1996).
-!- CATALYȚIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                              !- MISCELLANBOUS: This DNA polymerase requires a protein as a primer.
!- SIMILARITY: Belongs to the DNA polymerase type-B family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                  Gaps
                                                                                                                                                                                                                                                                      Avian adenovirus gall (strain Phelps) (Fowl adenovirus 1) (CELO).
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Aviadenovirus
                                                                                                                                                                                                                                                                                                                                                                     "The complete DNA sequence and genomic organization of the avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=96186720; PubMed=8627769;
Chiocca S., Kurzbauer R., Schaffner G., Baker A., Mautner V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 1; Length 1121;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U46933; AAC54904.1; -.
InterPro; IPR006172; DNA_DOL_B.
InterPro; IPR00486; DNA_DOL_B.
InterPro; IPR00486; DNA_DOL_B 2; I.
PRINTS; PR00106; DNAPOLB 2; I.
PRINTS; PR00106; DLBC; I.
PROSTITE; PS00116; DNA_POLYMERASE B; I.
Transferase; DNA-directed DNA_POlymerase; DNA_replication;
                                                        47.7%; Score 41; DB 1; Length 415; 61.5%; Pred. No. 9.7; tive 1; Mismatches 4; Indels
            NUCLEOPHILE (BY SIMILARITY).
BASE (BY SIMILARITY).
054D366586CEB32F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1121 AA; 129395 MW; AS5B9B6A54D3BDE1 CRC64;
                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA polymerase (EC 2.7.7.7).
Porphyrin biosynthesis; Oxidoreductase; NADP. ACT_SITE 50 NUCLEOPHILE (BY ACT_SITE 94 94 BASE (BY SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            543 AA.
                                                                                                                                                                                          PRT; 1121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
             50 50 M
94 94 B
415 AA; 45453 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   731 ROOFRYADDPEQEE 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RORYLYTDDAQOTE 14
                                                 Query Match
Best Local Similarity 61.5-
Best Local 8; Conservative
                                                                                                        4 YLYTDDAQQTEAH 16
                                                                                                                                82 YLYTLÖMÖETVRH 94
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                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                              NCBI_TaxID=10553;
                                                                                                                                                                                                                                                                                                                                                                                                                       (N) (N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZN08_HUMAN
P17098;
                                                                                                                                                                                         DPOL_ADEG1
Q64751;
                                                                                                                                                                                                                                                                                                                                                            Cotten M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
ZNO8 HUMAN
ID ZNO8 HC
AC P17098;
DT 01-AUG-
DT 01-AUG-
                                                                                                                                                                               DPOL_ADEG1
                                                                                                                                                                     RESULT 4
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0
                                                                                                                                                                                                           TISSUE FROM N.A.

TISSUE Placenta;

MEDIARE-POLE5933; PubMed=2106481;

MEDIARE-POLE5933; PubMed=2106481;

A lania L., Donti E., Pamuti A., Pascucci A., Pengue G.,

Lania L., Donti E., Pamutia G., Lanfrancone L., Pelicci P.-G.;

Tomba isolation, expression analysis, and chromosomal localization of Genomics 6:333-340(1990).

Tomba isolation, and principle of Genomics 6:333-340(1990).

L. FUNCTION: May function as a transcription factor.

C. I SUBCELLUIAR LOCATION: Nuclear (Probable).

C. I TISSUE SPECIFICITY: UBIQUITORSLY PRESENT IN MANY HUMAN CELL LINES CONTINENTALION.

C. I TISSUE SPECIFICITY: UBIQUITORSLY PRESENT IN MANY HUMAN CELL LINES CONTINENTALION.

C. I TINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pfam; PF00096; zf-C2H2; 7.

PFNUTS; PR00046; ZINCFINGER.

SMART; SM00349; KRAB; 1.

SMART; SM00355; ZnF_C2H2; 7.

PROSITE; PS00028; KRAB; 1.

PROSITE; PS00028; KRAB; 1.

PROSITE; PS00157; ZINC_FINGER_C2H2 1; 7.

PROSITE; PS00157; ZINC_FINGER_C2H2 2; 7.

Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005634; C:nucleus; NAS.
GO; GO:0003677; F:DNA binding; NAS.
GO; GO:0008270; F:zinc ion binding; NAS.
GO; GO:0008255; P:regulation of transcription, DNA-dependent; NAS.
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
10-OCT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 8 (Zinc finger protein HF.18) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 543;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61772 MW; ADD987504ECAC019 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.5%; Score 40; DB 1;
53.3%; Pred. No. 20;
ive 3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRAB.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 KRAB domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C2H2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C2H2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001909; KRAB.
InterPro; IPR007087; Znf_C2H2.
InterPro; IPR007086; Znf_C2H2_sub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M29581; AAA61314.1; -.
PIR; B34612; B34612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 RGEYLYTYDSOLTDS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RORYLYTDDAGOTEA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:13154; ZNF8.
MIM; 194532; -.
                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P08046; 1A1H.
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us-10-060-765-7.rsp

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Durbin R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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0
                                                                                                                                                                                              MEDLINE=91251227; PubMed=1645789;
LOPEZ S., LOPEZ I.V., Romero P., Mendez E., Soberon X., Arias C.F.;
Lopez S., Lopez I.V., Romero P., Mendez E., Soberon X., Arias C.F.;
Lopez I.V., Romero P., Mendez E., Soberon X., Arias C.F.;
Lopez I.V., Romero P., Mended amino acid sequence and
prediction of the secondary structure of the VP4 protein.";
J. Virol. 65:3738-3745(1991).
-!- STBCELLULAR LOCATION: Outer capsid.
-!- STBCELLULAR LOCATION: Outer capsid.
-!- PTM: VP8 is one of two trypsin cleavage products of VP4; the other
product is VP5.
-!- SIMILARITY: Belongs to the rotaviruses VP4 protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                           01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
[Contains: Outer capsid proteins VP5 and VP9].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.5%; Score 40; DB 1; Length 776; 50.0%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B6A6C9CF81541014 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OUTER CAPSID PROTEIN VP4.
OUTER CAPSID PROTEIN VP8.
OUTER CAPSID PROTEIN VP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC.) (F
N-LINKED (GLCNAC.)) (F
N-LINKED (GLCNAC.)) (F
N-LINKED (GLCNAC.)) (F
N-LINKED (GLCNAC.)) (F
N-LINKED (GLCNAC.)) (F
N-LINKED (GLCNAC.)) (F
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N-LINKED (GLCNAC.)) (F
N-LINKED (GLCNAC.)) (F
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N-LINKED (GLCNAC.)) (F
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ID _SUR2_CAEEL STANDARD; PRT; 1587 AA.
AC Q10669; 045497; Q90365;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                       Viruses; dsRNA viruses; Reoviridae; Rotavirus NCBI TaxID=10919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC
                                    776 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 30;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M63231; AAA47100.1; -.
PIR; A40342; VPXRXM.
InterPro; IPR00416; Cap VP4.
InterPro; IPR008985; Conalike_lec_gl.
Pfam; PF00426; VP4; 1.
Coat protein; Glycoprotein. OUTER CAP!
CHAIN
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N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86772 MW;
                                                                                                                                      Porcine rotavirus (strain YM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 gyryrkbGegirah 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
32
56
97
1116
132
132
178
183
198
325
670
670
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                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                    VP4 ROTPY P25174;
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CARBOHYD
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                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Singh N., Han M.; sine, functions late in the let-60 ras-mediated "sut-2, a novel gene, functions late in the let-60 ras-mediated signaling pathway during Caenorhabditis elegans vulval induction."; Genes Dev. 9:2251-2265(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IF4E APLCA

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-!- FUNCTION: Functions in the let-60 ras signaling pathway; acts downstream of let-60 during C.elegans vulval induction.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 1587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1405 1587 GLN/HIS-RICH.
505 505 Y -> FLD (in isoform b).
FTIG=VSP (04435.
1587 AA, 183906 MW, Al25FGA74922BIIC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dobson R.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 1
Pred. No. 68;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q10669-2; Sequence=VSP_004435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q10669-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS, AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACIDIC
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Bristol N2;
MEDLINE=96018822; PubMed=7557379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U33051; AAA85507.1; -.
EMBL; Z92834; CAB07385.2; -.
EMBL; Z92834; CAB07394.2; -.
WOTMPEP; F39B2.44; CE28023.
WOTMPEP; F39B2.45; CE28024.
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1553 QQQYLYMQQLQQHQQH 1568
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 43.8%;
Matches 7; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16
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SUR-2 OR F39B2.4.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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us-10-060-765-7.rsp

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                                                                                                                                                                                                                                                                                                                                  MEDLINE=99009053; PubMed=9792652;

A MEDLINE=99009053; PubMed=9792652;

A "Phosphorylation of elfed at a conserved serine in Aplysia.";

"Der J.R., Pepio A.M., Yanow S.K., Sossin W.S.;

"Phosphorylation of elfed at a conserved serine in Aplysia.";

"I Biol. Chem. 273:29469-29474 (1998).

"I Biol. Chem. 273:29469-29474 (1998).

"I Biol. Chem. 273:29469-29474 (1998).

"I Recognizes and binds the 7-methylguanosine-containing mRNA secondary structures.

"I Synthesis and facilitates ribosome binding by inducing the unwinding of the mRNAs secondary structures.

"I Synthesis and facilitates ribosome binding by inducing the unwinding of the mRNAs secondary structures.

"I Synthesis and the amulti-submit complex, the composition of the synthesis and internal and internal environmental conditions.

"I is composed of at least EIP4A, EIF4E and EIF4G. EIF4E is also known to interact with other partners (By similarity).

"I TM: Phosphorylation increases the ability of the protein to bind to mRNA caps and to form the EIF4F complex.

"I SIMILARITY: Belongs to the eukaryotic initiation factor 4E family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                     Apogastropoda; Heterobranchia; Buthyneura; Opisthobranchia; Anaspidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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MEDLINE=21275457; PubMed=11380623;
Tanabe O., Hirata D., Usui H., Nishito Y., Miyakawa T., Igarashi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, delta 2 isoform (PP2A, B subunit, B' delta 2 isoform)
PRAR2 OR PBP2 OR SPAC6F12.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein biosynthesis; Translation regulation; Initiation factor; RNA-binding; Phosphorylation.
MOD RES 207 207 PHOSPHORYLATION (BY PKC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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Gukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (BY PKC).
9EE00CB6DE8162E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                627 AA.
                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PHOSPHORYLATION.
TISSUE=Nerve;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                          Aplysioidea, Aplysiidae, Aplysia.
NCBI_TaxID=6500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPRO1040; TIF_eIF_4E. Prom; Prom; PRO1652; IF4E; 1. Prom; PD03597; TIF_eIF_4E; 1. PROSITE; PS00813; IF4E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF085810; AAC36720.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 AA; 24646 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 LWTRDAOKTEA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 LYTDDAQQTEA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P07260; 1AP8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takeda M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P78759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2AD2_SCHPO
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RX MEDLINE=172.8

RA WOOD V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., RADLINE=21848401; PubMed=11859560;

RA WOOD V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgourso J., Peat N., Hayles J., Basham D., Bowman S., Chillingworth T., Churcher C.M.,

RA Gentles S., Goble A., Hamilin N., Harris D., Hidalgo J., Hodgeon G., Gentles S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA, Jones L., Jones M., Leather S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., Stanter S., States S., Stevens K., States S., Stevens K., Stevens K., Stevens K., Stevens K., Stevens K., Stevens K., Stevens K., Stevens K., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., Hurst S., McGonet W., Gaillbert H., Wanbutt R., Punnelle B., Dreano S., Gloux S., Lelaure V., McDonald S., McDonald S., Rocket M., Gaillardin C., Fallada V.B., Garzon A., Thode G., Bominguez A., Revuelta J., Moreno S., Armstrong J., Forsburg S.L., Robackowski G., Ussery D., Barrell B.G., Nurse P., Shaldone Bequence of Schizosaccharomyces pombe.";

Ry Nature 415:871-880 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBGINIT: PP2A consists of a common heterodimeric core enzyme, composed of a 36 kDa catalytic subunit (subunit C) and a 65 kDa composed of a 36 kDa catalytic subunit (subunit A), that associates constant regulatory subunit (PR65 or subunit A), that associates with a variety of regulatory subunits. Proteins that associate with the core dimer include three families of regulatory subunits B (the R2/B/PR55/B55, R3/B''/PR72/PR130/PR59 and R5/B'/B56 families), the 48 kDa variable regulatory subunit, viral proteins, and cell signaling molecules.
SUBCELDULAR LOCATION: Cytoplasmic and nuclear.
SIMILARITY: Belongs to the phosphatase 2A regulatory subunit B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 4:363-369(1997).
-!- FUNCTION: The B regulatory subunit might modulate substrate selectivity and catalytic activity, and also might direct the localization of the catalytic enzyme to a particular subcellular compartment. Has a role in cell shape control and septum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98162722; PubMed-9501991;
Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
"Identification of open reading frames in Schizosaccharomyces pombe
                                                                                                                                             "Isolation and characterization of parl(+) and par2(+): two Schizosaccharomyces pombe genes encoding B' subunits of protein
                                                                      SEGUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION. MEDLINE=20221714; PubMed=10757751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 215-627 FROM N.A.
                                                                                                                                                                                                                               Genetics 154:1025-1038(2000)
with calcineurin.";
Genes Cells 6:455-473(2001).
                                                                                                                             Jiang W., Hallberg R.L.;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                            phosphatase 2A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid sequence analysis.";
Virology 182:407-412 [1991].
-!- SUBCELLULAR LOCATION: Outer capsid.
-!- PIM: VP8 is one of two trypsin cleavage products of VP4; the other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OUTER CAPSID PROTEIN VP4.
OUTER CAPSID PROTEIN VP8 (POTENTIAL).
OUTER CAPSID PROTEIN VP5 (POTENTIAL).
N.LINKED (GLCNAC...) (POTENTIAL).
N.LINKED (GLCNAC...) (POTENTIAL).
N.LINKED (GLCNAC...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Outer layer protein VP4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 1; Length 776; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                  Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
EMBL; AB041232; BAB40598.1; -.
BMBL; 298533; CAB11096.1; -.
EMBL; D89107; BAB13770.1; -.
GeneDB_SPombe; SPACFT2.12; -.
GO; GO;0007043; P:cell cycle; ISS.
GO; GO:0016043; P:cell organization and biogenesis; ISS.
GO; GO:0016288; P:cytokinesis; ISS.
GO; GO:007067; P:mitosis; ISS.
InterPro; IRR002554; BS6.
Fran, PF01603; BS6; I.
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                                                                                                                                                                                                                                                                                                          627 AA; 72464 MW; 82AD6FD5EA5097C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1992 (Rel. 23, Last sequence update)
10-0CT-2003 (Rel. 42, Last amnotation update)
10-cr capsid protein VP4 (Hemagglutinin) (Outer Contains: Outer capsid proteins VP4 NP4 (Pemagglutinin)
                                                                                                                                                                                                                                                                                                                                                                  45.3%; Score 39; DB 1; 46.2%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human rotavirus (serotype 1 / strain 69M).
Viruses, dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=10947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     776 AA
                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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Interpro; IPR008985; ConA_like_lec_gl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91220682; PubMed=1850912;
Qian Y., Green K.Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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32
56
97
132
198
776 AA;
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                           Nuclear protein.
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P26451;
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CARBOHYD
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SECUENCE FROM N.A.
Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
Federspiel N., Hyman K., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampel G., Seki X., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMed G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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MEDLINE=20461235; PubMed=11004187;
Munson G.P., Lam D.L., Outten F.W., O'Halloran T.V.;
Munson G.P. a copper-responsive two-component system on the chromosome of Escherichia coli K-12.";
J. Bacteriol. 182:5864-5871(2000).
                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99420866; PubMed=10493123;
Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
"Enrichment of low abundance proteins of Escherichia coli by
hydroxyapatite chromatography.";
Electrophoresis 20:2181-2195(1999).
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Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
CUSC ECOLI STANDARD; PRT; 457 AA. P772I; Q9L5Y3; Q9X444; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) Cation efflux system protein cusC precursor. CUSC OR IBBB OR B0572.
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                                                                                                                                                                                                                                                   Escherichia coli
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EMBL; AB2099; BAB4326.1; -.

EMBL; AP30205.1; -.

EMBL; AP30205.1; -.

EMBL; AP5061 BAF70174.1; -.

BRE; B64790; B64790.

R Eccene; ETG1423; Cusc.

DR InterPro; IPR001423; DPC.

DR PAR ; P800313; PROKL LIPOPROTEIN; 1.

DR PROSITE; P800013; PROKRR LIPOPROTEIN; 1.

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PROSITE; P800013;
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MEDLINE=22697381; PubMed=12813074;

Franke S., Grass G., Rensing C., Nies D.H.;

Franke S., Grass G., Rensing C., Nies D.H.;

Franke S., Grass G., Rensing C., Nies D.H.;

Franke S., Grass G., Rensing C., Nies D.H.;

J. Bacterichia coli...;

J. Bacterichia coli...;

J. Bacterich. 185:3804-3812(2003).

J. Bacterich. Part of a cation efflux system that mediates resistance of copper and silver. In pathogenic strains it allows the bacteria to invade brain microvascular endothelial cells (BMEC) thus allowing it to cross the blood-brain barrier and cause neonatal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: The cus efflux system is composed of cusA, cusB, cusC and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- MISCELLANEOUS: The cus system plays an important role in copper tolerance under anaerobic growth and, under extreme copper stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                              MEDLINE=21391920; PubMed=11399769; O'Halloran T.V.; Outten F.W., Huffman D.L., Hale J.A., O'Halloran T.V.; uthe independent cue and cus systems confer copper tolerance during aerobic and anaerobic growth in Escherichia coli."; J. Biol. Chem. 276:30670-30677 (2001).
                                                                                                                                                                                                                                                                                      Franke S., Grass G., Nies D.H.; "The product of the ybdE gene of the Escherichia coli chromosome is involved in detoxification of silver ions."; Microbiology 147:965-972(2001).
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-!- INDUCTION: Transcriptionally regulated by cusR in response to copper and silver ions.
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FUNCTION IN COPPER HOMEOSTASIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-0157:H7 / EDL933 / ATCC 700927;
STRAIN-0157:H7 / EDL933 / ATCC 700927;
PETJA N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
PetJA N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Posfai G., Hackett J., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.,
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anchor (Potential).
                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=83334;
S -> F (IN STRAIN K1 / R5218).
R -> G (IN STRAIN K1 / R5218).
Q -> R (IN STRAIN K1 / R5218).
S -> P (IN STRAIN K1 / R5218).
G -> GWQQ (IN STRAIN K1 / R5218).
W, BB5B2B6B6719F7A1 CRC64;
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                                                                                               1; Length 457;
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                                                                                                                                                                                                                                                                                           10-0CT-2003 (Rel. 42, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) Cation efflux system protein cusC precursor. CUSC OR Z0711 OR ECS0610.
                                                                                                   .DB
                                                                                                                              Mismatches
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SEQUENCE FROM N.A.
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                                                                                                  44.2%; Score 38; 58.3%; Pred. No.
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MEDLINE=21156231; PubMed=11258796;
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10-0CT-2003 (Rel. 42, Last anno
                                                                          50269 MW;
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457 AA;
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SYR STAEP
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SYR_STAEP
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"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).

-I- FUNCTION: Part of a cation efflux system that mediates resistance to copper and silver (By similarity).

-I- SUBUNIT: The cus efflux system is composed of cusA, cusB, cusC and cust (By similarity).
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-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
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InterPro; IPR003423; OEP.
InterPro; IPR003423; OEP.
InterPro; IPR003423; OEP.
Pfam; PF02321; OEP; 2.
PROSITE; PROKER LIPOPROTEIN; 1.
PROSITE; PROSITE; INTERPROTE IN THE STATEM PROTEIN CUSC.
SIGNAL 1 17 BY SIMILARITY.
CHAIN 18 460 CATION EFFLUX SYSTEM PROTEIN CUSC.
LIPID 18 18 N-palmitoyl cysteine (Probable).
  PIR; E8555; BOSSOS; BOSSOS; INTERPRO; IRRODA37; PROK_lipoprot_S.
InterPro; IPRO00437; Prok_lipoprot_S.
PEMSITE; PRO1013; PROKAR IIPOPROTEIN; 1.
PROSITE; PS00013; PROFA IIPOPROTEIN; 1.
Outer membrane; Signal; Inpoprotein; Palmitate; Complete proteome.
SIGNAL 17 EBY SIMILARITY.
18 460 CATION EFFLUX SYSTEM PROTEIN CUSC.
18 460 CATION EFFLUX SYSTEM PROTEIN CUSC.
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-!- INDUCTON: Transcriptionally regulated by cusR in response to
copper and silver ions (Probable).
-!- SIMILARITY: Belongs to the fusA/nodT family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bscherichia coli O6.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                         N-palmitoyl cysteine (Probable).
S-diacylglycerol cysteine (Probable)
FE79EDB715ABC922 CRC64;
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Pred. No. 38;
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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MEDLINE=22388234; PubMed=12471157;
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NCBI_TaxID=217992;
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18 18 S-1
460 AA; 50715 MW;
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
ARGS OR SE0380.
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InterPro; IPR001412; IRNA-synt ld C.
InterPro; IPR001412; IRNA-synt ld C.
Pfam; PF00450; IRNA-synt ld C; 1.
Pfam; PF00750; IRNA-synt ld C; 1.
Pfam; PF00750; IRNA-synt ld C; 1.
PRINTS; PR01038; IRNASNYTHARG.
TIGRRAMS; TIGR00456; argS; 1.
PR05ITE; PS00178; AA TRNA LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                           Gaps
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Mol. Microbiol. 49:1577-1593 (2003).
-!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA (Arg) = AMP + diphosphate + L-arginyl-tRNA (Arg).
-!- SUBGNIT: Monomer (By similarity).
-!- SUBGNIT: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J., 
Zhon Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z., 
Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M., 
"Genome-based analysis of virulence genes in a non-biofilm-forming
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                                                    DB 1; Length 460;
                                                                                                           2; Indels
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460 AA; 50709 MW; 4C1D618F06AD66B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                553 AA.
                                                                                                        3; Mismatches
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                                                    Score 38; DB
Pred. No. 38;
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InterPro; IPR001278; Arg_tRNA-synt_1c.
InterPro; IPR005148; N.
                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                 44.2%;
58.3%;
                             148 RONYLATEEAOR 159
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STRAIN=ATCC 12228;
PubMed=12950922;
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P39033;
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MEDLINE=92356070; PubMed=1322955;
Isegawa Y., Nakagomi O., Nakagomi T., Ueda S.;
Isegama T., Nakagomi O., Nakagomi F., Ueda S.;
A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotavirus strain FRV-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
[Contains: Outer capsid proteins VP5 and VP8].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE=89012172; PubMed=2845121; Nishikawa K., Taniguchi K., Torres A., Hoshino Y., Green K., Kapikian A.Z., Chanock R.M., Gorziglia M.; Comparative analysis of the VP3 gene of divergent strains of the roctaviruses simian SAll and bovine Nebraska calf diarrhea virus."; J. Virol. 62:4022-4026(1988).
                                                                                                                                                                                                                                          .... capping protein v_P4 (Hemagglutinin) (Outer layer protein VP4) (Contains: Outer capsid proteins VP5 and VP8].
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OUTER CAPSID PROTEIN VP8.
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                                                                                                                                                                                                                                                                                                                                                        Nebraska calf diarrhea virus (strain Lincoln) (NCDV).
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
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Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=39009;
                                                                                                                                                         01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-AUG-2003 (Rel. 142, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Oute
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3; Mismatches
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Interpro; IPR008985; ConA like lec_gl.
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QYTYTRDGEEVTAH 315
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Coat protein; Glycoprotein.
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                                                                                       STANDARD;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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NCBI_TaxID=10932;
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                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Gen. Virol. 73:1939-1946(1992).
-!- SUBCELLUIAR LOCATION: Outer capsid.
-!- FTM: VPB is one of two trypsin cleavage products of VP4; the other product is VP5.
-!- SIMILARITY: Belongs to the rotaviruses VP4 protein family.
J. Gen. Virol. 73:1939-1946(1992).
-i- SUBCELLULAR LOCATION: Outer capsid.
-i- PTM: VPR is one of two trypsin cleavage products of VP4; the other product is VP5.
-i- SIMILARITY: Belongs to the rotaviruses VP4 protein family.
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01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
[Contains: Outer capsid proteins VP5 and VP8].
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Viruses, dsRNA viruses, Reoviridae, Rotavirus.
NCBI_TaxID=39013;
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PIR; JQ1639; JQ1639.
Interpro; IPR000416; Cap VP4.
InterPro; IPR008985; ConA_like_lec_gl.
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Coat protein; Glycoprotein.
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Pfam; PF00426; VP4; 1.
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Yeager M., Berriman J.A., Baker T.S., Bellamy A.R.;
Trager M., Berriman J.A., Baker T.S., Bellamy A.R.;
Three-dimensional structure of the rotavirus haemagglutinin VP4 by
cryo-electron microscopy and difference map analysis.";
EMBO J. 13:1011-1018(1994).
-:- SUBCELLULAR LOCATION: Outer capsid.
-:- PTM: VP8 is one of two trypsin cleavage products of VP4; the other
product is VP5.
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LoCT-2003 (Rel. 42, Last annotation update)
Outer capsid protein VP4 (Hemaga]utinin) (Outer layer protein VP4)
[Contains: Outer capsid proteins VP5 and VP8] (Version 1).
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MEDILINE=86645921, PubMed-898038,
LOPEZ S., Arias C.F., Bell J.R., Strauss J.H., Espejo R.T.,
"Primary structure of the cleavage site associated with trypsin
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 1; Length 775;
Pred. No. 69;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                         4148D0C91A89B18A CRC64;
                                                                                                                                                   OUTER CAPSID PROTEIN VP4.
OUTER CAPSID PROTEIN VP9.
OUTER CAPSID PROTEIN VP5.
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Viruses; dsRNA viruses; Reoviridae; Rotavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enhancement of rotavirus SA11 infectivity."; Virology 144:11-19(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              776 AA
                                  EMBL; D10970; BAA01747.1; -. PIR; JQ1638; JQ1638.
InterPro; IPR000416; Cap VP4.
InterPro; IPR008985; ConA_like_lec_gl.
Pfam; PF00426; VP4; 1.
Coat protein; Glycoprotein.
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1 775
OUTER CAPSI
  email to license@isb-sib.ch)
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=89183617; PubMed=2538804;
Mitchell D.B., Both G.W.;
Michell D.B., Both G.W.;
"Complete nucleotide sequence of the simian rotavirus SAll VP4 gene.";
Nucleic Acids Res. 17:212-2122(1989).
-!- SUBCELLUIAR LOCATION: Outer capsid.
-!- PIM: VP8 is one of two trypsin cleavage products of VP4; the other
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                                                                                                                                                                                                                                                                                                                                                OUTER CAPSID PROTEIN VP4.

OUTER CAPSID PROTEIN VP8 (POTENTIAL).
OUTER CAPSID PROTEIN VP5 (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-2003 (Rel. 42, Last annotation update)
0uter capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
[Contains: Outer capsid proteins VP5 and VP8] (Version 2).
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-!- SIMILARITY: Belongs to the rotaviruses VP4 protein family.
-!- CAUTION: SEE ALSO VERSION 1 OF THIS PROTEIN.
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Pred. No. 69;
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Viruses; dsRNA viruses; Reoviridae; Rotavirus.
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                                                                                                                                                                        EMBL, Y00336; CRA68424.1; -.
PIR; A04129; VPXR4S.
InterPro; IPR000416; Cap VP4.
InterPro; IPR008885; ConA like lec_gl.
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InterPro; IPR000416; Cap VP4.
InterPro; IPR008985; ConA_like_lec_gl.
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                                                                                                                                                                                                                                                                                                                           Coat protein; Glycoprotein.
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                                                                                                                                                                                                                                                                                                  Pfam; PF00426; VP4; 1.
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6; Conserv
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-! SUBCELGULAR LOCATION: Outer capsid.
-!- PIM: VP8 is one of two trypsin cleavage products of VP4; the other product is VP5.
-!- SIMILARITY: Belongs to the rotaviruses VP4 protein family.
InterPro; IPR000416; Cap VP4.
InterPro; IPR008985; ConA_like_lec_gl.
Pfam; PF00426; VP4; 1.
Coat protein; Glycoprotein.

CHAIN
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         OUTER CAPSID PROTEIN VP4.
OUTER CAPSID PROTEIN VP8 (POTENTIAL).
OUTER CAPSID PROTEIN VP5 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=93286580; PubMed=8389807;
Taniguchi K., Urasawa I., Urasawa S.;
Taniguchi K., Urasawa I., Urasawa S.;
"Independent regregation of the VP4 and the VP7 genes in bovine rotaviruses as confirmed by VP4 sequence analysis of G8 and G10
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OUTER CAPSID PROTEIN VP9.
OUTER CAPSID PROTEIN VP5.
N-LINKED (GLCNAC. . .) (PC
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                                                                                                                                              EA9B43CE96CC53CF CRC64;
                                             N-LINKED (GLCNAC. . . ) (
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Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=36440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC
                                                                                                                                                                                                                                                                                                                                    01-UUN-1994 (Rel. 29, Created)
01-UUN-1994 (Rel. 29, Last sequence update)
01-UUN-1993 (Rel. 42, Last annotation update)
01-ter capsid protein VP4 (Hemagglutinin) (Out
                                                                                                                                   N-LINKED (GLCNAC
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Pred. No.
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Pred. No. (
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                                                                                                                                                  86774 MW;
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                                                                                                                                                                        44.2%;
llarity 42.9%;
Conservative
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Coat protein; Glycoprotein. CHAIN 1 776
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776 AA;
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Best Local Similarity
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776 AA;
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P36305;
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 15:4361-4361(1987).

-- SUBCELLULAR LOCATION: Outer capeid.

-- PTM: VPB is one of two trypsin cleavage products of VP4; the other product is VP5.

-- SIMILARITY: Belongs to the rotaviruses VP4 protein family.
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                                                  01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-JAN-1988 (Rel. 42, Last amordation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=87231020; PubMed=3035492;
Potter A.A., Cox G., Parker M., Babiuk L.A.;
"The complete nucleotide sequence of bovine rotavirus C486 gene
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Pred. No. 69;
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776 AA
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InterPro; IPR000416; Cap VP4.
InterPro; IPR008985; ConA_like_lec_gl.
Pfam; PF00426; VP4; 1.
Coat protein; Glycoprotein.
CHAIN
PRT;
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                                                                                                                                                                                                                                                                             Bovine rotavirus (strain C486)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10931;
   VP4 ROTBC
P08713;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
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VP4_ROTSF
ID VP4_R
AC P1746
DT 01-AU
DT 10-OC
DE OUTER
DE CONTER
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STRAIN=9a5c;
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CARBOHYD
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OSTA XYLFA
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                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                            MEDILINE=89012172; PubMed=2845121;
Nishikawa K., Taniguchi K., Torres A., Hoshino Y., Green K.,
Kapikian A.Z., Chanock R.M., Gorziglia M.;
"Comparative analysis of the VP3 gene of divergent strains of the rotaviruses simian SA11 and bovine Nebraska calf diarrhea virus.";
J. Virol. 62:4022-4026(1988).
-!- SUBCELLUIAR LOCATION: Outer capsid.
-!- PTM: VP8 is one of two trypsin cleavage products of VP4; the other product is VP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
10-OCT-2003 (Rel. 142, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
[Contains: Outer capsid proteins VP5 and VP8].
                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEĞUENCE FROM N.A.
MEDLINE=89912172; PubMed=2845121;
Nishikawa K., Taniguchi K., Torres A., Hoshino Y., Green K.,
Kapikian A.Z., Chanock R.M., Gorziglia M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 1; Length 776;
Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86692 MW; 3F7DE298DB298FC7 CRC64;
                                                                                                                                                                                                                                                                                                                                   OUTER CAPSID PROTEIN VP4.
OUTER CAPSID PROTEIN VP9.
OUTER CAPSID PROTEIN VP5.
                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=10926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC
           Simian 11 rotavirus (strain SA11-FEM).
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     776 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                        InterPro; IPR000416; Cap VP4.
InterPro; IPR008985; ConA like_lec_gl.
Pfam; PF00426; VP4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                      EMBL; M23188; AAA47355.1; ALT_SEQ.
PIR; B31159; VPXRT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 QYTYTRDGEEVTAH 315
                                                                                                                                                                                                                                                                                                                             Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             з купутрраостван 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                    776 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                       SEQUENCE FROM N.A.
                                 NCBI_TaxID=10925;
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RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Ra Simpson A.J.G., Reinach F.C., Arruda P., Baia G.S., Baptista C.S., Rapson A.J.G., Ralves L.M.C., Arruda J.E., Baia G.S., Baptista C.S., Rayarenga R., Alves L.M.C., Arruda J.E., Baia G.S., Baptista C.S., Rabeno M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Earlones M.R.S., Rabeno M.H., Colmboc C., Costa R.F., Costa M.C.R., Costa-Neto C.M., Racincani A.D., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Raga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Raga J.S., Franca S.C., Franco M.C., Frohme M. Fraga J.S., Franca S.C., Franco M.C., Frohme M. F., Gomes E.L., Kitajima J.P., R. Forieger J.E., Kuramae E.E., Landster E.L., Kitajima J.P., R. Freeger J.E., Kuramae E.E., Landster E.L., Martino C.L., R. Machado J.A., Marches M.V., Martins E.B., L., Martins E.M.F., Martins E.M.F., Martins E.M.F., Marcher M.Y., Martins E.A.L., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.F., Martins E.M.
"Comparative analysis of the VP3 gene of divergent strains of the rotaviruses similar SA11 and bovine Nebraska calf diarrhea virus.";
J. Virol. 62:4022-4026(1988).
-!- SUBCELLUIAR LOCATION: Outer capsid.
-!- PIM: VP8 is one of two trypsin cleavage products of VP4; the other product is VP5.
-!- SIMILARITY: Belongs to the rotaviruses VP4 protein family.
| InterPro; IPR000416; Cap VP4.
| InterPro; IPR008985; Conalike_lec_gl.
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(POTENTIAL).
(POTENTIAL).
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Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 1; Length 776; Pred. No. 69; 5; Indels 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    OUTER CAPSID PROTEIN VP4.
OUTER CAPSID PROTEIN VP5.
N-LINKED (GLCNAC. . ) (POTI
N-LINKED (GLCNAC. . ) (POTI
N-LINKED (GLCNAC. . ) (POTI
N-LINKED (GLCNAC. . ) (POTI
N-LINKED (GLCNAC. . ) (POTI
N-LINKED (GLCNAC. . ) (POTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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28-FFB-2003 (Rel. 41, Created)
28-FFB-2003 (Rel. 41, Last sequence update)
28-FFB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Organic solvent tolerance protein precursor
IMP OR OSTA OR XF0837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20365717; PubMed=10910347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 OYTYTRDGEEVTAH 315
                                                                                                                                                                                                                                                                                                                                                                                                                  Coat protein; Glycoprotein.
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Best Local Similarity 42...
Best Local Similarity
Gonservative
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56
116
1132
1149
1188
386
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                            part of a targeting/usher system for outer membrane components (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., vallada H., van Sluys M.A., Verjovski-Almeida S., Vettore A.L., zago M.A., Zatz M., Meidanis J., Setubal J.C., "The genome sequence of the plant pathogen Xylella fastidiosa."; Nature 406.151-159(2000).

-: FUNCTION: Determines N-hexane tolerance. Involved in outer membrane permeability. Essential for envelope biogenesis. Could B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 792 ORGANIC SOLVENT TOLERANCE PROTEIN.
792 AA: 91001 MW; EB97FP8CFD35A422 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 1; Length 792;
Pred. No. 70;
0; Mismatches 5; Indels
                                                                                                                                                                                                         SUBCELLULAR LOCATION: Outer membrane (By similarity). SIMILARITY: Belongs to the imp/ostA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kylella fastidiosa (strain Temeculal / ATCC 700964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last Bequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Organic solvent tolerance protein precursor.
IMP OR OSTA OR PD1836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               792 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMÁP; MF_01411; -; 1.
InterPro; TPR007533; OstA_C.
POTENT PRO453; OSTA_C; 1.
Outer membrane; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 185:1018-1026(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE003923; AAF83647.1; -. PIR; B82756; B82756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 RYLYDDGKWQTRA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 RYLYTDDAQQTEA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=183190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kitajima J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fastidiosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OSTA XYLFT
Q87AI9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSTA XYLFT
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                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
FUNCTION: Determines N-hexane tolerance. Involved in outer membrane permeability. Essential for envelope biogenesis. Could be part of a targeting/usher system for outer membrane components (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garrett J.B., Knutzon D.S., Carroll D., "Composite transposable elements in the Xenopus laevis genome."; Mol. Cell. Biol. 9:3018-3027(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.2%; Score 38; DB 1; Length 792; 61.5%; Pred. No. 70; cive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.2%; Score 38; DB 1; Length 130
63.6%; Pred. No. 1.2e+02;
ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein, Transposable element.
SECHTENCE 1308 AA: 149577 MW; C9A9C98CDC169C19 CRC64;
                                                                                                                    -!- SUBCELLULÂR LOCATION: Outer membrane (By similarity) -:- SIMILARITY: Belongs to the imp/ostA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
Transposon TX1 hypothetical 149 kDa protein (ORF 2).
Transposon TX1 hypothetical 149 kDa protein (ORF 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1308 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAWAP; MF 01411; -; 1.

Interbro; IRR00743; OstA_C.

Pfam; PF04453; OstA_C; 1.

Outer membrane; Signal; Complete proteome.

22
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InterPro; IPR000477; RVTSe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=89384562; PubMed=2550791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF03372; Exo_endo_phos; 1.
Pfam; PF00078; rvt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE012560; AA029668.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 792 O
792 AA; 90768 MW;
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PIR; B32494; B32494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 RYLYDDGKWOTRA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 RYLYTDDAQQTEA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1308 AA;
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Best Local Similarity
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P14381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - i - SIMILARITY: WITH THE POLYMERASE PROTEIN OF OTHER CORONAVIRUSES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=39297139; PubMed=8517032; MEDLINE=39297139; PubMed=8517032; Meulenberg J.J.M., Hulst M.M., de Meijer E.J., Moonen P.L.J.M., den Besten A., de Kluyver E.P., Wensvoort G., Moormann R.J.M.; Lelystad virus, the causative agent of pordine epidemic abortion and respiratory syndrome (PEARS), is related to LDV and EAV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         suggested. Also contains a protease domain.
CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
                                                                                                                                                                                                                                                                                                                                                                                                                            Lelystad virus (LV) (Porcine reproductive and respiratory syndrome
                                                                                                                                                                                                                                                    01-0CT-1993 (Rel. 27, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2004 (Rel. 43, Last annotation update)
POL polyprotein (ORFLA) [Contains: RNA-directed RNA polymerase (EC 2.7.7.48); Helicase; Protease (EC 3.4.21.-)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF TOROVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kroese M.V., Moormann R.J.M.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                             PRT; 3859 AA.
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Peptidase_C31.
Peptidase_C32.
Peptidase_C33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arteriviridae, Arterivirus.
                                                                                                                                                                                                STANDARD;
                                                ORYLYADPSPQ 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virology 192:62-72(1993)
QRYLYTDDAQQ 12
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InterPro; IPR008743;
InterPro; IPR008760;
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MEROPS; C32.001; -.
MEROPS; C33.001; -.
MEROPS; S32.UPW; -.
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PIR; A45392; A45392.
PIR; B36861; B36861.
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                                                                                                                                                                                                      RPOA LELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       virus)
                                                                                                                                                                        RPOA_LELV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G. Bacteriol. 176:7601-7613(1994).

-i. FUNCTION: REGULATES THE TRANSCRIPTION OF GENES INVOLVED IN THE BIOSYNTHERSIS OF PATHERIAL ADHESIN-III.

-i. SIMILARITY: HIGH TO E.COLLI DARA, SOME, TO E.COLI PAPB.

-i. CAUTION: It is uncertain whether Met-1 or Met-17 is the initiator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Garcia M.-I., Labigne A., le Bouguenec C.L.; "Nucleotide sequence of the afimbrial-adhesin-encoding afa-3 gene cluster and its translocation via flanking IS1 insertion sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
InterPro; IPR007095; RNA_pol_DS_PS.

R InterPro; IPR007094; RNA_pol_PSvir.

R InterPro; IPR007056; Viral_helicasel.

R Efan; PR05410; Peptidase_C31; 1.

R Fan; PR05411; Peptidase_C32; 1.

R Fan; PR05579; Peptidase_C33; 1.

R Fan; PF05579; Peptidase_C32; 1.

R Fan; PF0579; Peptidase_C32; 1.

R Fan; PF0579; Peptidase_C32; 1.

R Fan; PF0579; Peptidase_C32; 1.

R Fan; PF05776; WCCH; 1.

R MA-directed RNA polymerase; Transferase; Helicase; ATP-binding; M Hydrolase; Serine protease; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                     SIMILARITY).
SIMILARITY).
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 1; Length 3859;
                                                                                                                                                                                                                                                   CYS-RICH.
TRYPSIN-LIKE SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
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T -> V (IN REF. 3).

V -> I (IN REF. 3).
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                     HELICASE
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MEDLINE=95095929; PubMed=8002584;
                                                                                                                                                                                                                                                                                                                                                                                                                                  44.2%;
54.5%;
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Best Local Similarity
6; Conserve
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ID AFAA ECOLI
AC P53515;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                   Vaccinia virus (strain WR).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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STRUMLN=India-1967 / Isolate Ind3;
MEDLINE=94152154; PubMed=8109158;
Shchelkunov S.N., Blinov V.M., Resenchuk S.M., Totmenin A.V.,
Sandakkhiev L.S.;
"Analysis of the nucleotide sequence of a 43 kbp segment of the
genome of variola virus India-1967 strain.";
Virus Res. 30:239-258(1993).
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MEDLINE-94088747; PubMed-8264798;
Massung R.F., Esposito J.J., Liu L., Qi J., Utterback T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 273;
                                                                                                                                                                                                                                                                                          Gershon P.D., Jones E.V., Moss B., Ahn B.-Y.; submitted (JUL-1990) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR005057; Pox_E8.
Pfam; PF03394; Pox E8; 1.
PIRSP; PIRSP015690; VAC_E8R; 1.
SEQUENCE 273 AA; 31888 MW; 6C274DCEE6353629 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.0%; Score 37; DB 1;
66.7%; Pred. No. 32;
tive 3; Mismatches
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
             (Rel. 20, Created)
(Rel. 20, Last sequence update)
(Rel. 20, Last annotation update)
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MEDLINE=93202281; PubMed=8384129;
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157 RYVYTDNAK 165
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Best Local Similarity
Matches 6; Conserv
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NCBI_TaxID=10255;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                  Orthopoxvirus.
NCBI_TaxID=10254;
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                01-NOV-1991
01-NOV-1991
01-NOV-1991
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ID VE08_VARV
                                                                                                Protein E8.
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P., Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.;
                                                                                                                                                                                     Transcription regulation, Activator, Trans-acting factor, Plasmid.
SEQUENCE 101 AA; 11743 MW; F55914BC263BDD6B CRC64;
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Pfam; PP03394; Pox_B8; 1.
PIRSF; PIRSF015690; VAC_E8R; 1.
SEQUENCE 273 AA; 31935 MW; 648DEADFF23EC9DD CRC64;
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(Rel. 17, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                58.3%; Pred. No. 10;
ive 1; Mismatches
                                                                                                                                                                                                                                                                            Score 37;
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                                         EMBL; X76688; CAAS4113.1; -.
EMBL; X76688; CAAS4114.1; ALT_INIT.
PIR; D55545; D55545.
InterPro; IFR004356; Fim_regulat.
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PRINTS; PR01554; FIMREGULATRY.
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Matches 6; Conservative
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Best Local Similarity 58.3.
The Conservative
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01-FEB-1991
16-OCT-2001
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VE08 VACCV
ID VE08 VACCV
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RESULT 29 VE08 VACCC

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MAYER V. Collumbia;

MAYER V. Collumbia;

MAYER V. Collumbia;

MAYER V. Schueller C., Wambut R., Murphy G., Volckaert G.,

MAYER K.F.X., Schueller C., Wambut R., Entian K.-D., Terryn N.,

A Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,

Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Melchselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,

A Weichselgartner M., Puigdomenech P., Watson M., Schmidtheini T.,

A Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,

A Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,

Langham S.-A., McCullagh B., Bilham L., Robben J.,

Van der Schueren J., Grymonprez B., Chuang Y.-O., Vandenbussche F.,

A Bracken M., Weltjens I., Vor M., Bastiaens I., Aert R., Defcor E.,

A Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thallana (Mouse-ear cress).

Bukaryota, Viridiplantae, Etreptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicocyledons; core eudicots; rosids;

eurosids II, Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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28-FEB-2003 (Rel. 41, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
Gamma-soluble NSF attachment protein (Gamma-SNAP) (N-ethylmaleimide-genstive factor attachment protein, gamma).
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"Functional and molecular identification of novel members of the ubiquitous membrane fusion proteins alpha- and gamma-SNAP (soluble N-ethylmaleimide-sensitive factor-attachment proteins) families in Dictyostelium discoideum.";
Eur. J. Biochem. 267:2062-2070(2000).
                                                                                                                 "Potential virulence determinants in terminal regions of variola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٠;
Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
Venter C.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.0%; Score 37; DB 1; Length 273; 66.7%; Pred. No. 32; cive 3; Mismatches 0; Indels
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EMBL; L22579; AAA60797.1; -.
PIR; B36842; B36842.
PIR; B36842; T28487.
InterPro; IPR005057; Pox_E8.
Pffam; PF03394; Pox_E8; 1.
PRSF; PRSF015690; VAC_E8R; 1.
SEQUENCE 273 AA, 31896 MW; 02859D3F756A53AE CRC64;
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MEDLINE=20193631; PubMed=10727946;
                                                                                                                                                          smallpox virus genome.";
Nature 366:748-751(1993).
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Best Local Similarity
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RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Benediser S., Hampel S., Feldpauser M., Lamberth S., Van den Daele H.,
Be Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Clark L., Doggett J., Hall S., Kay W., Lennard N., McLay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Pettett A., Rajandream M.A., Scharfe M., Grimm M., Lochnert T. H.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Lochnert T. H.,
RA Gabel C., Fuchs M., Farrmann B., Granderath K., Dauner D., Herzl A.,
RA Gabel C., Fuchs M., Yicale D., Ligoria R., Pitzavandi E.,
RA Schnabl S., Hiller R., Schmidt W., Lecharry A., Aubourg S.,
Achabl S., Hiller R., Schmidt W., Lecharry A., Aubourg S.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Cascuber E.,
RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
Raccaria P., Bevan M., Wilson R., Schotz S., Francs P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
Raccaria P., Bevan M., Wilson R., Abbott S., Stocker S.,
Raccaria P., Bevan M., Wilson R., Abbott A., Scott K., Johnson D.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker K., Johnson D.,
RA Schoelle P., Courney D., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
Ramerille P., Courney D., Cloud J., Abbott A., Scott K., Johnson D.,
RA Atchool B., Zidanic M., Styne G., Sun H., Lanar B., Yordan C.,
RA Atchool B., Zidanic M., Styne S., Shekker M., Matero A., Shah R.,
RA Bentley D., Fulton B., Miller M., Debnis D., Allonson A.,
RA Bentley D., Reston R., Vull D., Shekker M., Matero A., Shah R.,
RA Bentley D., Reston R., Vull D., Shekker M., Matero A., Shah R.,
RA Bentley D., Raseston R., Vull D., Shekker M., Matero A., Shah R.,
Radenat S., Shohdy N., Hasesgawa A., Hameed A., Lodhi M., Johnson A.,
RH Hainn H., Main M., Radis B., Dokok 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K.A.;
Feldmann K.A.;
Feldmann K.A.;
Feldmann K.A.;
Feldmann K.A.;
Formath CDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Required for vesicular transport between the endoplasmic reticulum and the Golgi appearatus. Binds to SNARE complex and then recruits NSF to disassemble it (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic peripheral membrane protein (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
-!- SIMILARITY: Belongs to the SNAP family.
-!- CAUTION: Ref.2 sequences differ from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transport; Protein transport; Endoplasmic reticulum; Golgi stack; Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A -> S (IN REF. 3).
3EECE3B64D038BAD CRC64;
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EMBL; AL080253; CAB45807.1; ALT_SEQ.
EMBL; AL161553; CAB79041.1; ALT_SEQ.
EMBL; AV086673; AAM65730.1; -.
InterPro; IPR000744; NSF attach.
InterPro; IPR008941; TPR-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 402:769-777(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46
129
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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SIP2 YEAST
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InterPro; IPR002305; tRNA-synt_lb.
InterPro; IPR002305; tRNA-synt_lb.
InterPro; IPR002306; Trp_tRNA-synt_l.
InterPro; IPR002306; Trp_tRNA-synt_lb.
Pflun's; PR01039; TRNA-synt_lb; 1.
PRINTS; PR01039; TRNA-SYNTHTRP.
PROSITE; PS00178; AA TRNA LIGASE 1; 1.
PROSITE; PS00178; AA TRNA LIGASE 1; 1.
Aminoacyl-tRNA synthétase; Protein biosynthesis; Ligase; AIP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diphosphate + L-tryptophanyl-tRNA(Trp).
-!-SUBUNIT: Homodimer (By similarity).
-!-SUBCELLUTAR LOCATION: Cytoplasmic.
-!-SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=970661201; PubMed=8905231; Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Mayajima N., Hirosawa M., Suquira M., Satamoto S., Kimura T., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Tabata S.; Yamada M., Tabata S.; Shimpo S., Ethe genome of the genome of the genome of the genome of the sential procedure analysis of the genome of the sential procedure determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
3-PARX-2000 (Rel. 39, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res. 3:109-136(1996).
-!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 337;
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 Indels
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202 202 ATP (BY SIMILARITY).
337 AA; 37763 MW; A7808E60A78D312D CRC64;
                                                                                                                                                                                                                                                                                                 Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
 4 ;
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 0; Mismatches
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                                                                                                                                                              PRT;
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HSSP; P00953; 1D2R.
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   7; Conservative
                                                                     200 YLYAHDLÖQAE 210
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203
202
                                     4 YLYTDDAQOTE 14
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es 7; Conserv
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RESULT 34

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                                                                                                                                                                                                                                                                                                                                                                                                                               NEGUENCE FROM N.A.
MEDLINE=97298309; PubMed=9153757;
Feuermann M., Simeonava L., Souciet J.-L., Potier S.;
"Analysis of 11.7 kb DNA sequence from the left arm of chromosome VII
reveals 11 open reading frames: two correspond to new genes.";
Yeast 13:475-477(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kail M., Juettner E., Vaux D.;
"Landa clone B22 contains a 7676 bp genomic fragment of
Saccharomyces cerevisiae chromosome VII spanning the VAM7-SPM2
intergenic region and containing three novel transcribed open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specific targets.
-!- PIM: Phosphorylated by SNF1 in vitro.
-!- SIMILARITY: Belongs to the 5'-AMP-activated protein kinase beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005886; C:plasma membrane; IDA.
GO; GO:0005886; C:plasma membrane; IDA.
GO; GO:000579; F:SNFIA/AMP-activated protein kinase activity; IMP.
GO; GO:0007574; P:cell aging (sensu Saccharomyces); IMP.
GO; GO:0007467; P:filamentous growth; IMP.
GO; GO:0006468; P:protein amino acid phosphorylation; IMP.
GO; GO:0007165; P:signal transduction; IMP.
PF04739; AMPKBI; 1.
                                                                                                                                                                                                                                                                                                                                     Yang X., Jiang R., Carlson M.;
"A family of proteins containing a conserved domain that mediates interaction with the yeast SNF1 protein kinase complex.";
EMBO J. 13:5878-5886(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Could be an adaptor that promote the activity of SNF1 towards
                                                                                                               Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast 12:799-807(1996).
                                                                                                                                                                                                                               Drebot M.A., Jansma D., Himmelfarb H.J., Friesen J.D.; submitted (JUL-1992) to the EMBL/GenBank/DDBJ databases.
                                                 01-FEB-1994 (Rel. 28, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
SIP2 protein (SPM2 protein).
SIP2 OR SPM2 OR YGL208W.
                                                                                                                                                                                                                                                                                                                        MEDLINE=95112798; PubMed=7813428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96408772; PubMed=8813766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L31592; AAC37420.1; ...
EMBL; Z72730; CAA96922.1; ...
EMBL; U33774; AAC49497.1; ...
PIR; S51792; S51792.
GermOnline; 141256; ...
SGD; S0003176; SIP2.
                                (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z14128; CAA78503.1; -.
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STANDARD;
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                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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             P34164;
01-FEB-1994
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SEQUENCE

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RESULT 35

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                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=86149315; PubMed=3006051;
Hagen D.C., McCaffrey G., Sprague G.F. Jr.;
"Evidence the yeast STE3 gene encodes a receptor for the peptide pheromone a factor: gene sequence and implications for the structure of the presumed receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakayama N., Miyajima A., Arai K.;
"Nucleotide sequences of STE2 and STE3, cell type-specific sterile
genes from Saccharomyces cerevisiae.";
EMBO J. 4:2643-2648(1985).
                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIRS, B24670; B24670.

Germonline; 139933; -

Germonline; 139933; -

GGD; 80001661; STE3.

GO; GO:0006893; F:mating-type a-factor pheromone receptor act.

GO; GO:0007693; F:mating-type a-factor pheromone receptor act.

GO; GO:000760; F:signal transduction during conjugation with.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coupled receptor; Pheromone response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5DBF611076B8CA91 CRC64;
                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 83:1418-1422(1986)
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Pred. No. 59;
                                                                    (Rel. 42, Last annotation update)
470 AA.
                                                    Last sequence update)
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                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M12239; AAA35113.1; --
EMBL; X03011; CAA5795.1; --
EMBL; X74151; CAA52261.1; --
EMBL; Z28177; CAA82019.1; --
                                                                                       factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00899; GPCRSTE3
Transmembrane; G-protein
 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
53
98
134
228
285
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206
267
300
470 AA;
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Best Local Similarity
             P06783;
01-JAN-1988 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                                      STE3 OR YKL178C.
                                                                    10-OCT-2003
                                                                                       Pheromone A
   STE3 YEAST
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MEDLINE=96189014; PubMed=8736346;

MEDLINE=96389014; PubMed=8736346;

MEDLINE=96389014; PubMed=8736346;

MEDLINE=96389014; PubMed=8736346;

Sequencing C., Perret X., Broughton W.J., Rosenthal A.;

Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.

NGR234 using dye terminators and a thermostable 'sequenase': a beginning.";

-!- FUNCTION: COULD BE REQUIRED FOR THE FORMATION OF A FUNCTIONAL NITROGENASE FE PROTEIN. PROBABLY ACCEPTS ELECTRONS FROM FIXA/FIXB AND REDUCES A QUINONE.

-!- COPACTOR: FAD (Potential).

-!- SIMILARITY: Belongs to the ETF-QO / fixC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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"Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:334-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nitrogen fixation; Oxidoreductase; FAD; Flavoprotein; Plasmid
                                                                                                                                                                                                                                                                                                                                                                               Plasmid sym pNGR234a.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.0%; Score 37; DB 1; Length 435; 46.7%; Pred. No. 54;
                                   Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium
   46404 MW; CBB4FCE0070A563F CRC64;
                                   Score 37; DB 1;
Pred. No. 51;
                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                    435 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000100; AAB91888'1;
InterPro; IPR001327; FAD_pyr_redox.
PRINTS; PR00368; FADPNR.
                                                                      7
                                                                                                                                                                                                                                                                                                                                                               (strain NGR234).
                                     43.0%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORYLYTDDAQQTEAH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORFWVIDDISHIGMH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                               320 ERYYYTLDROOS 331
                                                                        Conservative
                                                                                                           2 QRYLYTDDAQQT 13
                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z68203; CAA92415.
                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
   415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                            FIXC OR Y4UP.
                                                                                                                                                                                                                                                                                                                                                               Rhizobium sp.
                                                                                                                                                                                                                                                                                                                         protein.
                                                                                                                                                                                                                                    FIXC RHISN
Q53208;
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Perret

Length 470;

Query Match

Matches

STE3_YEAST

RESULT 36

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Matches

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                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF03485; N-Arg; 1.
Pfam; PF03485; N-Arg; 1.
Pfam; PF0750; tRNA-synt 1d; 1.
Pfam; PF0756; tRNA-synt 1d; 1.
TIGRPAM; TIGR00456; args; 1.
PROSITE; PF00178; AA TRNA TRNA 1.0.
PROSITE; PF00178; AA TRNA TRNA 1.0.
PROSITE; PF00178; AS TRNA PROTEIN biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=21311952; PubMed=11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,

Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,

Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,

Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,

Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,

Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA (Arg) = AMP diphosphate + L-arginyl-tRNA (Arg).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               553 AA; 62365 MW; 84F0AAAA2212E30C CRC64;
                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PERSONAL ASSESSION SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SENSONAL SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aureus.";
Lancet 357:1225-1240(2001).
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                                   STANDARD;
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DT 28-FE

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                                   SOLUTION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEINTS; PRO1038; TRNASNTHARG.
TIGREAMS; TIGRO0456; args; 1.
PROSITE; PS00178; AA TRNA LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Arginyl--ENA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS)
ARGS OR SAVO607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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-!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +
diphosphate + L-arginyl-tRNA(Arg).
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Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus (strain Mu50 / ATCC 700699).
Bacteria, Firmicutes; Bacillales; Staphylococcus.
9
                                                                                                                                                                                                                                                                                                                                                                                     553 AA.
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1; Mismatches
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HAMAP; MF_00123; '-; 1.
InterPro; IPR001278; Arg_tRNA-synt_lc.
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InterPro; IPR008909; tRNA-synt ld_C.
InterPro; IPR001412; tRNA-synt_I.
                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Pfam; PF00750; tRNA-synt ld; 1.
Pfam; PF05746; tRNA-synt ld C; 1.
                                                                                                                                                                        226 YTFVQDLÓÓVEGH 238
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Best Local Similarity 60...
6; Conservative
                                                                                    4 YLYTDDAQQTEAH 16
        6; Conservative
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518 TDDIEKTKAH 527
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Q932F6;
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Gaps
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43.0%; Score 37; DB 1; Length 553; 60.0%; Pred. No. 71; 1; Indels tive 3; Mismatches 1; Indels
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
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O8NXT8;
28-FEB-2003
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Search completed: March
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00750; KRNA-synt 1d; 1.
Pfam; PF05746; KRNA-synt 1d; 1.
PRIAM: PRO1038; TRNASYNTHARG.
TIGRRAMS; TIGRO0456; args; 1.
PROSTIE; PS00178; AA TRNA LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; AIP-binding;
Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS) ARGS OR MW0571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                Lancet 359:1819-1827(2002).
-!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +
diphosphate + L-arginyl-tRNA(Arg).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                      SEQUENCE FROM N.A.
MEDIJNE=22040717; PubMed=12044378;
MEDIJNE=22040717; PubMed=12044378;
MEDIJNE=22040717; PubMed=12044378;
MAGDI T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EC 1.8.1.8)
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Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.0%; Score 37; DB 1; Length 553; 60.0%; Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    553 AA; 62381 MW; 9B10AAB5C212E30C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Thiol:disulfide interchange protein dsbD precursor Priolindisulfide reductase)
DSBD OR VV11247.
                                                              Dacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          593 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF_00123; -; 1.
InterPro; IPR001278; Arg_tRNA-synt_lc.
InterPro; IPR0018148; N.
InterPro; IPR008909; tRNA-synt_ld_C.
InterPro; IPR001412; tRNA-synt_l.
Pf048; PF03485; N-Arg; 1.
                                                       Staphylococcus aureus (strain MW2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP004824; BAB94436.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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518 TDDIEKTKAH 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vibrio vulnificus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                      NCBI_TaxID=196620;
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                                                                                                                                                                                                                                                                                    acquired MRSA."
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Q8DCZ0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
"Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Required to facilitate the formation of correct disulfide bonds in some periplasmic proteins and for the assembly of the periplasmic c-type cytochromes. Acts by transferring electrons from cytoplasmic thioredoxin to the periplasm. This transfer involves a cascade of disulfide bond formation and reduction steps (By similarity).
-!- CATALATIC ACTIVITY: Protein dithiol + NAD(P) + = protein disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THIOL: DISULFIDE INTERCHANGE PROTEIN DSBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase, Redox-active center; Electron transport; NAD;
Transmembrane; Inner membrane; Cytochrome c-type biogenesis; Signal;
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                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                   (By similarity).
-!- SIMILARITY: Belongs to the thioredoxin family. DsbD subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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Pred. No. 76;
3; Mismatches
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Potential
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InterPro; IPR003834; Ctytoch TM.
InterPro; IPR003864; Thiored.
InterPro; IPR006663; Thioredox_dom2.
Pfam; PP020813; DSDD, 1.
Pfam; PP00085; thiored; 1.
PROSITE; PS00194; THIOREDOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2, 2004, 16:05:26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE016801; AA009703.1; -.
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54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome
SIGNAL 1
                                                                                                                                                                                                                                    + NAD (P) H
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March 2, 2004, 16:00:38; Search time 2.2667 Seconds
(without alignments)
678.999 Million cell updates/sec Run on:

US-10-060-765-7 86 1 RQRYLYTDDAQQTEAH 16 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMAKLES	Description	I-1	hypothetical prote	hypothetical prote	н	cal	hypothetical prote		zinc finger protei		Q.		-	1	hypothetical prote		probable sugar upt	probable phosphopr	beta-glucosidase (probable membrane	probable GDSL-m	yclB prot	probable			probable per	outer layer		
200	ΩI	T00526	T26063	S28726	T00525	T25023	C70385	JE0181	B34612	\$59382	VPXRYM	T21986	T21993	C36819	G90294	T18857	B95927	T11663	JC5869	T33962	AI0633	T01629	B64790	B90705	E85555	F81042	A81989	VPXR4S	. JQ1638	
	DB	. 2	N	7	~1	7	N	~	N	7	Н	7	7							~				~						
	Length	349	2225	93	349	332	403	529	543	995	776	1661	1663	259	263			627	735	235	285	344	457	460	460	580	580	747	775	
•	Query Match	53.5	0	47.7	47.7	46.5		46.5	46.5	46.5	46.5	46.5	46.5	45.3	45.3	45.3	45.3	45.3	45.3	44.2	44.2	44.2	44.2	44.2	44.2		44.2	44.2	44.2	
	Score	46	43	41	41	40	40	40	40	40	40	40		39	39			39	39	38	38	38	38	38	38	38	38	38	38	
	Result No.	 r-1	8	٣	41	2	9	7	80	60	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	

RESULT 2
T26063
T26063
Hypothetical protein W01F3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26063
R;Cummings, P.
R;Cummings, P.
R;Cummings, P.
R;Reference to the EMBL Data Library, March 1997

layer]	layer	outer layer protei	layer	outer layer protei	outer layer protei	hypothetical outer	organic solvent to	WD repeat domain p	transposable eleme	hypothetical prote	hypothetical prote	two-component hybr	orf la protein - L	afaA protein - Esc	hypothetical prote
VPXRT2	VPXRT1	VPXRB3	JQ2022	VPXRS1	S03611	S24410	B82756	T48933	B32494	A99580	T18499	AG1897	B36861	D55545	AE3288
1	Н	н	Н	+	7	7	~	~	7	7	7	N	~1	N	7
775	176	176	176	776	176	776	792	1051	1308	1426	1619	1645	2396	101	145
44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	43.0	43.0
38	38	38	38	38	38	38	38	38	38	38	38	38	38	37	37
30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: C70385
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: ĞB;AE000717; NID;g2983492; PIDN;AAC07076.1; PID;g2983498; GB:AE0006
A,Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 392, 353-358, 1998
A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A,Reference number: A70300; MUID:9819666; PMID:9537320
A,Accession: C70385
A,Status: preliminary; nucleic acid sequence not shown; translation not shown A,Molecule type: DNA
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <STO>
A;Crose.references: GB:AE002093; NID:g3176707; PIDN:AAD12023.1; GSPDB:GN00139
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z81593; PIDN:CAB04743.1; GSPDB:GN00023; CESP:T20B3.5
A;Experimental source: clone T20B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
Cispecession: T25023
R;Mortimore, B.
B;Mortimore, B.
B;Mortimore, B.
B;Mortimore and B.
B;Mortimore and B.
B;Reference number: Z19970
A;Reference number: Z19970
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-332 <WIL>
A;Residues: 1-332 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.5%; Score 40; DB 2; Length 403; 37.5%; Pred. No. 30; tive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
46.5%; Score 40; DB 2; Length 332;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 8; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                               Length 349;
                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Map position: 5
A,Introns: 110/1, 246/3
C,Superfamily: Caenorhabditis hypothetical protein C49G7.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein T20B3.5 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                            Query Match 47.7%; Score 41; DB 2; Best Local Similarity 46.7%; Pred. No. 17; Matches 7; Conservative 4; Mismatches
                                                                                                                                                                          A,Gene: T20K24.6; At2g19050
A,Map position: 2
A,Introns: 82/1; 123/3; 198/3; 291/1
C,Superfamily: myrosinase-associated protein MyAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein aq 985 - Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RORYLYTDDAQQTEAH 16
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8 RIDYIHTADFQQTVLH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 ORRYVYWDNVHSTEA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RORYLYTDDAQOTEA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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Matches 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C, Genetics:
A, Gene: CESP: T20B3.5
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T25023
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A, Residues: 1-349 < ROUD
A, Residues: 1-349 < ROUD
A, Cross-references: EMBL: AC002392; NID: 93176701; PID: 93176707
A, Experimental source: cultivar Columbia
R, Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Blsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
                                                                                                                                                                             A.Experimental source: clone WOIF3
Genetics
A.Gene: CESP:WOIF3.3
A.Map position: 5
A.Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable GDSL-motif lipase/hydrolase [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T20K24.6
S;Species: Arabidopsis thaliana (mouse-ear cress)
C;Dete: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001
C;Accession: T00525; H84571
S;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, Bubmitted to the EMBL Data Library, July 1997
A;Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.
A;Reference number: Z14167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-i-225.4WIL>
A;Cross-references: EMBL:Z92815; PIDN:CAB07294.1; GSPDB:GN00023; CESP:W01F3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein 1 (insertion sequence ISL1) - Lactobacillus casei
C;Species: Lactobacillus casei
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X02734; NID:g1279518; PIDN:CAA26516.1; PID:g43974
A;Experimental source: insertion sequence ISL1; strain C239
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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R;Shimizu-Kadota, M.; Kiwaki, M.; Hirokawa, H.; Tsuchida, N.
Mol. Gen. Genet. 200, 193-198, 1985
A;Title: ISLI: a new transposable element in Lactobacillus casei.
A;Reference number: S28726; MUID:85295506; PMID:2993817
A;Accession: S28726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Mobile element: insertion sequence ISL1
C;Superfamily: Shigella flexneri conserved hypothetical protein 1
                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 2; Length 2225;
Pred, No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 2; Length 93;
Pred. No. 3.7;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  50.0%;
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477 QRYFYNEDSQKCE 489
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.0.
The Conservative
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Best Local Similarity 61...
8; Conservative
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A; Residues: 1-93 <SHI>
                                  A; Accession: T26063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: T00525
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Cjaccession: A40342
R;Lopez, S.; Lopez, I.; Romero, P.; Mendez, E.; Soberon, X.; Arias, C.F.
Virol. 65, 3738-3745, 1991
A;Title: Rotavirus YM gene 4: analysis of its deduced amino acid sequence and prediction A;Reference number: A40342; MUID:91251227; PMID:1645789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Molecule type: genomic RNA
A, Residues: 1-776 < LOP-
A, Residues: 1-776 < LOP-
A, Cross-references: GB:M61231; NID:g33323; PIDN:AAA47100.1; PID:g33324
C, Superfamily: rotavirus outer layer protein VP3
C, Superfamily: rotavirus outer layer protein; glycoprotein; hemagglutinin
F;1-241/Product: outer layer protein VP8 #status predicted < VP8-
F;242-247/Region: cleavage processing #status predicted
F;248-776/Reduct: outer layer protein VP5 #status predicted < VP5-
F;17,32,56,97,116,132,151,178,183,198,325,670/Binding site: carbohydrate (Asn) (covalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 37/3; 102/2; 229/3; 317/3; 375/2; 505/3; 546/1; 668/3; 833/1; 904/2; 941/3; 9
A;Accession: S59382
A;Molecule type: DNA
A;Residues: 1-566 <FAV>
A;Cross-references: EMBL:U20162; NID:g632669; PIDN:AAB67493.1; PID:g632672; MIPS:YLR417w
A;Experimental source: strain S288C (AB972)
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                outer layer protein VP3 - porcine rotavirus C (strain YM)
NiAlternate names: hemagdlutinin; VP4 protein
NiContains: outer layer protein VP5; outer layer protein VP8
C;Species: porcine rotavirus C
C;Species: 30-Jun.1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 776;
                                                                                                                                                                                                                                                                                         Length 566;
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                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F39B2.4a - Caenorhabditis elegans
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A;Molecule type: DNA
A;Residues: 1-1661 <WIL>
                                                                                                                                                                                                                                                                                            7,
                                                                                                                                                                                                                                                                                            DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
                                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R.Dobson, R. submitted to the EMBL Data Library, March 1997 Streference number: Z19498 A;Accession: T21986
                                                                                                                                                                                                           SGD:S0004409; MIPS:YLR417w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                            Score 40;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.5%;
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52 QRIIYIDDAKPTQ 64
                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
7; Conserve
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A40342
                                                                                                                                                                                                              A; Cross-references: A; Map position: 12R
                                                                                                                                                                                  A; Gene: SGD: VPS36
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                                                                                                                                                                                                   Oligo-1, 6-glucosidase (EC 3.2.1.10) - Bacillus flavocaldarius KP1228
C;Species: Bacillus flavocaldarius KP128
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 20-Sep-1999
C;Accession: JEO18
Biosci. Biotechnol. Biochem. 62, 1093-1102, 1998
A;Rtashiwabara, S.; Matsuki, Y.; Kishimoto, T.; Suzuki, Y.
Biosci. Biotechnol. Biochem. 62, 1093-1102, 1998
A;Rtle: Clustered proline residues around the active-site cleft in thermostable oligo-1
A;Reference number: JEO181; MUID:98357218; PMID:9692189
A;Reference number: JEO181
A;Molecule type: DNA
A;Residues: J-529 *KAS>
A;Cross-references: DBBJ:AB003697
C;Superfamily: alpha-glucosidase; alpha-amylase core homology
C;Reywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              zinc finger protein ZNFB - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Jun-1990 #sequence_revision 09-Oct-1992 #text_change 01-Dec-2000
C;Accession: B34612
R;Lania, L.; Donti, E.; Pannuti, A.; Pascucci, A.; Pengue, G.; Feliciello, I.; La Mantia A;Itie: CDNA isolation, expression analysis, and chromosomal localization of two human A;Reference number: A34612; MUID:9016993; PMID:2106481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GB:M29581; NID:g340447; PIDN:AAA61314.1; PID:g340448; GB:J04751
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C;Superfamily: zinc finger protein ZPP-36; LIM metal-binding repeat homology
C;Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein YLR417w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L9931.3
C;Species: Saccharomyces cerevisiae
C;Date: 30-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 29-Oct-1999
C;Accession: S59382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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46.5%; Score 40; DB 2; Length 529;
Best Local Similarity 43.8%; Pred. No. 41;
Matches 7; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 543
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A;Description: The sequence of S. cerevisiae cosmid 9931.
A;Reference number: S59376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
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ilarity 53.3%; Pred. No. 42;
Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: GDB:120510; OMIM:194532
                                                                        CKRYVYVDTRSEDETH 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RORYLYIDDAQQTEAH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 RGEYLYTYDSQITDS 178
                                    16
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                                    RORYLYTDDAQQTEAH
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les 8; Conserv
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-543 < LAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB: ZNF8
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Best Local S:
Matches 8
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A;Cross-refe
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Mismatches

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Conservative

7;

Matches

16

1 RQRYLYTDDAQQTEAH

1627 QQQYLYMQQLQQHQQH 1642

R.Dobson, R. submitted to the EMBL Data Library, March 1997 submitted to the EMBL Data Library, March 1997 A;Reference number: 219498 A;Accession: T21993 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA.

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A;Reaidues: 1-278 <WIL>
A;Reaidues: 1-278 <WIL>
A;Cross-references: EMBL:Z79596; NID:e1323798; PIDN:CAB01858.1; GSPDB:GN00028; CESP:C02.
A;Experimental source: clone C02C6
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A,Description: Sulfolobus solfataricus complete genome.
A,Reference number: A99139
A,Acession: G90294
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-263 <KUR>
A,Cross-references: GB:AE006641; NID:g13814594; PIDN:AAK41614.1; GSPDB:GN00155
C,Genetics:
A,Genetics:
A,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein C02C6.3 - Caenorhabditis elegans Cispecies: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000 C; Accession: T18857 R; Swinburne, J. Siswinburne, J. Subwinted to the EMBL Data Library, August 1996 A; Reference number: Z19032
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C;Superfamily: Caenorhabditis elegans hypothetical protein C02C6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 2; Length 278;
Pred. No. 29;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                       Length 263;
                                                                                                                                                                                                                                                                                  Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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7
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Pred. No. 28;
3; Mismatches
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                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                  2 QRYLYTDDAQQTEA 15
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Best Local Similarity 70.v.
70.v.
71. Conservative
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C11 protein - rabbit fibroma virus
C;Species: rabbit fibroma virus, Shope fibroma virus
C;Species: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 07-May-1999
C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 07-May-1999
C;Accession: C36819
R;Strayer, D.S.; Jerng, H.H.; O'Connor, K.
Virology 185, 585-595, 1991
Virology 185, 585-595, 1991
A;Atitle: Sequence and analysis of a portion of the genomes of Shope fibroma virus and ma A;Reference number: A41700; MUID:92074222; PMID:1660196
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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Farrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Map position: 1
A,Introns: 37/3; 102/2; 229/3; 317/3; 375/2; 505/3; 546/1; 670/3; 835/1; 906/2; 943/3;
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A;Cross-references: EMBL:Z92834; PIDN:CAB07394.1; GSPDB:GN00019; CESP:F39B2.4b
A;Experimental source: clone F39B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein SS01380 [imported] - Sulfolobus Bolfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #Bequence_revision 24-May-2001
                                                                                                                                                                                                                 hypothetical protein F39B2.4b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21993
              Gaps
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C;Superfamily: vaccinia virus D10R protein; mutT domain homology
F;123-157/Domain: mutT domain homology <MUTT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1663;
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                Indels
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1629 <u>gógylymgológhogh</u> 1644

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1 RORYLYTDDAQQTEAH 16

Local Similarity

Query Match

A; Gene: CESP: F39B2.4b

Score 39; DB 2 Pred. No. 27; 2; Mismatches

45.3%; 58.3%;

Conservative 4 YLYTDDAQQTEA 15 YTWTDDAORVSA 36

Query Match
Best Local Similarity
7; Conserva

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A,Status: translation not shown A,Molecule type: DNA A,Residues: 1-259 <STR>

Gaps

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probable membrane transporter STY1164 [imported] - Salmonella enterica subsp. enterica sprobable membrane transporter STY1164 [imported] - Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: this species has also been called Salmonella typhi C;Date: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: A10633
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D; Wain, J; Churcher, Lh. T; Connerton, P; Cronin, A; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C; Quail, M; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Parry, C; Quail, M: Rutherford, R; Simmonds, M: Skelton, J.; Stevens, K.; A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSPDB:GN00023; CESP:F46E10.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-235 <BLA>
A;Cross-references: EMBL:U64852; PIDN:AAB04972.1; GSPDB:GN00023; CESP:W01A11.7
A;Experimental source: strain Bristol N2; clone W01A11
C; Comment: This enzyme is involved in cellulose synthesis and its degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F46E10.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 05-Nov-1999
C;Accession: T33962; T29650
R;Johnson, D.; Bradshaw, H.
submitted to the EMBL Data Library, February 1999
A;Description: The sequence of C. elegans cosmid F46E10.
A;Reference number: Z21446
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                                                                                                                                                                      DB 2; Length 735; 90;
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                                                                                                                                                                                                                                             Indels
                                   C;Superfamily: beta-glucosidase
C;Keywords: glycosidase; hydrolaase
E;1-26/Domain: signal sequence #status predicted <SIG>
F;27-735/Product: beta-glucosidase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-213 < JOH>
A;CosH-creences: EMBL:AF125955; PIDN:AAD14716.1; GSPD
A;Experimental source: strain Bristol N2; clone F46E10
B;Blanchard, M; Bradshaw, H.
submitted to the EMBL Data library, July 1996
A;Description: The sequence of C. elegans cosmid WOLAll.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: DNA
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                                                                                                                                                                                                                   Pred. No. 90;
1; Mismatches
                                                                                                                                                                                         Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CESP: F46E10.6; CESP: W01A11.7
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                                                                                                                                                                                      45.3%;
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Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: 93/3; 140/3; 185/3
                                                                                                                                                                                                                                                                                                                                                                          718 TDDSQQTTMH 727
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A;Accession: T29650
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A;Status: preliminary
A,Molecule type: DNA
A;Residues: 1-285 <PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable phosphoprotein phosphatase (BC 3.1.3.16) regulatory chain - fission yeast (Schi
C;Species: Schizosaccharomyces pombe
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Accession: T11663
A Status: preliminary; translated from GB/EMBL/DDBJ
A Status: preliminary; translated from GB/EMBL/DDBJ
A Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-627 < BAR>
A, Cross-references: EMBL: Z98533; NID:e1071719; PID:e334113
A, Cross-references: EMBL: Z98533; NID:e1071719; PID:e334113
B, Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A, Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A, Reference number: Z17323; MUID:98162722; PID:9501991
A, Reference number: Z172984
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A,Residues: 27-55 <702.
A,Experimental source: strain BPR2001
A,Note: the residues and 714 and 715 are interchanged in the authors' translation
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A;Experimental source: strain BPR2001
A;Accession: PC4505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosfidues: 215-627 < XOS.
A;Cross-references: EMBL:D89107; NID:g1749421; PIDN:BAAL3770.1; PID:g1749422
A;Experimental source: strain PR745
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75;
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50;
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Pred. No. 75;
3; Mismatches
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Pred. No. 5
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A;Note: SPAC6F12.12
C;Keywords: phosphoric monoester hydrolase
                                                                                                                                                                   45.3%;
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Best Local Similarity 46.2%;
Matches 6; Conservative
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Best Local Similarity 53.8'
Matches 7; Conservative
                                                                                                                                                                                                                                                                                         2 QRYLYTDDAQQTE 14
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A; Residues: 1-735 <TON>
                A; Contents: annotation
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                                                   C,Genetics:
A,Gene: SMb21103
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probable resistance protein ylcB [imported] - Escherichia coli (strain O157:H7, substra C;Species: Bscherichia coli (cjate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: E85555 B;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe lller, L.; Grotheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca Nature 409, 529-533, 2001 A;Fifte: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
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A; Experimental source: strain 0157:H7, substrain EDL933
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable resistance protein [imported] - Escherichia coli (strain 0157.H7, substrain RI)
                                                                                                                                                                                              A;Cross-references: GB:AE000162; GB:U00096; NID:g1786782; PIDN:AAC73673.1; PID:g1786785
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: B90705
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and Gasternoce number: A99629; MUID:21156231; PMID:11258796
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A,Realdudes: 1-460 <HR>
A,Realdudes: 1-460 <HR>
A,Cross-references: GB:BA000007, PIDN:BAB34033.1, PID:g13360068, GSPDB:GN00154
A,Experimental source: strain 0157:H7, substrain RIMD 0509952
C,Genetics:
A,Gene: ECs0610
C,Superfamily: nodulation protein nodT
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                                                                                                                             A;Accession: B64790
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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pred. No. 79;
3; Mismatches 2; Indels
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1465, 1997
A,Title: The complete genome sequence of Escherichia coli K-12.
A,Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 2; Length 457;
Pred. No. 79;
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                                                                                                                                                                                                                                                                                                                                        A;Gene: yclB
(Superfamily: nodulation protein nodT
C;Keywords: transmembrane protein
F;6-22/Domain: transmembrane #status predicted <TMM>
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Best Local Similarity 58.3%;
Matches 7; Conservative
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148 RONYLATEEAOR 159
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A;Molecule type: DNA
A;Residues: 1-460 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable GDSL-motif lipase/hydrolase At2g19010 [imported] - Arabidopsis thaliana N;Alternate names: AFG protein homolog F19F24.21; hypothetical protein T20K24.2 (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 19-Feb-1999 #sequence revision 19-Feb-1999 #text_change 16-Feb-2001 C;Accession: T01629; T00521; D84571 B4571 B4571 B5.20.2 Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul submitted to the EMBL Data Library, April 1998 II BAC F19F24 genomic sequence. A;Reference number: Z14153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL:AC002392; NID:g3176701; PID:g3176703
A; Cross-references: EMBL:AC002392; NID:g3176701; PID:g3176703
A; Experimental source: cultivar Columbia
R; Experimental source: cultivar Columbia
R; Experimental source: cultivar Columbia
R; Experimental source: cultivar Columbia
R; Experimental source: cultivar Columbia
R; Experimental S; Ranis S; Experimental S; E; Umayam, E.; Tallon, E.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A)Residues: 1-344 <ROU>
A)Cross-references: EMBL:AC003673; NID:g3004543; PID:g3004563
A)Cross-references: EMBL:AC003673; NID:g3004543; PID:g3004563
A)Experimental source: cultivar Columbia
R)Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, July 1997
A)Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.
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C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: B64799
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
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         A; Cross-references: GB: AL513382; PIDN: CAD08252.1; PID: g16502299; GSPDB: GN00176
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                                                                                                                                   Length 285;
                                                                                                                                                                                        3; Indels
                                                                                                                                DB 2;
46;
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C;Superfamily: myrosinase-associated protein MyAP
                                                                                                                                                                                           4; Mismatches
                                                                                                                                   Score 38;
Pred. No.
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A, Status: translated from GB/EMBL/DDBJ
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                                                                                                                                44.2%;
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                                                                                                                                                                                                                                                                                                               ORYIVTDSIEETK 58
                                                                                                                                                                                                                                                       2 ORYLYTDDAQQTE 14
                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: Z14167
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nes 7; Conserv
                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA A;Residues: 1-344 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T00521
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                                                                              A; Gene: STY1164
                                                                                                                                                                                                                                                                                                                  46
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B64790
                                                     Genetics;
                                                                                                                                                                                                  Matches
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A, Gene: ylcB C, Superfamily: nodulation protein nodT

148 RÓNYLATEBÁOR 159

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1 RORYLYTDDAGO 12

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Outer layer protein VP4 - human rotavirus A (serotype G3, strain AU-1)
NyAlternate names: hemagglutinin; outer capsid protein VP4
N;Contains: outer layer protein VP5; outer layer protein VP8
C;Species: human rotavirus A
C;Species: human rotavirus A
C;Accession: JQ1638
R;Isegawa, Y; Nakagomi, O; Nakagomi, T; Ueda, S.
J, Gen. Virol. 73, 1939-1946, 1992
A;Aritle: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav
A;Reference number: JQ1638; MUID:92356070; PMID:1322955
A;Accession: JQ1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Map position: segment 4

C,Superfamily: roctavirus outer layer protein VP3

C,Superfamily: roctavirus protein; hemagglutinin; outer capsid protein

C,Reywords: glycoprotein; hemagglutinin; outer capsid evP8>

F;1-241/Product: outer layer protein VP8 #status predicted evP8>

F;242-247/Region: cleavage processing #status predicted evP5>

F;248-775/Product: outer layer protein VP5 #status predicted evP5>

F;17,32,97,132,183,198,237,567,613/Binding site: carbohydrate (Asn) (covalent) #status p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.
J. Gen. Virol. 73, 1939-1946, 1992
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav
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                                                                                                     C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 1.4e+02;
3; Mismatches 5; Indels
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44.2%; Score 38; DB 1; Length 747

Best Local Similarity 42.9%; Pred. No. 1.4e+02;

Matches 6; Conservative 3; Mismatches 5; Indels
outer layer protein VP3 - simian rotavirus SA11 (fragment)
C;Species: simian rotavirus SA11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: segment 4
C;Superfamily: rotavirus outer layer protein VP3
                                                                                                                                                                                                                                                                                                                                                              A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: genomic RNA
A;Residues: 1-747 (LDP>
A;Cross-references: GB:M11158; NID:g61868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 QYTYTRDGEEVTAH 312
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Best Local Similarity 42.5%
Best Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: genomic RNA
A;Residues: 1-775 <1SE>
                                                                                  A; Note: host (monkey)
                                                                                                                                                                                                                                                                                                                                       A; Accession: A04129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hemolysin activation protein HecB, probable NMB1780 [imported] - Neisseria meningitidis cispecies: Neisseria meningitidis cispecies: Neisseria meningitidis cispecies: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 Cispecession: P80.04 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 Cispecession: P80.04 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Sauders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherry, B.A.; Tri, H.; Qin, H.; Vanathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000, E.S.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A; Authores Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8. A; Status: preliminary A; Molecule type: DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE002528; GB:AE002098; NID:g7227034; PIDN:AAF42120.1; PID:g722703
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                      Query Match
44.2%; Score 38; DB 2; Length 460;
Best Local Similarity 58.3%; Pred. No. 79;
Matches 7; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.2%; Score 38; DB 2; Length 580; 63.6%; Pred. No. 1e+02;
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3; Indels

1; Mismatches

Best Local Similarity 63.6 Matches 7; Conservative

A; Residues: 1-580 <TET>

A; Gene: NMB1780

Genetics:

Query Match

361 ROTYKYIDDAE 371

RESULT 26

1 RQRYLYTDDAQ 11

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/ Match 44.2%; Score 38; DB 2; Length 580; Local Similarity 63.6%; Pred. No. 1e+02; res 7; Conservative 1; Mismatches 3; Indels
                                                                                                                                    361 ROTYKYIDDAE 371
                                                                                               1 RORYLYTDDAQ 11
             Query Match
                                   Best Loca
Matches
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A;Gene: NMA0686; NMA0687

RESULT 27

A; Accession: JQ1639

Query Match Best Local Similarity Matches 6; Conserv

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outer layer protein VP4 - bovine rotavirus A (serotype 5)

outer layer protein VP4

N,Alternate names: hemagglutinin; outer capsid protein VP4

N,Contains: outer layer protein VP5; outer layer protein VP8

N,Contains: outer layer protein VP5; outer layer protein VP8

C;Species: bovine rotavirus A requence revision 24-Feb-1994 #text_change 02-Jun-2000
C;Accession: JQ2022

R;Taniguchi, K; Urasawa, T; Urasawa, S.

J, Gen. Virol. 74, 1215-1221, 1993

A;Title: Independent segregation of the VP4 and the VP7 genes in bovine rotaviruses as A;Pitle: Independent segregation of the VP4 and the VP7 genes in bovine rotaviruses A;Accession: JQ2022

A;Molecule type: genomic RNA

A;Molecule type: genomic RNA

A;Molecule type: GB:D13395; NID:G393327

A;Cross references: GB:D13395; NID:G393327

A;Note: this translation is not annotated in GenBank entry ROBASVP4, release 113.0
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C; Superfamily: roctavirus outer layer protein VP3
C; Superfamily: roctavirus outer layer protein or Siperfamily: roctavirus outer layer protein; hemagglutinin; outer capsid predicted <VP8>
F; 1-241/Product: outer layer protein VP8 #status predicted <VP8>
F; 248-77/Region: cleavage processing #status predicted <VP5>
F; 248-77/Region: cleavage processing #status predicted <VP5>
F; 248-77/Region: cleavage processing #status predicted <VP5>
F; 258-77/Fbroduct: outer layer protein VP5 #status predicted <VP5>
F; 56, 97, 132, 151, 198, 456, 507, 670/Binding site: carbohydrate (Asn) (covalent) #status pre
                                                                                                                                               (covalent) #status
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Nucleic Acids Res. 15, 4361, 1987
A,Title: The complete nucleotide sequence of bovine rotavirus C486 gene 4 cDNA.
A,Reference number: A29529; MUID:87231020; PMID:3035492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: segment 4
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: glycoprotein; hemagglutinin
F;32,56,97,132,151,183,198,456,507,596,602/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               outer layer protein VP3 - bovine rotavirus A (strain C486)
N;Alternate names: hemagglutinin
C;Species: bovine rotavirus A
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
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A,Molecule type: genomic RNA
A,Residues: 1-776 <POI>
A,Cross-references: GB:Y00127; NID:g61854; PIDN:CAA68325.1; PID:g61855
C,Genetics:
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: glycoprotein; hemagglutinin; outer capsid protein
F;1-241/product: outer layer protein VP8 #status predicted <VP8>
F;248-776/Product: outer layer protein VP5 #status predicted <VP5>
F;248-776/Product: outer layer protein VP5 #status predicted <VP5>
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                                                                                                                                                                                                                    Score 38; DB 1; Length 776;
Pred. No. 1.4e+02;
3; Mismatches 5; Indels
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42.9%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.2%;
                                                                                                                                                                                                                            Query Match

Best Local Similarity 42.9%;
Matches 6; Conservative
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Best Local Similarity 42...
Best Local Si Conservative
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NyAlternate names: glycoprotein VP3; outer layer protein VP3
NyContains: outer layer protein VP3; outer layer protein VP3
NyContains: outer layer protein VP5; outer layer protein VP8
C;Species: Nebraska calf diarrhea virus
C;Species: Nebraska calf diarrhea virus
C;Accession: C31159
R;Nishikawa, K.; Taniguchi, K.; Torres, A.; Hoshino, Y.; Green, K.; Kapikian, A.Z.; Chan J.Yirol. Cs. 4022-4026, 1988
A;Title: Comparative analysis of the VP3 gene of divergent strains of the rotaviruses si A;Reference number: A94694; MUID:89012172; PMID:2845121
A;Accession: C31159
A;Residues: 1-775 <NIS>
C;Genetics:
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NyAlternate names: glycoprotein VP3; hemagglutinin; outer capsid protein VP3

N;Contains: outer layer protein VP5; outer layer protein VP8

C;Species: simian rotavirus SAll

A;Note: Note: (monkey)

B;Note: Nature (monkey)

C;Accession: B3ll59

C;Accession: B3ll59

C;Accession: M; Taniguchi, K; Torres, A; Hoshino, Y; Green, K; Kapikian, A.Z.; Chan, N; Niahikwaw, K; Taniguchi, K; Torres, A; Hoshino, Y; Green, K; Kapikian, A.Z.; Chan, N; Niahikwaw, K; Torres, A; Hoshino, Y; Green, K; Kapikian, A.Z.; Chan, N; Niahikwa, K; Torres, A; Hoshino, Y; Green, K; Kapikian, A.Z.; Chan, N; Niahikwa, K; Torres, A; Hoshino, Y; Green, K; Kapikian, A; Chan, N; Niahicher Comparative analysis of the VP3 gene of divergent strains of the rotaviruses single N; Nicol.
                                                                                                                                                                                                                                               A,Map position: segment 4

S.Superfamily: roctavirus outer layer protein VP3
C.Superfamily: roctavirus hemagglutinin, outer capsid protein
C.Keywords: glycoprotein; hemagglutinin, outer capsid prodicted <VP8>
F;12-241/Froduct: outer layer protein VP8 #status predicted <VP8>
F;242-247/Region: cleavage processing #status predicted <VP5>
F;248-775/Product: outer layer protein VP5 #status predicted <VP5>
F;248-775/Product: outer layer protein VP5 #status predicted <VP5>
F;248-775/Product: outer layer protein Site: carbohydrate (Asn) (covalent) #status predi
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C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: glycoprotein, hemagglutinin; outer capsid protein
F;1-241/Product: outer layer protein VP8 #status predicted <VP8>
F;248-775/Product: outer layer protein VP5 #status predicted <VP5>
F;56,97,132,151,183,199,456,507,596,602/Binding site: carbohydrate (Asn) (covalent) #sta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.2%; Score 38; DB 1; Length 775
42.9%; Pred; No. 1.46+02;
Mismatches 5; Indels
                           A, Reference number: JQ1638; MUID: 92356070; PMID: 1322955
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Best Local Similarity 42.9%;
Matches 6; Conservative
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QYTYTRDGEEVTAH 315
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A;Residues: 1-776 <NIS>
C;Genetics:
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A; Residues: 1-775 <ISE>
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A; Map position: segment

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Matches

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RESULT 34 VPXRS1

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Apperimental source: strain 936.

Apperimental source: strain 936.

RySimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.B.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.B.; Frenca, A.J.S.

submitted to GenBank, June 2000

A,Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm A,Authors: Ferreira, W.L.; Kamper, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigir J.D.; Junqueira, M.L.; Kamper, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigir J.D.; Junqueira, M.L.; Kamper, M.Y.; Menck, C.F.M.; Miracca, E.C.; Martins, E. A,Authors: Martins, E.M.F.; Matchkuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; A,Authors: Martins, E.M.F.; Matchkuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; A,Authors: da Silva, A.C.R.; da Silva, F.R.; de Sa, R.G.; Santelli, R.V.; Sawasa A,Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvaira, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A;Genetics: annotation
C;Genetics: A,Gene: XF0837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Species: Nylella fastidiosa
C;Accession: B82756
C;Accession: B82756
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347.
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB: AE003923; GB: AE003849; NID: 99105736; PIDN: AAF83647.1; GSPDB: GN001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organic solvent tolerance precursor XF0837 [imported] - Xylella fastidiosa (strain 9a5c)
                                  C;Accession: S24410
R;Mattion, N.M.; Estes, M.K.
Arch. Virol. 120, 109-113, 1991
A;Tile: Sequence of a rotavirus gene 4 associated with unique biologic properties.
A;Reference number: S24410; MUID:92028406; PMID:1656916
A;Accession: S24410
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C,Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 19-Feb-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 776;
                                                                                                                                                                                                                                                                                                                                                                                                                                  44.2%; Score 38; DB 2; Length 776 42.9%; Pred. No. 1.4e+02; rative 3; Mismatches 5; Indels
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C, Superfamily: rotavirus outer layer protein VP3
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Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 42.93
Matches 6; Conservative
                                                                                                                                                                                                                                                                         A;Molecule type: genomic RNA
A;Residues: 1-776 <MAT>
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A;Molecule type: DNA
A;Residues: 1-792 <SIM>
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A;Title: Comparative analysis of the VP3 gene of divergent strains of the rotaviruses si A;Reference number: A94694; MUID:89012172; PMID:2845121
A;Accession: A31159
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C;Superfamily: rotavirus outer layer protein vP3
C;Keywords: glycoprotein; hemagglutinin; outer capsid protein
F;1-241/Product: outer layer protein VP8 #status predicted <VP5>
F;248-776/Product: outer layer protein VP5 #status predicted <VP5>
F;328-776/Product: outer layer protein VP5 #status predicted <VP5>
F;32,56,97,116,132,149,198,386/Binding site: carbohydrate (Asn) (covalent) #status predi
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                                                                                                                                                                                                                                                                                                                  outer layer protein VP3 - simian rotavirus SA11 (strain SA11-SEM) N;Alternate names: glycoprotein VP3; hemagglutinin; outer capsid protein VP3 N;Contains: outer layer protein VP5; outer layer protein VP8 C;Species: simian rotavirus SA11
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C.Species: Bimian rotavirus SA11
C.Species: Or-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 20-Sep-1999
C.Accession: S03611
R;Mitchell, D.B.; Both, G.W.
Nucleic Acids Res. 17, 2122, 1989
A;Title: Complete nuclectide sequence of the simian rotavirus SA11 VP4 gene.
A;Reference number: S03611; MuID:89183617; PMID:2538804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: host (monkey)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 16-Jul-1999
C;Accession: A31159
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                                  5; Indels
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C;Species: simian rotavirus SAll
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                                     Mismatches
                                     3;
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302 QYTYTRDGEEVTAH 315
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                                        6; Conservative
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A, Residues: 1-776 <NIS>
                                                                                                         3 RYLYTDDAQQTEAH
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A; Residues: 1-776 <MIT>
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C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: A99580
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Ress. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
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A;Molecule type: DNA
A;Residues: 1-1426 <KUR>
A;Cross-references: GB:AL445566; PID:914089960; PIDN:CAC13718.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                              A;Map position: 3
A;Introns: 36/3; 121/3; 205/3; 336/2; 668/3; 739/1; 773/1; 853/2; 894/2; 932/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transposable element Txlc protein 2 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 21-Jul-2000
C;Accession: B32494
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A;Molecule type: DNA
A;Residues: 1-1308 <GR>
A;Cross-references: GB:M26915; NID:g214844; PIDN:AAA49976.1; PID:g214846
C;Superfamily: pol polyprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Garrett, J.E.; Knutzon, D.S.; Carroll, D. Mol. Cell. Biol. 9, 3018-3027, 1989
A;Title: Composite transposable elements in the Xenopus laevis genome. A;Reference number: A32494; MuID:89384562; PMID:2550791
A;Accession: B32494
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                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1051 <JOR>
A;Cosa-references: BMBL:AL353818; GSPDB:GN00661; ATSP:F14L2.80
A;Experimental source: cultivar Columbia; BAC clone F14L2
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submitted to the Protein Sequence Database, April 2000 A;Reference number: Z25008 A;Accession: T48933
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44.2%; Score 38; DB 2;
Best Local Similarity 70.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches
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Matches 7; Conservative
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Then 8; Conserva
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A;Gene: ATSP:F14L2.80
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A; Genetic code: SGC3
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45
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US-10-219-466-78

US-10-219-479-78

US-10-219-481-78

US-10-219-481-78

US-10-230-260-78

US-10-230-260-78

US-10-216-78-78

US-10-216-78-78

US-10-216-78-78

US-10-219-468-78

US-10-219-468-78

US-10-219-468-78

US-10-219-470-78

US-10-219-470-78

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Sequence 8, Application US/10060765

PUblication No. US20020164713A1

SERREAL INFORMATION

APPLICANT: Itch, No. US20020164713Aluyuki

APPLICANT: Itch, No. US20020164713Aluyuki

APPLICANT: TEVENENTON: HUWAN FGF-21 GENE AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS

FILE REFERENCE: PP-16758.001/201130.408

FILE REFERENCE: PP-16758.001/201130.408

FILE REFERENCE: 2000-11-16

NUMBER OF SEQ ID NOS: IT

SEQ ID NOS 8

LENGTH: 15

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 8

LENGTH: 15

HUMAN SEQ ID NOS: 17

SEQ ID NO 9

LENGTH: 15

HUMAN SEQ ID NOS: 17

SEQ ID NO 9

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APPLICANT: ECONS, Michael
APPLICANT: ECONS, Michael
APPLICANT: WHITE, Kenneth
APPLICANT: WHITE, Kenneth
APPLICANT: WITCH
APPLICANT: WITCH
APPLICANT: MEITINGER, Thomas
TITLE OF INVENTION: NOVEL FIEROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
TITLE OF INVENTION: NOVEL FIEROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
CURRENT APPLICATION NUMBER: US/09/901,938
CURRENT FILING DATE: 2001-07-10
RICHARD PRICE FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 34
SOFTWARE PARENT HIN Version 3.0
SEQ ID NO 33
LENGTH: 136
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; Sequence 36, Application US/09802154
; Publication No. US20030105302A1
; GENERAL INFORMATION:
    APPLICANT: Itch, No. US20030105302Aluyuki
    APPLICANT: Kavanaugh, W. Michael
    TITLE OF INVENTION: HUMAN FGF-23 GENE AND GENE EXPRESSION
    TITLE OF INVENTION: HUMAN FGF-23 GENE AND GENE EXPRESSION
    TITLE OF INVENTION: HUMAN FGF-23 GENE AND GENE
    TITLE OF INVENTION: HUMAN FGF-369/802,154
    CURRENT APPLICATION NUMBER: US/09/802,154
    CURRENT FILING DATE: 2001-03-07
    NUMBER OF SEQ ID NOS: 46
    SOFTWARE: FaelSEQ for Windows Version 4.0
    SEQ ID NO 36
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Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
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TITLE OF INVENTION: HUMAN FGF-23 GENE AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS
FILE REPERENCE: PP-17150.0011/201130.40901
CURRENT APPLICATION NUMBER: US/09/801,968
CURRENT FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 68
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Matches 15; Conservative
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CORGANISM: Homo Sapiens
US-09-901-938-33
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
US-09-801-968-36
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US-10-379-334-33

US-10-379-334-33

Sequence 33, Application US/10379334

Publication No. US20030181379A1

APPLICANT: BCONS, Michael

APPLICANT: BCONS, Michael

APPLICANT: STROW, Tim

APPLICANT: STROW, Tim

APPLICANT: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE

TITLE OF INVENTION: NOVEL FIBROBLAST

CURRENT FILING DATE: 2003-03-04

PRIOR APPLICATION NUMBER: US/10/991,938

PRIOR APPLICATION NUMBER: 60/219,137

PRIOR PLILNG DATE: 2000-07-19

PRIOR FILING DATE: 2000-07-19

NUMBER OF SEQ ID NOS: 34

SOFTWARE PARENTIN VERSION 3.0

SEQ ID NOS: 34

SOFTWARE PARENTIN VERSION 3.0
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    Length 136;
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100.0%; Score 89; DB 9; 1
ilarity 100.0%; Pred. No. 7.9e-05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2. Application US/09755695;
Patent No. US20020081663A1
GENERAL INFORMATION:
APPLICANT: CONKIEN, DAITELL C.
APPLICANT: CONKIEN, DAITELL C.
TITLE OF INVENTION: NOVEL FGF HOMOLOG ZFGFI1
FILE REPERBREE: 00-03
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US/09/755,695
CURRENT FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FREESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 2
LENGTH: 208
TYPE: PRT
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Matches 15; Conservative
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Matches 15; Conservative
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ORGANISM: Homo Sapiens
        Query Match
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Matches 15; Conserva
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US-09-755-695-2
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APPLICATION NUMBER: 60/091982
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PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR APPLICATION NUMBER: 60/095916
PRIOR FILING DATE: 1998-08-17
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PRIOR FILING DATE: 1998-08-17
PRIOR PLICATION NUMBER: 60/09594
PRIOR FILING DATE: 1998-08-17
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PRIOR PELING DATE: 1999-01-10
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PRIOR PLING DATE: 1999-03-19
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PRIOR APPLICATION NUMBER: 60/126773
PRIOR PLING DATE: 1999-04-29
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US-10-230-163-78
; Sequence 78, Application US/10230163
; Publication No. US20030036635A1
; PUBLICATION:
; APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1999-11-16
APPLICATION UNMBER: 60/169445
FILING DATE: 1999-12-07
APPLICATION NUMBER: 60/169495
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APPLICATION NUMBER: 60/115733
FILING DATE: 1999-01-12
APPLICATION NUMBER: 60/119549
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                                                               APPLICATION NUMBER: 60/115565
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Query Match

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PRION APPLIANG MARIE: 1938-09-14

PRIOR APPLICATION NUMBER: 60/10192

PRIOR FILING DATE: 1938-09-24

PRIOR FILING DATE: 1938-10-28

PRIOR FILING DATE: 1938-10-29

PRIOR FILING DATE: 1938-10-29

PRIOR APPLICATION NUMBER: 60/106464

PRIOR APPLICATION NUMBER: 60/106905

PRIOR PILING DATE: 1938-10-30

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PRIOR APPLICATION NUMBER: 60/10801

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PRIOR FILING DATE: 1938-12-25

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PRIOR APPLICATION NUMBER: 60/101738
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PRIOR FILING DATE: 1998-09-24
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APPLICATION NUMBER: 60/123618
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Gaps ö Length 208; Indels ö 100.0%; Score 89; DB 14; 100.0%; Pred. No. 0.00012; Mismatches Sequence 78, Application US/10230338; Publication No. US20030044934A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin P. APPLICANT: Genoyers, Luc; APPLICANT: Gerriteen, Mary APPLICANT: Goddard, Audrey; APPLICANT: Goddard, Paul J. PRIOR FILING DATE: 1999-03-10

PRIOR APPLICATION NUMBER: 60/125259

PRIOR FILING DATE: 1999-03-19

PRIOR PILING DATE: 1999-03-29

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PRIOR FILING DATE: 1999-04-05

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PRIOR PILING DATE: 1999-01-09

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PRIOR PILING DATE: 1999-11-09

PRIOR PILING DATE: 1999-11-09

PRIOR PILING DATE: 1999-11-09 Godowski, Paul J. Grimaldi, J. Christopher Gurney, Austin L. Smith, Victoria ; 144 HLPGNKSPHRDPAPR 158 1 HLPGNKSPHRDPAPR 15 Query Match 100. Best Local Similarity 100. Matches 15; Conservative US-10-230-338-78 셤 ò

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APPLICANT:

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PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 66/064103
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
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PRIOR PILING DATE: 1998-03-25
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Publication No. US20030050448A1
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GRGANISM: Homo Sapien
US-10-218-631-78
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APPLICANT: Gerriteen, Mary
APPLICANT: Gerriteen, Mary
APPLICANT: Geddadd, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victorial
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APPLICANT: Watanabe, Colin L.
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          APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: PSS30PL02
CURRENT APPLICATION NUMBER: US/10/230,338
CURRENT FILING DATE: 2002-08-28
PRIOR PILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-00-17
PRIOR FILING DATE: 1997-10-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 HLPGNKSPHRDPAPR 158
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Best Local Similarity 100.
Matches 15; Conservative
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; ORGANISM: Homo Sapien
US-10-230-338-78
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GENERAL INFORMATION:

APPLICANT: BAKET, Kevin P.
APPLICANT: Gearlisen, Mary
APPLICANT: Gedard, Audrey
APPLICANT: Gedard, Audrey
APPLICANT: Gedard, Audrey
APPLICANT: Gedreki, Paul J.
APPLICANT: Gedreki, Paul J.
APPLICANT: Grampli, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Vactoria
APPLICANT: Stephan, Vactoria
APPLICANT: Stephan, Vactoria
APPLICANT: Stephan, Vactoria
APPLICANT: Stephan, Vactoria
APPLICANT: Stephan, Vactoria
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
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APPLICANT: Wood, William I.
APPLICANT: WOOD, WILL STORDER
CURRENT APPLICATION NUMBER: 10/119,480
RING PRILNG DATE: 2002-04-09
RRIOR FILING DATE: 2002-04-09
RRIOR FILING DATE: 1997-09-17
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
LENGTH: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 89; DB 14; Length 208; Best Local Similarity 100.0%; Pred. No. 0.00012; Matches 15; Conservative 0; Mismatches 0; Indels 0
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RESULT 14
US-10-227-873-78
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APPLICANN: Goddard, Audray
APPLICANN: Goddard, Audray
APPLICANN: Goddard, Audray
APPLICANN: Goddard, Audray
APPLICANN: Gurnaldi, J Christopher
APPLICANT: Gurnaldi, J Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
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APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: ACIDS ENCODING THE SAME
FILE REFERENCE: P359016
CURRENT APPLICATION NUMBER: US/10/119, 480
PRIOR APPLICATION NUMBER: 60/06287
PRIOR APPLICATION NUMBER: 60/06287
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-17
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100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                   Length 208;
                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-216-159A-78; Sequence 78, Application US/10216159A; Publication No. US20030069397A1; GENERAL INFORMATION:
                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HLPGNKSPHRDPAPR 15
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ORGANISM: Homo Sapien
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-414-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-216-159A-78
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144 HLPGNKSPHRDPAPR 158

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APPLICANT: Gerritsen, mary
APPLICANT: Goddard, hudrey
APPLICANT: Goddard, hudrey
APPLICANT: Goddard, baul J.
APPLICANT: Goddard, baul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wadanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: BECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PL72
CURRENT APPLICATION NUMBER: US/10/27,873
CURRENT APPLICATION NUMBER: G0/059113
PRIOR APPLICATION NUMBER: G0/062287
PRIOR FILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: G0/06349
PRIOR PILING DATE: 1997-10-21
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PRIOR APPLICATION NUMBER: G0/06349
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLIFEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLIFEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3530PIC11
CURRENT APPLICATION NUMBER: US/10/218,849
CURRENT FILING DATE: 2002-08-12
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
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                                                                                            APPLICANT: Baker, Kevin P.
APPLICANT: Besnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Geddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Swith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watenabe, Colin L.
APPLICANT: Wacenabe, Colin L.
APPLICANT: Wacenabe, Colin L.
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Publication No. US20030073816A1
GENERAL INFORMATION:
Sequence 78, Application US/10218849
Publication No. US20030073814A1
GENERAL INFORMATION:
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Gerritsen, Mary
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APPLICANT: Gerdard, Audrey
APPLICANT: Gerdard, Paul J.
APPLICANT: Grandld, J. Christopher
APPLICANT: Grandld, J. Christopher
APPLICANT: Grandld, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
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APPLICANT: Watanabe, Lolin L.
APPLICANT: Watanabe, Lolin L.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
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APPLICANT: Wood, William I.
APPLICANT: NOWBER: 10/119,480
FRIOR FILING DATE: 1097-10-17
FRIOR PELICATION NUMBER: 60/059113
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PRIOR FILING DATE: 1999-07-26
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Publication No. US20030073817A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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APPLICATION NUMBER: 60/149320
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APPLICANT Grimaldi, J. Christopher
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APPLICANT Grimaldi, J. Christopher
APPLICANT Gunaldi, J. Christopher
APPLICANT Smith, Victoria
APPLICANT Smith, Victoria
APPLICANT Watanabe, Colin L.
APPLICANT Watanabe, Colin L.
APPLICANT WACO, William I.
APPLICANT WOOd, William I.
APPLICANT WOOd, William I.
APPLICANT WOOD SERRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: BECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
CURRENT FILING DATE: 1202-04-08-14
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ORGANISM: Homo Sapien
US-10-219-076-78
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US-10-219-076-78
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A APPLICATION NUMBER: 60/10138

R PILING DATE: 1998-09-13

R APPLICATION NUMBER: 60/101477

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R APPLICATION NUMBER: 60/101738

R APPLICATION NUMBER: 60/101741

R APPLICATION NUMBER: 60/101741

R APPLICATION NUMBER: 60/101786

R FILING DATE: 1998-09-25

R APPLICATION NUMBER: 60/10196

R FILING DATE: 1998-09-25

R APPLICATION NUMBER: 60/101916

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FILING DATE: 1998-08-10
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APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Suith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Retanabe, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: Mood, William I.
APPLICANT: Mood, William I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C82
CURRENT FILING DATE: 2002-04-09
PRIOR PELICATION NUMBER: 60/0659113
PRIOR PELING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
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         Length 208;
                                                                Indels
Query Match
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0;
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VB-10-230-434-78

Sequence 78, Application US/10230434

Publication No. US20030078380A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc

APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/079656
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FILING DATE: 1998-03-27
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APPLICANT: Destroyers, Juc.
APPLICANT: Destroyers, Juc.
APPLICANT: Destroyers, Juc.
APPLICANT: Destroyers, Juc.
APPLICANT: Gedorati, Paul J.
APPLICANT: Gedorati, Paul J.
APPLICANT: Gedorati, Paul J.
APPLICANT: Gedorati, J. Christopher
APPLICANT: Gedorati, J. Christopher
APPLICANT: Gedorati, J. Christopher
APPLICANT: Gedorati, J. Christopher
APPLICANT: Wood, Milliam I.
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APPLICANT: WWWER: 60/062373
PRIOR FILING DATE: 1998-06-12
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; Sequence 78, Application US/10219003
; Publication No. US20030088063A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels (
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CRGANISM: Homo Sapien
US-10-219-464-78
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LENGTH: 208
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APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Retanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: WATANABER C. PELDE SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: PSSSOPICE.
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CURRENT APPLICATION NUMBER: 10/119,480
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Remaining Prior Application data removed - See File Wrapper or PALM.
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3530P1C57
CURRENT APPLICATION NUMBER: US/10/219,464
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Best Local Similarity 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels
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Gerritsen, Mary
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Stephan, Jean-Philippe F.
Watanabe, Colin L.
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; Publication No. US20030088065A1
; GENERAL INFORMATION:
                          Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) TYPE: PRT
) ORGANISM: Homo Sapien
US-10-219-075-78
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US-10-219-464-78
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APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Besnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria I.
APPLICANT: Smith, Victoria I.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: MACHIGA I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERBNUE: P3530PLG47
CURRENT PILICATION NUMBER: US/10/219,466
CURRENT PILING DATE: 2002-08-13
CURRENT FILING DATE: 2002-08-14

PRIOR PELICATION NUMBER: 10/119,480

PRIOR PELICATION NUMBER: 10/119,480

PRIOR PELING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: 60/06287

PRIOR APPLICATION NUMBER: 60/06287

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/064103

PRIOR APPLICATION NUMBER: 60/068913

PRIOR APPLICATION NUMBER: 60/068913

PRIOR APPLICATION NUMBER: 60/078910

PRIOR PILING DATE: 1998-03-20

PRIOR PILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079294

PRIOR PILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/07928

PRIOR APPLICATION NUMBER: 60/07928

PRIOR APPLICATION NUMBER: 60/07928

PRIOR PILING DATE: 1998-03-25

PRIOR PILING DATE: 1998-03-27

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 246
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PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/069113
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-01-17
PRIOR PELICATION NUMBER: 60/06287
PRIOR PELICATION NUMBER: 60/063549
PRIOR APPLICATION NUMBER: 60/063549
PRIOR APPLICATION NUMBER: 60/064103
PRIOR APPLICATION NUMBER: 60/064103
PRIOR PRILING DATE: 1997-10-21
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APPLICATION NUMBER: 60/069873
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Publication No. US20030088066A1
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goddard, Audrey
                        Best Local Similarity 100.
Matches 15; Conservative
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ORGANISM: Homo Sapien
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US-10-230-260-78
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APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austrul J.
APPLICANT: Gother, Austrul J.
APPLICANT: Gurney, Austrul J.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECREDED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: 00/062813
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-13
PRIOR PLILING DATE: 1997-10-13
PRIOR PLILING DATE: 1997-10-13
PRIOR FILING DATE: 1997-10-13
PRIOR FILING DATE: 1999-12-17
PRIOR FILING DATE: 1999-12-17
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                        PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR APPLICATION NUMBER: 60/079728
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
LENGTH: 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 89; DB 14; Length 208; 100.0%; Pred. No. 0.00012; tive 0; Mismatches 0; Indels (
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Publication No. US20030088067A1
GRNERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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Best Local Similarity 100.0
Matches 15; Conservative
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; ORGANISM: Homo Sapien
US-10-219-479-78
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ORGANISM: Homo Sapien
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US-10-219-479-78
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERRACE: P3530P1C28
CURRENT APPLICATION NUMBER: US/10/219,481
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 60/065213
PRIOR APPLICATION NUMBER: 60/065287
PRIOR APPLICATION NUMBER: 60/065287
PRIOR APPLICATION NUMBER: 60/065287
PRIOR APPLICATION NUMBER: 60/065287
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR PLING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/069873
PRIOR PLING DATE: 1998-03-20
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-26
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                                            Indels
Pred. No. 0.00012; Mismatches 0;
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Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Stephan, Vean-Philippe F.
Watanabe, Colin L.
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Publication No. US20030088068A1
GENERAL INFORMATION:
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144 HLPGNKSPHRDPAPR 158
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
, ORGANISM: Homo Sapien
US-10-232-231-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                   APPLICANT: Grindli, v. Caristopher, Abstin L. APPLICANT: Smith, Victoria APPLICANT: Smith, Victoria APPLICANT: Stephan, Jean-Philippe F. APPLICANT: Stephan, Jean-Philippe F. APPLICANT: Watanabe, Colin L. APPLICANT: Wood, William I. TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ADDITION NUMBER: US/10/230,260
CURRENT APPLICATION NUMBER: US/11/9,480
FRIOR FILING DATE: 2002-04-09
FRIOR FILING DATE: 1997-09-17
FRIOR FILING DATE: 1997-10-17
FRIOR FILING DATE: 1997-10-17
FRIOR FILING DATE: 1997-10-17
FRIOR FILING DATE: 1997-10-31
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FRIOR FILING DATE: 1998-03-26
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APPLICANT: Goddwaki, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, COLIN L.
APPLICANT: WATANAWINI SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: 10/119,480
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 HLPGNKSPHRDPAPR 158
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRGANISM: Homo Sapien US-10-230-260-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-232-231-78
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US-10-232-233-78

Sequence 78, Application US/10232233

Sequence 78, Application US/10232233

Publication No. US20030088072A1

Sequence 78, Application No. US20030088072A1

APPLICANT: Baker, Kevin P.

APPLICANT: Godowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Grinneldi, J. Christopher

APPLICANT: Grinneldi, J. Christopher

APPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin L.

APPLICANT: Watanabe, Colin L.

APPLICANT: APPLICANT: ACIDS ENCODING THE SAME

TITLE OF INVENTION: ACIDS ENCODING THE SAME

TITLE OF INVENTION: ACIDS ENCODING THE SAME

TITLE OF INVENTION: ACIDS ENCODING THE SAME

TITLE OF INVENTION: ACIDS ENCODING THE SAME

TITLE OF INVENTION: ACIDS ENCODING THE SAME

TITLE OF INVENTION NUMBER: US/10/232,233

CURRENT APPLICATION NUMBER: US/10/139,480

PRIOR APPLICATION NUMBER: US/119,480

PRIOR APPLICATION NUMBER: US/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-17
PRIOR PLICATION NUMBER: 60/063549
PRIOR PLICATION NUMBER: 60/064103
PRIOR PLING DATE: 1997-10-38
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1998-03-26
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PRIOR FILING DATE: 2002-04-09
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062187
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR PILING DATE: 1997-10-31
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UMBER: 60/079294
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1 HLPGNKSPHRDPAPR 15
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC7
CURRENT APPLICATION NUMBER: US/10/216,165
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-31
PRIOR PRILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
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PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
LENGTH: 208
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Best Local Similarity 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels (
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Publication No. US20030092866A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Gerzitsen, Mary
APPLICANT: Gerzitsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Wictoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 HLPGNKSPHRDPAPR 158
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US-10-216-165-78
                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo Sapien
US-10-232-233-78
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US-10-216-165-78
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REAGE FILING DATE: 1999-1-23

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| PRIOR FILING DATE: 1999-1-23
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| PRIOR FILING DATE: 1999-1-0-1-23
| PRIOR FILING DATE: 1999-1-0-1-23
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| PRIOR FILING DATE: 1999-1-0-1-23
| PRIOR FILING DATE: 1999-1-0-1-23
| PRIOR PADICATION NOMES: 60/12559
| PRIOR PADICATION NOMES: 60/12559
| PRIOR PADILACTION NOMES: 60/12559
| PRIOR PADILACTION NOMES: 60/12559
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILER REFERENCE: P3530P1C30
CURRENT APPLICATION NUMBER: US/10/219,478
CURRENT FILING DATE: 2002-08-03
PRIOR APPLICATION NUMBER: (0/069113
PRIOR APPLICATION NUMBER: (0/062287)
PRIOR APPLICATION NUMBER: (0/062287)
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-17
PRIOR PLICATION NUMBER: (0/06287)
PRIOR PLICATION NUMBER: (0/063549)
PRIOR FILING DATE: 1997-10-28
PRIOR PLICATION NUMBER: (0/069873)
PRIOR PLICATION NUMBER: (0/069873)
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-22
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
PRIOR PLICATION NUMBER: (0/079294)
PRIOR FILING DATE: 1998-03-25
PRIOR PLILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-26
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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Stephen, Gean-Philippe F.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: ALGORATED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
LENGTH: 208
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 208;
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100.0%; Pred. No. 0.00012;
iive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: US/10/19,536
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/05287
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 HLPGNKSPHRDPAPR 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-219-478-78
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APPLICANT: Godwski, Paul J.
APPLICANT: Godwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: ACTOR SERGETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACTOR ENCODING THE SAME
FILE REFERENCE: P3530PIC34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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NUMBER OF SEQ ID NOS: 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/219,468 CURRENT FILING DATE: 2002-08-13
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Publication No. US20030092869A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Gernitsen, Mary
APPLICANT: Gernitsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gramaddi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR APPLICATION NUMBER: 60/079656
PRIOR PILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
                                                         Sequence 78, Application US/10219468 Publication No. US20030092888A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/064103
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PRIOR APPLICATION NUMBER: 60/069873
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Best Local Similarity 100.0%;
Matches 15; Conservative
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                                                                                                                                                APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CORGANISM: Homo Sapien
US-10-219-468-78
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US-10-219-478-78
                                          US-10-219-468-78
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LENGTH: 208
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Gaps

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Query Match
Best Local Similarity 100.0
Matches 15; Conservative
         ; ORGANISM: Homo Sapien
US-10-233-205-78
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APPLICANT: Goldowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3530PLC115
CURRENT APPLICATION NUMBER: 10/10/233,205
CURRENT FILING DATE: 2002-08-29
PRIOR FILING DATE: 1097-10-19
PRIOR PLILNG DATE: 1997-10-19
PRIOR APPLICATION NUMBER: 60/063287
PRIOR PLILNG DATE: 1997-10-28
PRIOR PLILNG DATE: 1997-10-28
PRIOR PLILNG DATE: 1997-10-28
PRIOR PLILNG DATE: 1997-10-21
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NUMBER OF SEQ ID NOS: 246
PRIOR APPLICATION NUMBER: 60/069873
PRIOR PLING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-27
REMAINING DATE: 1998-03-27
REMAINING PATE: 1998-03-27
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Best Local Similarity 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo Sapien
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LENGTH: 208
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APPLICANT: GGETILGEN, MARY
APPLICANT: GGGGARSI, Paul J,
APPLICANT: GGGGARSI, Paul J,
APPLICANT: GCTGAGA, AUGUST
APPLICANT: GTGAGA, AUGUST
APPLICANT: GTGAGA, J. Christopher
APPLICANT: GATIMAIA, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: WAGA Hilliam I.
APPLICANT: WAGA Hilliam I.
APPLICANT: WAGA HILLIAM ACIDS ENCODING THE SAME
TITLE DF INVENTION: ACIDS ENCODING THE SAME
FILE REPRENCE: D5330PLC45
CURRENT FAILING DATE: 2002-044-09
PRIOR APPLICATION NUMBER: 60/062913
PRIOR PRILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PRILING DATE: 1997-09-17
PRIOR PELLOCATION NUMBER: 60/06387
PRIOR APPLICATION NUMBER: 60/06387
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Length 208;
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       100.0%; Score 89; DB 14; 100.0%; Pred. No. 0.00012;
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; Sequence 78, Application US/10219470
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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FILE REFERENCE: P3530P1C36
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LENGTH: 208
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APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
TILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TILLE OF INVENTION: ACIDS ENCODING THE SAME
TILLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P$330P1059
FULL REPERENCE: $3330P1059
FULL REPERENCE: $2002-08-14
FRICH PILLING DATE: 2002-08-14
FRICH FILLING DATE: 100-17
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APPLICANT: Goddweki, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Onlin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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Pred. No. 0.00012;
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
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       No. US20030096960A1
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                                                                                                                        Desnoyers, Luc
Gerritsen, Mary
                                              GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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US-10-219-470-78
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APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND CURRENT APPLICATION NUMBER: US/10/19,480
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-01-17
PRIOR FILING DATE: 1997-01-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-28
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PRIOR FILING DATE: 1997-10-31
PRIOR PRILING DATE: 1997-10-31
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NUMBER OF SEQ ID NOS: 246
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Best Local Similarity 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels
FILE KEFERENCE: 19350FLC39,
CURRENT APPLICATION NUMBER: US/10/219,474
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR PILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06287
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Publication No. US20030096962A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Gestoyers, Luc
APPLICANT: Geritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
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ORGANISM: Homo Sapien
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RAPLICATION NUMBER: 60/095312

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RAPLICATION NUMBER: 60/095318

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R FILING DATE: 1998-05-13
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R FILING DATE: 1998-05-22
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R FILING DATE: 1998-06-25
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R APPLICATION NUMBER: 60/091982
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APPLICANT: Bearowers, Luc
APPLICANT: Goddard, Audrey
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APPLICANT: Goddard, Audrey
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Monday
APPLICANT: Wood, William I.
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
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PRIOR PILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR APPLICATION WUMBER: 60/079728
PRIOR APPLICATION DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
LENGTH: 208
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Best Local Similarity 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0
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; ORGANISM: Homo Sapien
US-10-219-524-78
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NUMBER: 60/089532 1998-06-17 1998-06-17 1998-06-17 1998-06-18 1998-06-18 NUMBER: 60/08905 1998-06-24 NUMBER: 60/090657 1998-06-24 NUMBER: 60/090691 1998-06-25 NUMBER: 60/090691 11998-06-25 NUMBER: 60/090691 11998-06-25 NUMBER: 60/090695	07-07 1 60/0953 1 60/0953 08-04 1 60/0959 1 60/0967 1 60/0967 1 60/0967 1 60/098 1 60/0998	1998-09-15 NUMBER: 60/100390 1998-09-16 NUMBER: 60/100627 1998-09-16 NUMBER: 60/100919 1998-09-17 NUMBER: 60/10019 1998-09-23 NUMBER: 60/101477 1998-09-24 NUMBER: 60/101741 1998-09-24 NUMBER: 60/101741 1998-09-24 NUMBER: 60/101741 1998-09-24 NUMBER: 60/101741 1998-09-24 NUMBER: 60/10196 11998-09-24 NUMBER: 60/10196 11998-09-24 NUMBER: 60/10192 11998-09-24 NUMBER: 60/10192 11998-09-24 NUMBER: 60/10192 11998-09-24 NUMBER: 60/10648 11998-10-29 NUMBER: 60/10648
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R FILING DATE: 1998-08-31
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R APPLICATION NUMBER: 60/099816
R FILING DATE: 1998-09-10
R PILING DATE: 1998-09-11
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R APPLICATION NUMBER: 60/10038
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R APPLICATION NUMBER: 60/101738
R FILING DATE: 1998-09-24
R PILING DATE: 1998-09-24
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R APPLICATION NUMBER: 60/101786
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R APPLICATION NUMBER: 60/099598
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R APPLICATION NUMBER: 60/099811
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RILING DATE: 1998-11-03
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APPLICATION NUMBER: 60/099812
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APPLICATION NUMBER: 60/100390
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APPLICATION NUMBER: 60/100627
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APPLICATION NUMBER: 60/100848
FILING DATE: 1998-09-18
APPLICATION NUMBER: 60/100919
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APPLICATION NUMBER: 60/101477
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APPLICATION NUMBER: 60/106464
                                                                                     FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
                 APPLICATION NUMBER: 60/090557
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APPLICATION NUMBER: 60/090691
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APPLICATION NUMBER: 60/095318
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APPLICATION NUMBER: 60/096146
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WOOd, WILLIAM J.
APPLICANT:
WOOD, WILLIAM J.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC80
CURRENT PAPLICATION NUMBER: US/10/227,881
CURRENT FILING DATE: 2002-04-09
RIOR APPLICATION NUMBER: 10/119,480
RIOR FILING DATE: 1997-09-17
RIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
RIOR APPLICATION NUMBER: 60/06287
PRIOR FILING DATE: 1997-10-18
RIOR APPLICATION NUMBER: 60/064103
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PRIOR APPLICATION NUMBER: 60/082804
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PRIOR FILING DATE: 1998-05-05
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PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
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APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/081819
FILING DATE: 1998-04-15
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APPLICANT: Baker, Kevin P.
       ; PRIOR APPLICATION NUMBER: 60/169835
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Gerritsen, Mary
                                                                             Best Local Similarity 100. Matches 15; Conservative
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PRIOR PEPLICATION NUMBER: 60/095302
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26	28	29	30	3 -	35	3.6	3.6		3.6	3.7	. cc	3.6	4 C	4	42	4.3	44	45

ALIGNMENTS

New nucleic acid molecule useful for treating disease, e.g. infertility, Fibroblast growth factor-21; FGF-21; cell growth; cell differentiation; hepatic cell; cirrhosis; infertility; impotence; testicular cancer; leukemia; lymphoma; autoimmune disease; thymus proliferative disorder. Epitope-bearing portion of human fibroblast growth factor-21 (FGF-21). AAB68419 standard; peptide; 15 AA Claim 17; Page 40; 61pp; English impotence, or testicular cancer 16-NOV-2000; 2000WO-US031745. 18-NOV-1999; 99US-0166540P. 11-MAY-2000; 2000US-0203633P. 23-JUL-2001 (first entry) Itoh N, Kavanaugh WM; (CHIR) CHIRON CORP. (KYOU) UNIV KYOTO. WPI; 2001-343823/36. WO200136640-A2. Homo sapiens. 25-MAY-2001. RESULT 1

The present sequence represents an epitope-bearing portion of human fibroblast growth factor-21 (FGF-21). FGF proteins regulate growth and differentiation of a variety of cell types. FGF-21 nucleic acids and polypeptides are useful for treating diseases and disorders characterised by inadequate numbers of hepatic cells, preferably cirrhosis of the liver. They may also be used in the treatment of infertility, impotence, and testicular cancer, as well as leukemia, lymphoma, autoimmune disease, or proliferative disorders of the thymus

Sequence 15 AA;

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Length 15;

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Fibroblast growth factor 9; FGF-9; cytostatic; vulnerary; osteopathic; antiarthritic; vasculogenesis; angiogenesis; FGFR; skeletal disorder; fibroblast growth factor receptor; cancer; bone fracture healing; bone growth; wound healing; achondroplasia; hypochondroplasia; osteoporosis; cartilage defect; multiple myeloma.
Score 89; DB 4; Length L., Pred. No. 7.1e-06;
                                                                                                                                                Human FGF21 core structure amino acid sequence.
                                                                                                ABB81312 standard; protein; 124 AA.
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                         Conservative
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                                                                                                                                                                                                                                                                                                                     Bogin O, Adar R,
                Similarity
                                                                                                                                                                                                                                   WO200236732-A2
                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                   10-MAY-2002.
        Query Match
Best Local Simi
Matches 15;
                                                                                                                 ABB81312;
                                                                                         ABB81312
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The present invention describes an active variant (1) of a fibroblast growth factor (FGF) having at least one mutation in the beta-8-beta-9 crowth factor (FGF) having at least one receptor subtype compared to the corresponding wild type FGF by decreasing the biological activity the corresponding wild type FGF by decreasing the biological activity mediated by at least one receptor subtype while retaining the activity of execopathic and antiarthritic activities. (1) has cytostatic, vulnerary, osteopathic and antiarthritic activities. (1) can be used as a regulator of vasculogenesis or angiogenesis. (1) is useful for preparing a phormal FGF receptors (FGFRS), especially skeletal disorders, cancer, cabnormal FGF receptors (FGFRS), especially skeletal disorders, cancer, cabnormal FGF receptors (FGFRS), especially skeletal disorders, and wound healing processes. (1) is useful in detection and treatment of various FGFR related disorders including skeletal disorders e.g. achondroplasia, and osteoporosis, and cartilage defects, multiple bladder and cervical carcinoma. The novel mutants are useful in high expression systems unitable for pharmaceutical production, targeting of drugs or other agents to tissues and cells having special carcinoma of the formuse or other agents to tissues and cells having special carcinoma of and serve as template for the formation of improved agonists and activity and cancers. The presents a FGFR in various disorders and carcers and cancers. The presents a FGFR care structure amino acid antagonists of FGFRs in various disorders and care structure amino acid cancer. The present sequence represents a FGF core structure amino acid sequence which is given in the exemplification of the present invention New variants of fibroblast growth factor, useful for treating skeletal disorders including osteoporosis, malignancies and to enhance wound and Disclosure; Fig 1; 74pp; English fracture healing.

Sequence 124 AA;

Query Match

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The sequence represents a fragment of a fibroblast growth factor-like (FGF-like) polypeptide. FGF-like protein and its associated nucleic acid play a role in modulating body growth, maturation or life-span. They are play a role in modulating by growth, maturation or life-span. They are considered to seem the second disease, mucositis, forbur's disease, cirrhosis, inflammatory bowel disease, mucositis, crohn's disease, cirrhosis, inflammatory bowel disease, mucositis, controllegenerative and iseases, damage to renal tubules as a result of acute tubular necrosis, has matopoietic cell reconstitution following chemotherapy, wasting syndromes (e.g., cancer associated cachexia), damage to the corneal cyndromes (e.g., cancer associated cachexia), damage to the corneal cyndromes (e.g., cancer associated cachexia), damage to the corneal cyndromes, myopathies, short stature maturation, alopecia, abnormalities of androgen target organs, premature maturation, alopecia, abnormalities of androgen target organs, bronchopulmonary dysplasia, acute respiratory distress syndrome, tumours of the eye or other tissues, atherosolerosis, hypercholesterolemia, stroke, osteoporosis, osteoarthritis, muscle atrophy, sarcopenia, cardiac function, immune system dysfunction, cancer, Parkinson's disease,
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                                                                                                                                                                                                                                                                                                                                                                                                           inflammatory bowel disease, Croin's disease; Obesity; tubular necrosis; renal tubule damage; gastrointestinal abnormality; wasting syndrome; neurodegenerative disease; haematopoietic cell reconstitution; cachaxia; chemotherapy; corneal epithelium damage; retinal tissue damage; myopathy; multiple sclerosis; short stature; delayed maturation; excessive growth; acromegaly; premature maturation; alopecia; bronchopulmonary dysplasia; androgen target organ abnormality; respiratory distress syndrome; stroke; cancer; atherosclerosis; hypercholesterolaemia; osteoporosis; baldness; descensed stamina; decreased cardiac function; immune system dysfunction; parkinson's disease; Alzheimer's disease; decreased cognitive function;
                                                                                                                                                                                                                                                                                                                                                                                          treatment; cirrhogis; mucositis; diabetes;
                  Gaps
                                                                                                                                                                                                                                                                                                                                                 Human Fibroblast Growth Factor-like (FGF-like) polypeptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated fibroblast growth factor-like polypeptide useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating, preventing or ameliorating cirrhosis, inflammatory bowel disease, mucositis, Crohn's disease, diabetes, obesity, stroke and
                  ;
                  Indels
Pred. No. 5.6e-05;
Migmatches 0;
                    Migmatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Page 116-117; 138pp; English.
                                                                                                                                                                                                                    AAU00965 standard; protein; 181 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                    Fibroblast Growth Factor; FGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-SEP-1999; 99US-00391861.
23-AUG-2000; 2000US-00644052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-SEP-2000; 2000WO-US024373.
                                                                                                          101 HLPGNKSPHRDPAPR 115
                                                                   1 HLPGNKSPHRDPAPR 15
                                                                                                                                                                                                                                                                                                            (first entry)
                       15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  senile dementia; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-226743/23.
Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200118172-A2.
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                                                                                                                                                                                                                                                                                                            24-MAY-2001
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ID AAU0
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WPI; 2002-479754/51

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                                                                                     .;
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                                                                                                                                                                                                                                                                                                                                     Human, fibroblast growth factor; FGF; zFGF11; chromosome 19; restenosis; proliferation; mesenchymal cell; osteoblastic lineage cell; osteoporosis; chromosomal disorder; chondrosarcoma; atherosclerosis; obesity; fracture; bone formation; diabetes mellitus; neural cell development; angiogenesis; amyotrophic lateral sclerosis; cerebrovascular stroke; neuropathy; ulcer; congenital disorder; wound healing; cardiac function; glomerulonephritis; surfactant production; anorectic; ischaemia; neogenesis; hyperplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel zFGF11 polypeptide and polynucleotide, a member of fibroblast growth factor family, for stimulating proliferation of mesenchymal, osteoblastic lineage cells and treating diabetes, obesity, osteoporosis,
 senile dementia, Alzheimer's disease, and decreased cognitive function
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                         Human fibroblast growth factor (FGF) homologue, zFGF11 protein.
                                                                                      ;
0
                                                           Length 181;
                                                                                     0; Indels
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/label= Human_mature_zFGF11_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Heparin binding domain"
                                                            DB 4;
8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                            hypertension; cytostatic; vasotropic; therapy
                                                           Score 89; DB
Pred. No. 8e-0
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .27
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                       AAE05078 standard; protein; 208 AA.
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0
                                                            100.0%;
100.0%;
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                                                                                                                                                117 HLPGNKSPHRDPAPR 131
                                                                                                                     1 HLPGNKSPHRDPAPR 15
                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ZYMO ) ZYMOGENETICS INC
                                                                           Local Similarity 100.
nes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen Z;
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                                  Sequence 181 AA;
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                                                                                                                                                                                                                                                    AAE05078;
                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
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                                                                             Best Loc
Matches
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tresults in bone formation useful for treating bone defects, fractures, categorosis and other deficiencies in bone structure and formation.

Zeteoprosis and other deficiencies in bone structure and formation.

ZEGRII is useful for treating disorders associated with diabetes
mellitus, neural cell development or degeneration, amyotrophic lateral
consists, cerebrovascular stroke, neuropathy associated with lack of
maintenance of neuronal differentiation and congenital disorders of the
merintenance of neuronal differentiation and congenital disorders of the
merintenance of neuronal development, promoting angiogenesis
nervous system or lack of neuronal development, promoting angiogenesis
on wound healing, for revasuularisation in eps. complications related to
conform the conformation and dispetic food ulcers improving cardiac
conformation, modulating surfactant production in the lung epithelium, to
conformation production in the lung epithelium, to
conformation particularly in the heart or brain and for inducing skeletal
conformation of systemic and pulmonary hypertension. Antagonists of zegrii
conformation in the linhibiting disorders associated with kidney epithelium
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                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 89; DB 4; Length 208; 100.0%; Pred. No. 9.2e-05;
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2001WO-US006666.
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2000US-0220664P.
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                                                                                                                                                                                                                                                                                                           such as glomerulonephritis
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                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                  Sequence 208 AA;
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25-JUL-2000;
26-JUL-2000;
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24-AUG-2000;
10-NOV-2000;
28-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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US2002081663-A1
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                                     27-JUN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the the proliferation of, or gene expression, in pericyte cells, for stimulating the proliferation of differentiation of chondrocyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating or inhibiting the proliferation of normal human blood, fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AU83592-AAU83713 represent human PRO protein sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28. .208
/note= "Mature fibroblast growth factor homologue,
zFGF11. This sequence is specifically claimed in claim 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, fibroblast growth factor; FGF, zFGF11; mesenchymal cell; FGFRIIIc; osteoblastic lineage cell; diabetes mellitus; neuropathy; neural cell develbyment, amyotrophic lateral sclerosis; cerebrovagcular stroke; neuronal differentiation; congenital disorder; nervous system disorder; cardiac function; wound healing.
                                                                                                                                                                                                                                               One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumors such as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or liver tumor.
                                                                                                                                                                                                                                                                                                                                                                               The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 RRO polymucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder.
                                                                                                                                      Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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/label=_Signal_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG32358 standard; protein; 208 AA.
                                                                                                                                                                                                                                                                                                                                              Claim 11; Fig 78; 359pp; English.
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                   10-MAX-2001; 2001US-00854208
10-MAX-2001; 2001US-00854280
25-MAX-2001; 2001WO-US017092
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       22-MAR-2001; 2001US-00816744
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Best Local Similarity luv..
Best Local Similarity Lov..
And 15; Conservative
                                                                                                                                        Desnoyers L,
C, Gurney AL,
                                                                                                  (GETH ) GENENTECH INC
                                                                                                                                                                                             WPI; 2002-172001/22.
                                                                                                                                                                                                                 N-PSDB; ABK33574
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                                                                                                                                        Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG32358;
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Human; extracellular messenger; neurological disorder; epilepsy; XWES-3; Alzheimer's disease; autoimmune disorder; renal tubular acidosis; stroke; acquired immune deficiency syndrome; AlDS; Addison's disease; cytostatic; developmental disorder; anaemia; Cushing's syndrome; endocrine disorder; vascular malformation; cell proliferative disorder; gene therapy; cancer; hypertpyroidism; proppituliarism; hypothyroidism; antiheminthic; hypertpyroidism; gonadal steroid hormone; panoreatic disorder; nootropic; diabetes mellitus; immunosuppressive; anti-inflammatory; antibacterial; antiviral; antifungal; parasitic; protozoal; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated human polypeptide (1) for zFGF11 (a fibroblast growth factor), and the encoding polynucleotide (II). (I) and (II) are used in methods of the invention stimulating proliferation of mesenchymal cells, detecting the presence of zFGF11 in a biological sample, detecting the presence of FGFRIIC in a biological sample and stimulating proliferation of osteoblastic lineage cells. The polypeptides, nucleic acid and/or antibodies of the invention may be used in treatment of disorders associated with diabetes mellitus, neural cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               development or degeneration, amyotrophic lateral sclerosis, cerebrovascular stroke, neuropathy associated with lack of maintenance of neuronal differentiation, and congenital disorders of the nervous system or lack of neuronal development. Molecules of the invention may also be useful for improving cardiac function and for promoting wound healing of the epidermis. The present sequence represents the amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptide for zFGFI1 (fibroblast growth factor) useful in treatment of disorders associated with diabetes mellitus, neural cell development or degeneration, amyotrophic lateral sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 89; DB 5; I
100.0%; Pred. No. 9.2e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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05-JAN-2001; 2001US-00755695.
                                                                          05-JAN-2000; 2000US-0174526P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cerebrovascular stroke.
                                                                                                                                                                                                                                                               Chen Z;
                                                                                                                                                     (CONK/) CONKLIN D C.
                                                                                                                                                                                                                                                                                                                                      WPI; 2002-626540/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABK91310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 208 AA;
                                                                                                                                                                                            (CHEN/) CHEN Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ното варіепв.
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                                                                                                                                                                                                                                                           Conklin DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human zFGF11
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Matches
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                                                                                                                                                                                                                                                                             The present invention relates to new extracellular messenger polypeptides and polynuclectides encoding them. XMES is useful in the diagnosis, treatment and prevention of neurological disorders (e.g. epilepsy, stroke, or Alzheimer's disease), autoimmune/inflammatory disorders (e.g. educined immune deficiency syndrome, AIDS, Addison's disease, or allergies), developmental disorders (e.g. renal tubular acidosis, anaemia allergies), asyndrome), endocrine disorders (e.g. hypophysectomy, aneurysm or vascular malforantion), and cell proliferative disorders (e.g. cancer), and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of extracellular messengers. XMES may also be used in the treatment of viral, bacterial, fungal, parasitic, protozoal and helminthic infections, trauma, disorders associated with hypopituitarism, hyperthyroidism or gonadal steroid hormones, and pancreatic disorders such as type II diabetes mellitus. The XMES may be used for somatic or germline gene therapy. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; PRO polypeptide; secreted and transmembrane protein; anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
                                                                                                                             Nguyen DB, Walia N, Gandhi AR, Azimzai Y; Lu Y, Baughn MR, Duggan BM, Lee S, Hafalia A;
                                                                                                                                                                                                            New extracellular messenger polypeptides and polynucleotides encoding them, useful for diagnosing, treating or preventing e.g. neurological, autoimmune, inflammatory, developmental and endocrine disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU80777 standard; protein; 208 AA.
                                                                                                                                                                                                                                                              Claim 1; Page 111; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence is human XMES-3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-2002; 2002US-00230163.
                                                          06-JUN-2000; 2000US-0210233P.
23-JUN-2000; 2000US-0213465P.
14-NOV-2000; 2000US-0249019P.
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                                     36-JUN-2001; 2001WO-US018476
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                                                                                                           (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO polypeptide #39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100..
Best Local 15; Conservative
                                                                                                                                 Yue H, He A,
O, Tang YT,
                                                                                                                                                                                WPI; 2002-154573/20.
                                                                                                                                                                                            N-PSDB; AAD28493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 208 AA;
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                                                                                                                                                          Policky JL;
                 13-DEC-2001
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                                                                                                                                              Bandman O,
                                                                                                                                   Lal P,
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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the diagnostis and treatment of tumours. Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ABU80739-ABU80860 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the
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                                                                                                                                                                                               Godowski PJ;
~~ Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                      One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Smith V, Stephan JF, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 208;
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100.0%; Pred. No. 9.2e-05;
Live 0; Mismatches 0;
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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25-JUL-2000; 2000US-0220638P.
01-JUN-2001; 2001MO-US017800.
29-JUN-2001; 2001MO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                 Desnoyers L,
                                                                                                                                                                   (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                    WPI; 2003-342045/32.
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Best Local Similarity
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Grimaldi JC,
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Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI;

Baker KP, Desnoyers L, Grimaldi JC, Gurney AL, (GETH) GENENTECH INC.

WPI; 2003-393229/37. N-PSDB; ACA68535.

2001WO-US017800. 2001WO-US021066.

25-JUL-2000; 01-JUN-2001;

12-AUG-2002; 2002US-00219003

US2003088063-A1

08-MAY-2003

29-JUN-2001; 2001WO-US021066 09-APR-2002; 2002US-00119480

One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.

The invention describes one hundred and eighty seven nucleic acids

Claim 11; Fig 78; 314pp; English

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Human; secreted and transmembrane protein; PRO; cardiant; cytostatic; antiangiogenic; hypotensive; vulnenry; antiarteriosclerotic; gene therapy; cardiovascular disorder; endothelial disorder; angiogenic disorder; cardiac hypertrophy; trauma; cancer; age-related macular degeneration; atherosclerosis; hypertension; arterial restenosis; rheumatoid arthritis; angina; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
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ABUB22
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The invention describes an isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 122 PRO (secreted and transmembrane) polypeptides whose sequences are fully defined in the specification; or (b) any of 122 nucleotide encoding sequences having e.g. 4834, 2504 or 1759 bp fully defined in the specification; or the FRO polypeptides or polymucleotides are useful complexities. The PRO polypeptides or polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour) in a mammal, for stimulating the release of TMF-alpha from human blood, for stimulating proliferation of pericyte cells, or for modulating colls, for stimulating proliferation of pericyte cells, or for modulating correcters (e.g. sports injuries or arthritis), or wounds. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, The PRO polypeptides are useful as molecular weight markers, or for chromosome also useful as molecular weight markers, or for chromosome canning libraries of human colls presence of those diseases. The PRO polypeptides are useful as hybridisation probes, or for screening libraries of human colls, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective control or transmembrane PRO polypeptide and no add sequence of a novel human secreted and transmembrane PRO polypeptide
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                                                                                                                                                                                                                                                                                                                                     New genes, and its encoded secreted and transmembrane polypeptides, useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or pericyte proliferation, especially for treating lung tumors, arthritis or
                                                                        Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
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                                                                                      Desnoyers L,
2, Gurney AL,
(GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             wounds in a mammal
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                                                                                                                              Grimaldi JC,
                                                                                      Baker KP,
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                                                                                                                                                                                                                                                                                                                                       encoding novel human secreted and transmembrane (PRO) polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, agerelated macular degeneration, atherosclerosis, hypertension, arterial restenoisis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, fibroblast growth factor 21; FGF-21; chromosome 19; 19q13.1-qter; diabetes; obesity; antidiabetic; anorectic; type 2 diabetes; type 1 diabetes.
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10-JAN-2002; 2002US-0347991P.
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Best Local S
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                                                                                                                                                                           The present sequence represents human fibroblast growth factor 21 (FGF-21). FGF-21 is located to chromosome 19, more specifically to 19q13.1-
cath. The present invention describes a method for treating a mammal exhibiting type 2 diabetes or type 1 diabetes, or treating a mammal cookesity which comprises administering to the mammal a composition cookesity which comprises administering to the mammal a composition comprising FGF-21 which has at least 95% amino acid sequence identity to the 20% amino acid sequence given in ABP96156. Also described: (1) inducing an increase in glucose uptake in adipocyte cells by administering FGF-21 to induce an increase in glucose uptake; and (2) administering a medicament for treating type 1 diabetes, type 2 diabetes cor obesity in a mammal using FGF-21 having 95% amino acid sequence identity to ABP96156. FGF-21 has antidiabetic and anorectic activities. The method is useful for treating a mammal exhibiting type 2 or 1 the method is preferably useful for treating a mammal for obesity. The method is preferably useful for treating to besity the method is preferably useful for besity the corresponding and for treating and mammal for type 2 diabetes, and for treating and mammal for obesity. The method is preferably useful for besity and for treating and mammal for type 2 diabetes, and for treating domestic animals for obesity
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                                                                                                     Treating a mammal exhibiting Type 2 diabetes or Type 1 diabetes or obesity, by administering composition comprising fibroblast growth factor
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Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte; differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
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100.0%; Pred. No. 9.2e-05;
iive 0; Mismatches 0; Indels
                                      Kharitonenkov A,
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                                                                                                                                                           Claim 3; Fig 1; 32pp; English.
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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nes 15; Conservative
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             (ELIL ) LILLY & CO ELI
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                                                                 WPI; 2003-248106/24
                                                                              N-PSDB; ABZ79797
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 208 AA;
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                                         Glasebrook AL,
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                                                                                                                                                                                                                                 The invention relates to a novel isolated nucleic acid encoding a fully defined PRO polypeptide. The molecules of the invention may be useful for stimulating proliferation or gene expression in periorre cells or the release of TNF-alpha from human blood. Other possible uses include the atimulation or inhibition of chondrocyte proliferation or inhibition of chondrocyte proliferation or proliferation of mannation of human dermal fibroblast cell proliferation and the detection of the presence of a tumour within a mammal. Purthermore, the nucleic acid may be useful for the manufacture of a medicament for diagnosing or treating a tumour within a mammal or for measuring or detecting the expression of an associated gene, as well as during gene therapy. The current sequence is that of the human PRO protein of the invention
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r Wood WI;
                                                New nucleic acid encoding for a PRO protein, useful for the manufacture of a medicament for diagnosing or treating tumors or for measuring or
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Smith V, Stephan JF, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Match 100.0%; Score 89; DB 6; Length 208; Local Similarity 100.0%; Pred. No. 9.2e-05; les 15; Conservative 0; Mismatches 0; Indels
                                                                                                                     detecting expression of an associated gene
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                                                                                                                                                                                      Claim 11; Fig 78; 315pp; English
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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N-PSDB; ABT44264.
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ID ABJ
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acid. The nucleic acid of the invention may be useful for preparing PRO polypeptides and anti-PRO antibodies for detecting the presence of a tummour in a mammal. Furthermore, the molecules of the invention may be useful for stimulating proliferation or gene expression in pericyte cells, the release of tummour necrosis factor (TNF) alpha from human blood, the proliferation or differentiation of fondrocyte cells and for inhibiting the proliferation of normal human dermal fibroblast cells. Finally, the molecules may be utilised during gene therapy. The current sequence is that of the human PRO protein of the invention
          888888888888888
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Sequence 208 AA;

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  Length 208;
                            0; Indels
  100.0%; Score 89; DB 6; I
100.0%; Pred. No. 9.2e-05;
                             Mismatches
                             .;
0
                                                        1 HLPGNKSPHRDPAPR 15
Query Match
Best Local Similarity 100.0
Matches 15; Conservative
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0;

Gaps

144 HLPGNKSPHRDPAPR 158

ABO34289 standard; protein; 208 AA. 19-SEP-2003 (first entry) ABO34289; RESULT 14 ABO34289

Human secreted/transmembrane polypeptide PRO 10196.

Human, chondrocyte stimulation; TNF-alpha stimulation; gene therapy; human dermal fibroblast stimulation; tumour; tissue typing;

affinity purification

Homo sapiens

US2003044934-A1.

06-MAR-2003

28-AUG-2002; 2002US-00230338.

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480. 29-JUN-2001; 09-APR-2002;

08-JAN-2003; 2003WO-US000010. 15-JAN-2002; 2002US-0348890P.

Kharitonenkov A;

Heuer JG,

WPI; 2003-618118/58.

(ELIL) LILLY & CO ELI

(GETH) GENENTECH INC.

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

WPI; 2003-492274/46. N-PSDB; ACD82214. New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes.

Claim 19; Fig 78; 315pp; English.

The invention relates to an isolated nucleic acid encoding a PRO polypeptide. Nucleic acids that encode PRO can be used to generate either transgenic animals or knock-out animals useful in developing and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy for replacing defective gene, in chromosome identification, as chromosome markers, or in generating probes to isolate full length PRO cDNA. The PRO POLYpeptides are useful for chondrocyte stimulation, TNR-alpha stimulation, human dermal fibroblasts stimulation and for detecting the presence of tumour in an mammal. The PRO polypeptides are useful as molecular markers for protein electrophoresis and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in

The present invention describes a method for the reduction of mortality and morbidity in critically ill patients, which involves the administration of fibroblast growth factor 21 (FGF-21) (1). (1) has cantiniflammatory, respiratory, antibacterial, immunosuppressive, vasotropic, haemostatic and nephrotropic activities, and can be used as a glucose level regulator, a glucose uptake stimulator, and an insulin esnsitivity enhancer. (1) can be used in the manufacture of a medicament for the reduction of morbidity and mortality in critically ill patients suffering from systemic inflammatory response syndrome (SIRS), respiratory distress, acute lung injury, acute respiratory distress acute lung injury, acute respiratory distress syndrome, multiple organ dysfunction syndrome, sepsis and chronic obstructive pulmonary disease (e.g. emphysema and chronic bronchitis). The SIRS includes pancreatitis, ischaemia, multiple trauma and tissue injury, haemorrhagic shock, immune-mediated organ injury, shock and renal

Use of fibroblast growth factor 21 for reduction of mortality and morbidity in patients suffering from e.g. systemic inflammatory response syndrome and acute respiratory distress syndrome.

Disclosure, Page 15-16; 22pp; English

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0
tissue typing, Anti-PRO antibodies are useful in diagnostic assays for PRO and in affinity purification of PRO from recombinant cell culture or natural sources. The present sequence represents the amino acid sequence of a human secreted/transmembrane PRO polypeptide
                                                                                                                                                                                                                                                                                                                                mortality; morbidity; fibroblast growth factor 21; FGF-21; antinflammatory; respiratory; antibacterial; immunosuppressive; vasotropic; haemostatic; nephrotropic; glucose level regulator; glucose uptake stimulator; insulin is spatievity enhancer; respiratory systemic inflammatory response syndrome; respiratory distress; acute lung injury; acute respiratory distress syndrome; multiple organ dysfunction syndrome; sepais; chronic obstructive pulmonary disease; emphysema; chronic bronchitis; pancreatitis; ischaemia; multiple trauma; tissue injury; haemorrhagic shock; immune-mediated organ injury; shock; renal failure.
                                                                                                                 Gaps
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                                                                                         Length 208;
                                                                                                                Indels
                                                                                         100.0%; Score 89; DB 6; I
100.0%; Pred. No. 9.2e-05;
                                                                                                                                                                                                                                                                                                            Human fibroblast growth factor 21 SEQ ID NO:1.
                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                  ADA37038 standard; protein; 208 AA.
                                                                                                                                                                144 HLPGNKSPHRDPAPR 158
                                                                                                                                            1 HLPGNKSPHRDPAPR 15
                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                   15; Conservative
                                                                                                       Best Local Similarity
                                                                    Sequence 208 AA;
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This invention relates to one hundred and twenty two novel nucleic acids encoding human PRO membrane bound proteins or receptors. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, auryival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are
                                                                                                                                                                                                                  0;
failure. FGF-12 regulates glucose levels in response to nutrient digestion; affects the overall metabolic state and counter-acts negative side effects that occur during the body's stress response to sepsis; reduces morbidity and mortality that occurs in critically ill patients; and stimulates glucose uptake and enhances insulin senativity. The present sequence represents the human FGF-21 amino acid sequence, which is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard A, Godowski PJ;
phan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human membrane bound receptor/protein PRO10196 amino acid sequence.
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                                                                                                                                                                                 Length 208;
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                                                                                                                                                                                 100.0%; Score 89; DB 7; I
100.0%; Pred. No. 9.2e-05;
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Smith V, Stephan JF,
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
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                                                                                                                                                                                                                                                                               HLPGNKSPHRDPAPR 158
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Grimaldi JC, Gurney AL,
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                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                 Sequence 208 AA;
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09-APR-2002;
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Matches
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received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the mamufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is the amino acid sequence of a human PRO protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New PRO polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human, secreted and transmembrane protein, PRO; cytostatic; vulnerary; antiarthritic, pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF) -alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes an isolated PRO (secreted and transmembrane) polymeptide (1). PRO982, PRO1160, PRO1187 or PRO1329 polymeptide are useful for stimulating the proliferation of or gene expression in
                                                                                                                                                                                                                                                                                                                   Gaps
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phan JF, Watanabe CK, Wood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                             Length 208;
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                                                                                                                                                                                                                                                                             100.0%; Score 89; DB 7; I
100.0%; Pred. No. 9.2e-05;
tive 0; Mismatches 0;
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Stephan JF,
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Smith V,
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-644806/61.
N-PSDB; ADB83567.
                                                                                                                                                                                                                                                                                                    Local Similarity
Les 15; Conserv
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Grimaldi JC,
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pericyte cells. PR0357, PR0229, PR01272 or PR04405 polypeptide are useful cells. PR0357, PR0229, PR01155, PR0136 or PR01419 polypeptide cells. PR0357, PR0357, PR01356, PR01349 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF) alpha from human blood. PR0982, PR0357, PR01365, PR01419, PR0214, PR0214, PR02137, PR01305, PR01036, PR010419, PR0214, PR02137, PR01305, PR01036, PR010181, PR01126, PR01031, PR01031, PR01031, PR01313, PR01256, PR01181, PR01317, PR01305, PR01313, PR01314, PR01317, PR01316, PR01317, PR01316, PR01318, PR01317, PR01316, PR01317, PR01316, PR01317, PR01316, PR01318, PR01317, PR01316, PR01318, PR01317, PR01316, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR01318, PR
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100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05; ive 0; Mismatches 0; Indels 100.08; *** 1 HLPGNKSPHRDPAPR 15 Query Match Best Local Similarity 100.0 Matches 15; Conservative 144 HLPGNKSPHRDPAPR Sequence 208 AA;

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Gaps

0;

ADB80674 standard; protein; 208 AA 04-DEC-2003 (first entry) ADB80674; RESULT 18 ADB80674

Novel human secreted and transmembrane protein PRO10196.

Human, secreted and transmembrane protein, PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF) - alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; gene therapy.

Ното варіепв.

US2003088068-A1

08-MAY-2003

13-AUG-2002; 2002US-00219481.

01-JUN-2001; 2001WO-US017800

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The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (1). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

to useful for stimulating the proliferation of or gene expression in

periopte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful

cells. PRO311, PRO357, PRO725, PRO1306 or PRO1419 polypeptide

cells. PRO311, PRO357, PRO725, PRO1306 or PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TMF)-

are useful for stimulating the release of tumour necrosis factor (TMF)-

are useful for stimulating the release of tumour necrosis factor (TMF)-

RRO125, PRO1314, PRO326, PRO351, PRO1035, PRO1419, PRO1419, PRO1414,

PRO1330, PRO1347, PRO1367, PRO1367, PRO1401, PRO1414, PRO1304,

RRO126, PRO1330, PRO1387, PRO1367, PRO1401, PRO1414, PRO1312,

RRO126, PRO1330, PRO1387, PRO1367, PRO1404, PRO1347, PRO1404, PRO1326,

RRO126, PRO1326, PRO4341, PRO1801, PRO4333, PRO1444, PRO1321, PRO1364, PRO1365, PRO1481, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO18
                                                                                                                                                                                                                                                      One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                      Wood WI;
                                                                                                                Goddard A, Godowski PJ;
phan JF, Watanabe CK, W
                                                                                                                Gerritsen ME, Goddard Smith V, Stephan JF,
                                                                                                                                                                                                                                                                                                                                                             Claim 11; Fig 78; 305pp; English
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                  Desnoyers L,
                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                          WPI; 2003-657982/62.
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                                                                                                                                              Grimaldi JC,
                                                                                                                     Baker KP,
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Gaps 0; 100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05; 0; Indels 0; Mismatches ADB73215 standard; protein; 208 AA. 1 HLPGNKSPHRDPAPR 15 Query Match Best Local Similarity 100. Matches 15; Conservative ADB73215; RESULT 19 ADB73215 g 田城北城市城田 ð

Novel human secreted and transmembrane protein PRO10196 04-DEC-2003 (first entry)

Sequence 208 AA

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22-MAY-2003
XXCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCX
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antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                                                                                                                    release;
    secreted and transmembrane protein; PRO; cytostatic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                  gene therapy
human;
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Homo sapiens.

JS2003096968-A1

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480. 29-AUG-2002; 2002US-00232223

(GETH) GENENTECH INC.

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Desnoyers L, Grimaldi JC, Baker KP,

2003-765525/72. WPI; 2003-765525, N-PSDB; ADB73214. New isolated PRO polypeptides useful as molecular weight markers in protein electrophoresis, useful for tissue typing, and for treating arthritis and tumors.

Claim 11; Fig 78; 308pp; English.

The invention describes an isolated PRO (secreted and transmembrane)

Cypyptide (I) PRO982, PRO1160, PRO1187 or PRO1392 polypeptide are

useful for stimulating the proliferation of or gene expression in

periove cells. PRO357, PRO212, PRO1272 or PRO4165 polypeptide are useful

cor stimulating the proliferation of differantiation of chondrocyte

cells. PRO357, PRO502, PRO3136, PRO1160, PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TMF)
alpha from human blood. PRO982, PRO3197, PRO175, PRO1160, PRO1419, PRO214,

PRO147, PRO3137, PRO5126, PRO1065, PRO6109, PRO1061, PRO1161,

PRO1266, PRO1181, PRO1186, PRO1187, PRO1197, PRO1174, PRO1111,

PRO1286, PRO1181, PRO1186, PRO1186, PRO1187, PRO1174, PRO1197,

PRO1181, PRO5139, PRO9183 or PRO11095, PRO1197, PRO1174, PRO1117,

PRO1181, PRO5129, PRO9183 or PRO11095 pRO1197, PRO1174, PRO3127,

PRO1181, PRO529, PRO9186, PRO1181, PRO1187, PRO1181, PRO1181,

PRO5181, PRO529, PRO9186, PRO1181, PRO1187, PRO1181, PRO1181,

PRO5181, PRO5182, PRO7184, Or PRO7182, PRO1188, PRO4132, PRO4189,

PRO5184, PRO5185, PRO7184, PRO1184, PRO1174, PRO5181, PRO4181,

PRO5184, PRO5185, PRO7184, PRO1184, PRO1197, PRO1181, PRO4186,

PRO5184, PRO5185, PRO7184, PRO1184, PRO1197, PRO1184, PRO4186,

PRO5184, PRO529, PRO9186, PRO1184, PRO1177, PRO1184, PRO4181,

PRO5184, PRO529, PRO9186, PRO1184, PRO1177, PRO1184, PRO4181,

PRO5184, PRO529, PRO9186, PRO1184, PRO1177, PRO1184, PRO4181,

PRO5184, PRO529, PRO9186, PRO1184, PRO1177, PRO1184, PRO4181,

PRO5184, PRO529, PRO9186, PRO1184, PRO1187, PRO1184, PRO5778, PRO4408,

PRO5184, PRO5184, PRO5004, PRO4981, PRO1174, PRO5778, PRO4408,

PRO5184, PRO5184 PRO5184, PRO5004, PRO4981, PRO7174, PRO5778, PRO4408,

PRO5185, PRO5186, PRO5004, PRO4981, PRO5778, PRO4408,

PRO5186, PRO5186, PRO5004, PRO4981, PRO5778, PRO4408,

PRO5187, PRO5187, PRO5004, PRO5004, PRO5778, PRO5778, PRO5778,

PRO5185, PRO5004, PRO5004, PRO4981, PRO5778, PRO5778, PRO5778,

PRO5185, PRO5004, PRO5004, PRO4981, PRO5778, PRO5778, PRO5778,

PRO5185, PRO5004, ransmembrane PRO polypeptide

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The Intellibration describes an insurance rect and transference are trained to the intellibration of or projection are useful for stimulating the proliferation of or gene expression in perioty-cells. PRO357, PRO259, PRO150. PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrossis factor (TNE)-are baseful for stimulating the release of tumour necrossis factor (TNE)-alpha from human blood. PRO363, PRO351, PRO155, PRO1419, PRO1419, PRO214, PRO247, PRO337, PRO566, PRO180, PRO1060, PRO1080, PRO1141, PRO1104, PRO1106, PRO1195, PRO1195, PRO1195, PRO1195, PRO1195, PRO1195, PRO1195, PRO1195, PRO1195, PRO1197, PRO1196, PRO1197, PRO1340, PRO1340, PRO1340, PRO3444, PRO1340, PRO1343, PRO3444, PRO1340, PRO3444, PRO1567, PRO1847, PRO1967, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO1867, PRO18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor alpha release;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated PRO polypeptide useful for tissue typing, gene therapy, amplecular weight markers in protein electrophoresis, and for treating arthritis and tumors.
                                                         Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes an isolated PRO (secreted and transmembrane)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colon tumour, breast tumour, prostate tumour; rectal tumour; liver tumour, tissue typing; chromosome mapping; gene mapping;
  Length 208;
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human secreted and transmembrane protein PRO10196.
100.0%; Score 89; DB 7; I
100.0%; Pred. No. 9.2e-05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                ADB78297 standard; protein; 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-2002; 2002US-00219478.
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                               144 HLPGNKSPHRDPAPR 158
                                                                                                            1 HLPGNKSPHRDPAPR 15
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                         Local Similarity 100.
hes 15; Conservative
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N-PSDB; ADB78296.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                            04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                         ADB78297;
  Query Match
                                                         Matches
                                                                                                                                                                                                                                               RESULT 20
                                                                                                                                                                                                                                                                            ADB78297
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PROJES, PRO229, PRO788, PRO1194, PRO1272, PRO1468, PRO4302, PRO4408, PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4914, PRO5778, PRO5732, etc., are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides involves tample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung is indicative of the presence of tumour in the mammal.
                                                                                                                                                                                                                                                                                                                                     tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or tumour, colon tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO157, PRO129, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and
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Sequence 208 AA;

Gaps . 100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05; rive 0; Mismatches 0; Indels 144 HLPGNKSPHRDPAPR 158 1 HLPGNKSPHRDPAPR 15 15; Conservative Local Similarity Query Match Matches

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RESULT 21 ADB84945

ADB84945 standard; protein; 208 AA. 04-DEC-2003 (first entry) ADB84945;

Human, PRO; secreted polypeptide, transmembrane polypeptide, tumour, cancer, lung; colon, breast; prostate, rectum, liver; tumour necrosis factor-alpha; TNF-alpha; blood, chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic. Human PRO polypeptide #39.

Ното варіелв.

US2003073817-A1

17-APR-2003

26-AUG-2002; 2002US-00227883.

01-AUG-2000; 2000US-0222425P. 01-JUN-2001; 2001W0-US017800. 29-JUN-2001; 2001W0-US021066. 09-APR-2002; 2002US-00119480. 01-AUG-2000;

(GETH) GENENTECH INC.

Goddard A, Godowski PJ; sphan JF, Watanabe CK, Wood WI; Gerritsen ME, Goddard Smith V, Stephan JF, Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

2003-730024/69 N-PSDB; ADB84944 New PRO polypeptides and nucleic acids encoding the polypeptides, useful e.g. in gene therapy, disease diagnosis, chromosome identification and tissue typing.

Claim 11; Fig 78; 314pp; English

transmembrane polypeptides) and the PRO polymucleotides encoding them.
The PRO polypeptides and polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TRP) alpha from human blood, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene chordrocyte cells, for stimulating the proliferation of or gene chordrocyte cells, for stimulating the proliferation of or gene chordrocyte cells, for stimulating the proliferation of or gene chordrocyte cells, in chromosome and gene mapping, in generating as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant creagents, in gene therapy, in chromosome identification, as chromosome reagents, in gene therapy, in chromosome identification, as chromosome condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartiage disorders (e.g. arthritis, sports injuries), involving inducing the re-differentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention. ö Gaps ·; invention relates to human PRO polypeptides (secreted and Length 208; 0; Indels 100.0%; Score 89; DB 7; I 100.0%; Pred. No. 9.2e-05; 0; Mismatches 144 HLPGNKSPHRDPAPR 158 1 HLPGNKSPHRDPAPR 15 Conservative Local Similarity tes 15; Conserv Sequence 208 AA; Query Match Matches à d

ADB78051

ADB78051 standard; protein; 208 AA. ADB78051;

04-DEC-2003

Novel human secreted and transmembrane protein PRO10196.

(first entry)

Human; secreted and transmembrane protein, PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; prostate tumour; prostate tumour; colon tumour; prostate tumour; colon tumour; prostate tumour; colon tumour; prostate tumour; p gene therapy

Homo sapiens

US2003092886-A1.

15-MAY-2003.

09-AUG-2002; 2002US-00216165. PARTHER STATES OF THE STATES O

25-JUL-2000; 2000US-0220607P. 01-JUN-2001; 2001UV-95017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Godowski PJ; Goddard A, Gerritsen ME, Desnoyers L, Baker KP,

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The invention describes an isolated PRO (secreted and transmembrane)

CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

CC useful for stimulating the proliferation of or gene expression in

Dericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are

CC cells. PRO31, PRO357, PRO229, PRO1275 pro1419 polypeptide

CC cells. PRO31, PRO357, PRO325, PRO1155, PRO1306 or PRO1419 polypeptide

CC are useful for stimulating the release of tumour necrosis factor (TMP)-

CC alba from human blood. PRO982, PRO357, PRO1306, PRO1419, PRO1419,

CC RRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1130,

CC PRO1025, PRO1134, PRO1826, PRO1105, PRO1031, PRO1419, PRO1412,

CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1431, PRO1341, PRO1330,

CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1444, PRO1414, PRO1326,

CRO9940, PRO6079, PRO9836 or PRO10056 polypeptide are useful for

CC PRO1887, PRO523, PRO788, PRO1194, PRO1331, PRO1484, PRO4322,

CRO9940, PRO6079, PRO9836 or PRO10056 polypeptide are useful for

CC PRO1881, PRO5229, PRO7184, or PRO1194, PRO1488, PRO4302, PRO4408,

CC PRO181, PRO5229, PRO7184, or PRO1408, PRO1488, PRO4312, etc.,

CC PRO181, PRO5229, PRO7184, or PRO4981, PRO1488, PRO4312, etc.,

CC PRO181, PRO5229, PRO7184, or PRO4981, PRO1488, PRO4332, etc.,

CC PRO181, PRO5229, PRO7184, or PRO4981, PRO1488, PRO4332, etc.,

CC PRO181, PRO5229, PRO7184, or PRO4981, PRO1348, PRO4332, etc.,

CC PRO181, PRO5229, PRO7184, or PRO4981, PRO1374, PRO5778, PRO4408,

CC Inhibiting the proliferation of normal human dermal tibroblast cells. PRO

CC Inhibiting the proliferation of normal human dermal tibroblast

CC Involves comparing the level of expression of the above PRO polypeptides

CC Involves comparing the test sample as compared to the control sample

CC Involves comparing the test sample as compared to the control sample

CC HUMOUT, colon tumour, breast tumour, prostate tumour, rectal tumour is linear mannal cells and presence of tumour, prostate tumour, rectal tumour problem mannal cells and propertic
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  Wood WI;
                                                                                                                        Novel isolated PRO polypeptide useful for tissue typing, gene therapy, molecular weight markers in protein electrophoresis, for treating
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  Watanabe CK,
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Stephan JF,
Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB87117 standard; protein; 208 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         typing, or as there and maeful for chromosome and
Grimaldi JC, Gurney AL,
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                                                 2003-765494/72
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                                                                                                                                                                          arthritis, tumor.
                                                                         N-PSDB; ADB78050
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ADB87117
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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polynucleotides encoding them.

The PRO polypeptides and polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TMF)-alpha from human blood, for stimulating the proliferation of differentiation of chondrocyte cells, for stimulating the proliferation of or gene capression in pericyte cells or for stimulating the proliferation of or gene normal human dermal fibroblasts. The PRO nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, in generating chordination probes, in chromosome and gene mapping, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents, in gene therapy, in chromosome identification, as chromosome antibodies, are useful for preparing a medicament for treating a mainibodies, are useful for preparing a medicament for treating a mainibodies, and the sesponsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartiage antibodies, such as pericyte-associated tumours and bone and/or cartiage antibodies, such as pericyte-associated tumours and bone and/or cartiage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                               Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
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                                                                                                                                                    13-AUG-2002; 2002US-00219479.
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29-JUN-2001; 2001MO-US021066.
09-APR-2002; 2002US-00119480.
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Grimaldi JC, Gurney AL,
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-657981/62.
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                                                               US2003088067-A1
                      Homo sapiens.
                                                                                                           08-MAY-2003
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Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
Human, PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.
                                                                                                                               24-FEB-2000; 2000WO-US005004.
02-WAR-2000; 2000WO-US005841.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                       14-AUG-2002; 2002US-00219536.
                                                                                                                        99US-0146222P
                                                                                                                                                                                                    Desnoyers L,
I, Gurney AL,
                                                                                                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                                                                              2003-777259/73.
                                                                                                                                                                                                                                       N-PSDB; ADB84698.
                                                                     US2003092890-A1
                                                                                                                                                                                                    Baker KP, Der
Grimaldi JC,
                                                    Homo sapiens
                                                                                                                        28-JUL-1999;
                                                                                      15-MAY-2003
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as New isolated PRO polypeptides, useful for tissue typing, gene therapy, molecular weight markers in protein electrophoresis, and for treating arthritis and tumors.

Claim 11; Fig 78; 308pp; English.

The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polypeptides encoding them.

The PRO polypeptides and polymuclectides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours rectal tumour, colon tumour, breast tumour, colon tumour, breast tumour, colon tumour, breast tumour, colon tumour, breast tumour, colon tumour, breast tumour, colon tumour, rectal tumour or liver tumour) in a mammal, for stimulating the proliferation of diamulating the proliferation of condition probes, in crimulating the proliferation of conditions probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant technology, in generating transgenic animals of therapeutically useful reagenes, in chromosome and gene mapping, in generating probes. The PRO polypeptides by recombinant technology, in generating probes. The PRO polypeptides, or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the recombined and secular markers for protein electrophoresis, and in tissue typing. This equence represents a human PRO polypeptide of the invention.

Sequence 208 AA;

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Gaps
                           ;
100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05; ive 0; Mismatches 0; Indels
  100.0%; r-
0;
                           15; Conservative
             Local Similarity
  Query Match
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144 HLPGNKSPHRDPAPR 158

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1 HLPGNKSPHRDPAPR 15
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ADB83814 standard; protein; 208 AA

ADB83814;

(first entry) 04-DEC-2003 Novel human secreted and transmembrane protein PRO10196.

release; human, secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping; gene therapy

Homo sapiens.

US2003069397-A1.

10-APR-2003.

09-AUG-2002; 2002US-00216159.

25-JUL-2000; 2000US-0220607P. 01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

WPI; 2003-657584/62. N-PSDB; ADB83813. New isolated polypeptides designated PRO polypeptides including polypeptides useful for stimulating the proliferation or differentiation of specific cell types, and for diagnosing cancer.

Claim 11; Fig 78; 314pp; English.

The invention describes an isolated PRO (secreted and transmembrane)

Complypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

Complying the proliferation of or gene expression in

Complying the proliferation of or gene expression in

Complying the proliferation of deficientiation of chondrocyte

Complying PRO357, PRO229, PRO1152, PRO1419 polypeptide

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Complying the same cell type, where a higher level of expression of the presence of tumour in the mammal. The tumour is lung time indicative of the presence of tumour in the mammal. The tumour of tumour is lungur tumour.

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RESULT 25 ADB83814

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes an isolated PRO (secreted and transmembrane) polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO351, PRO357, PRO1155, PRO1156, PRO1316 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TMF)-alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214, PRO347, PRO357, PRO56, PRO366, PRO1606, PRO10011, PRO1111, PRO1309,
typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PJ;
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                    human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiathritic; perioyte cell proliferation; chondrocyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNR)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated PRO polypeptide useful for tissue typing, gene therapy, molecular weight markers, for treating arthritis, tumor.
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Smith V, Stephan JF, Watanabe CK,
                                                                                                                         Score 89; DB 7; Length 208;
Pred. No. 9.2e-05;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                               Novel human secreted and transmembrane protein PRO10196.
                                                                                                                                                                                                                                                                   ADB72969 standard; protein; 208 AA
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09-APR-2002; 2002US-00119480.
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Best Local Similarity 100.
Matches 15; Conservative
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N-PSDB; ADB72968.
                                                                                                    Sequence 208 AA;
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Grimaldi JC,
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PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412, PRO1340, PRO1340, PRO1340, PRO1340, PRO1340, PRO1340, PRO1340, PRO1340, PRO1340, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO1341, PRO
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phan JF, Watanabe CK, Wood WI;
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29-JUN-2001; 2001MO-US021066.
09-APR-2002; 2002US-00119480.
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N-PSDB; ADC36806.
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1 HLPGNKSPHRDPAPR 15
                                                                                 Local Similarity
                                                                          Sequence 208 AA;
                                                                                                                                                JS2003096969-A1
                                                                                                                                                                    20-JUN-2000;
                                                                                                                                                               02-JUN-2000;
                                                                                                                                            Homo sapiens
                                                                                                                                                                  05-JUN-2000;
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                                                                                                                                                     22-MAY-2003.
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transmembrane polypeptides) and the PRO polymucleotides encoding them.

The invertion relates to numman kWO polypeptides encoding them.

The PRO polypeptides and polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, protect tumour, rectal tumour or liver tumour) in a mammal, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene chondrocyte cells, for stimulating the proliferation of or gene chordrocyte cells, for stimulating the proliferation of or gene chordrocyte cells, for stimulating the proliferation of or gene chordrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells or for stimulating the proliferation of or gene chypridisation probes, in chromosome and gene mapping, in generating as they by bridisation probes, in chromosome and gene mapping, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful cragents, in gene therapy, in chromosome identification, as chromosome condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sporte injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as condition which has responsive to the PRO polypeptides are useful as condition which an arkers in the PRO polypeptides are useful as condition and process or anti-PRO confit some markers for protein electrophoresis, and in tissue typing. This condition who have a human PRO polypeptide of the invention.
One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, or for preparing a medicament for treating
                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human PRO polypeptides (secreted and
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0
                                  Gaps
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0
Length 208;
100.0%; Score 89; DB 7; Length 20
100.0%; Pred. No. 9.2e-05;
tive 0; Mismatches 0; Indels
                                   15; Conservative
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ADC21797 standard; protein; 208 AA. 144 HLPGNKSPHRDPAPR 158 (first entry) Human PRO polypeptide #39.

Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.

2000US-0209832P. 2000US-0212901P. 2000US-0213807P. 2000US-0219556P. 2000US-0220585P. 2000US-0220605P. 29-AUG-2002; 2002US-00232255 22-JUN-2000; 2 20-JUL-2000; 2 25-JUL-2000; 2 25-JUL-2000; 2

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Gaps .

Length 208; Indels

Score 89; DB 7; I Pred. No. 9.2e-05; Mismatches 0;

0;

Local Similarity 100.

Matches

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Query Match

1 HLPGNKSPHRDPAPR 15

144 HLPGNKSPHRDPAPR

100.08; 100.0%; ADC49828 standard; protein; 208 AA.

RESULT 29 ADC49828 ID ADC498

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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polymucleotides encoding them.

The PRO polypeptides and polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours rectal tumour colon tumour, breast tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TNF) alpha from human blood, for stimulating the proliferation of differentiation of chondrocyte cells, for stimulating the proliferation of or gene chondrocyte cells, for stimulating the proliferation of chondrocyte cells, for stimulating the proliferation of chondrocyte cells, for stimulating the proliferation of chondrocyte cells, for stimulating the proliferation of chondrocyte cells, for stimulating the proliferation of chondrocyte cells, for stimulating the proliferation of chondrocyte cells in chromosome and gene mapping, in generating transpanic animals of therapeutically useful reagents, in gene therapy, in chromosome indemnification, as chromosome completes, and in generating probes. The PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injures), involving inducing the recondition which is responsive to the PRO polypeptides or anti-PRO disorders (e.g. arthritis, sports injures), involving inducing the recondition energe and unana PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated PRO polypeptide useful for tissue typing, as molecular weight markers in protein electrophoresis, for treating arthritis, tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goddard A, Godowski PJ;
phan JF, Watanabe CK, Wood WI;
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Smith V, Stephan JF,
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                                                                      2000US-0220666P.
2000US-0220893P.
2000US-022425P.
2000US-0227133P.
                                                                                                                                                                           2000WO-US023328
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Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH.) GENENTECH INC.
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N-PSDB; ADC21796.
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                                                                          25-JUL-2000; 26-JUL-2000; 201-AUG-2000; 3
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                                                                                                                                    22-AUG-2000;
23-AUG-2000;
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10-NOV-2000;
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(first entry)

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The invention describes an isolated PRO (secreted and transmembrane)

CD polypeptide (1). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
useful for stimulating the proliferation of or gene expression in

Dericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful

CD stimulating the proliferation of or gene expression in

CD stimulating the proliferation or differentiation of chondrocyte

CD stimulating the proliferation or differentiation of chondrocyte

CD SEQ14, PRO337, PRO352, PRO1155, PRO1306 or PRO1419, PRO1419, PRO1419,

CD SEQ14, PRO337, PRO352, PRO353, PRO125, PRO1306, PRO1419, PRO1419,

CD PRO125, PRO1181, PRO126, PRO1085, PRO1927, PRO1411, PRO1409,

CD PRO1286, PRO1390, PRO1347, PRO1305, PRO1917, PRO1411, PRO1309,

CD PRO1286, PRO1330, PRO1347, PRO1305, PRO1374, PRO1374, PRO1360,

CD PRO1887, PRO1387, PRO1305, PRO1449, PRO1379, PRO1361,

CD PRO1887, PRO1389, PRO4389, PRO4409, PRO1917, PRO1361, PRO1362,

CR PRO1887, PRO5725, PRO7184, PRO1305, PRO4333, PRO3444, PRO4322,

CR PRO1897, PRO5725, PRO7184, PRO1307, PRO4389, PRO4302, PRO4408,

CD PRO181, PRO5225, PRO7184, PRO1272, PRO1488, PRO4302, PRO4408,

CD Stimulating the proliferation of normal human dermal fibroblast cells. PRO

CD STIMULATION CD PRO1964, PRO1374, PRO5778, PRO4408,

CD STORD CD STORD CD PRO1964, PRO4981, PRO7774, PRO5778, PRO4408,

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                                                                                                                                                             human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New secreted and transmembrane PRO polypeptide useful for preparing medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody, e.g. cancer.
                                                                                                                      Novel human secreted and transmembrane protein PRO10196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; SEQ ID NO 78; 314pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUL-2000; 2000US-0220605P.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
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Grimaldi JC, Gurney AL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                      18-DEC-2003
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                       ADC49828;
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polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO351, PRO357, PRO1155, PRO1366 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214, PRO337, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO8400, PRO1080,
useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO127 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New PRO polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor alpha release;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; tumour; lung tumour;
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phan JF, Watanabe CK, W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                Length 208;
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human secreted and transmembrane protein PRO10196.
                                                                                                                                                                100.0%; Score 89; DB 7; I
100.0%; Pred. No. 9.2e-05;
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                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerritsen ME,
                                                                                                                                                                                                                                                                                                                                                                       ADC49027 standard; protein; 208 AA.
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                1 HLPGNKSPHRDPAPR 15
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                                                                                                                                                                                                      15; Conservative
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N-PSDB; ADC49026.
                                                                                                                                                                                     Local Similarity
                                                                                                                                Sequence 208 AA;
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Grimaldi JC,
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Godowaki PJ;

Goddard A, Gousser TF. Watanabe CK,

Gerritsen ME, Goddard Smith V, Stephan JF,

2002US-00119480

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
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PRO809, PRO1071, PRO1411, PRO1309
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PRO1005,
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADC49544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC49544
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The invention describes an isolated PRO (secreted and transmembrane)

CC polypeptide (1): PRO982. PRO1160, PRO1197 or PRO1329 polypeptide are useful for stimulating the proliferation of of onderfocyte cells. PRO357, PRO1292. PRO1292 or PRO4405 polypeptide are useful for stimulating the proliferation of differentiation of chondrocyte cells. PRO357, PRO352, PRO1272 or PRO4405 polypeptide are useful for stimulating the release of tumour necrosis factor (TMF) alpha from human blood. PRO921, PRO351, PRO1306, PRO1419, PRO1419, PRO214, PRO1417, PRO337, PRO351, PRO155, PRO1180, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                        useful
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, secreted and transmembrane protein, PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; chumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                     New PRO polypeptides and nucleic acids encoding the polypeptides, in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 89; DB 7; Length 20; 100.0%; Pred. No. 9.2e-05; ....ma+rhe8 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human secreted and transmembrane protein PRO10196.
Stephan JF,
                                                                                                                                                                                             Claim 11; SEQ ID NO 78; 315pp; English.
Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC47405 standard; protein; 208 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transmembrane PRO polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 HLPGNKSPHRDPAPR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HLPGNKSPHRDPAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
  Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
Les 15; Conserva
                                           2003-801156/75.
                                                                N-PSDB; ADC49543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC47405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 32
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dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                New PRO polypeptide for use as molecular weight markers for protein electrophoresis purposes and for detecting the presence of tumor in a
                                                                                                                                                    Gerritsen ME, Goddard
Smith V, Stephan JF,
                                                                                                                                                                                                                             Claim 11; Fig 78; 314pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transmembrane PRO polypeptide
                                                                                                       2001WO-US017800.
2001WO-US021066.
                                                                                  29-AUG-2002; 2002US-00232233.
                                                                                                 25-JUL-2000; 2000US-0220605P.
                                                                                                                      09-APR-2002; 2002US-00119480
                                                                                                                                                    Desnoyers L,
                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                          WPI; 2003-801157/75.
                                                                                                                                                                                 N-PSDB; ADC47404
                                                     US2003088072-A1.
                                                                                                                                                            Grimaldi JC,
                                       Homo sapiens
                                                                                                       01-JUN-2001;
                         gene therapy
                                                                    08-MAY-2003
                                                                                                                                                  Baker KP,
                                                                                                                                                                                                                mammal
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Goddard A, Godowski PJ; phan JF, Watanabe CK, Wood WI;

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The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

useful for stimulating the proliferation of or gene expression in

perioyte cells. PRO321, PRO1222, PRO1132, polypeptide are useful

for stimulating the proliferation or differentiation of chondrocyte

cells. PRO311, PRO357, PRO155, PRO1155, PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TNP)-

alpha from human blood. PRO982, PRO351, PRO136, PRO1419, PRO1419

PRO131, PRO3134, PRO526, PRO353, PRO525, PRO1066, PRO1180,

PRO1025, PRO1181, PRO126, PRO1065, PRO1192, PRO1411, PRO1411, PRO1310,

PRO1343, PRO1340, PRO1367, PRO1367, PRO1444, PRO1311, PRO1411,

PRO1343, PRO1376, PRO1367, PRO1369, PRO1444, PRO1311, PRO1411, PRO13139,

PRO1343, PRO1376, PRO1367, PRO1409, PRO1444, PRO1311, PRO1409,

PRO1887, PRO1928, PRO1367, PRO1801, PRO43131, PRO1444, PRO4312,

PRO1887, PRO1928, PRO1367, PRO1801, PRO1414, PRO1911, PRO1408,

PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1408, PRO4408,

PRO181, PRO229, PRO7184, or PRO1405 polypeptide are useful for atimulating the proliferation of normal human dermal fibroblast cells. PRO

polypeptides such as PRO6004, PRO4911, PRO1774, PRO5778, PRO4312, etc.,

are useful for detecting the presence of tumour in a mammal which

involves comparing the level of expression of the above PRO polypeptides

in a test sample of cells taken from the mammal, and a control sample of

cormal cells of the same cell type, where a higher level of expression of

the profile of the same cell type, where a higher level of expression of

cormal cells of the same cell type, where a higher level of expression of

the profile of the same cell type, where a higher level of expression of

cormal cells of the same cell type, where a higher level of expression of the same cell type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 208 AA;
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Gaps

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Length 208; Indels

/ Match 100.0%; Score 89; DB 7; L Local Similarity 100.0%; Pred. No. 9.2e-05; Les 15; Conservative 0; Mismatches 0;

Query Match

Best Loca Matches

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The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
useful for stimulating the proliferation of or gene expression in

pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful

for stimulating the proliferation or differentiation of chondrocyte

colls. PRO231, PRO357, PRO125, PRO1155, PRO1306 or PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TNF)-

alpha from human blood. PRO982, PRO357, PRO125, PRO1306, PRO1419, PRO214,

PRO247, PRO337, PRO526, PRO363, PRO531, PRO1081, PRO1419, PRO1412,

PRO1025, PRO1181, PRO826, PRO1005, PRO909, PRO1071, PRO1419, PRO1309,

PRO1026, PRO1330, PRO1347, PRO1305, PRO1927, PRO1274, PRO1320,

PRO10286, PRO1330, PRO1347, PRO1305, PRO144, PRO1279, PRO1340, PRO1322,

PRO1940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for

stimulating the proliferation of normal human dermal fibroblasts cells.

PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for

inhibiting the proliferation of normal human dermal fibroblast cells.

PRO5723, PRO5725, PRO7154, or PRO74081, PRO5778, PRO5778, PRO5732, etc.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO), for use in recombinantly producing a PRO polypeptide, as a hybridization probe, and in gene therapy.
                                                                                                                                                                                                                                                                                                                antiarthritic, pericyte cell proliferation, pericyte cell differentiation, chondrocyte cell differentiation, chondrocyte cell differentiation, chondrocyte cell differentiation, tumour necrosis factor alpha release, (TNF)-alpha release, dermal fibroblast cell proliferation, dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                             Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
                                                                                                                                                                                                                                                      Novel human secreted and transmembrane protein PRO10196.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Fig 78; 308pp; English
                                                                                                                                  ADC47150 standard; protein; 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JUL-2000; 2000US-0220666P.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US01066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-AUG-2002; 2002US-00219070.
                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Desnoyers L, ;, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-801246/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADC47149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003105288-A1.
                                                                                                                                                                                                                 18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ношо варієпв.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grimaldi JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baker KP,
                                                                                                                                                                           ADC47150;
                                                                                                 RESULT 33
                                                                                                                      ADC47150
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are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides in a test sample of calls taken from the mammal, and a control sample of normal cells of the same call type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful creating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmembrane PRO polypeptide.
          8¥866666666666668888
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Sequence 208 AA;

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0
           100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05;
                                  0; Indels
                                     Mismatches
                                     ..
                                                                                144 HLPGNKSPHRDPAPR 158
                                                             1 HLPGNKSPHRDPAPR 15
Query Match
Best Local Similarity luv..
Best Local Si Conservative
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Gaps

ADC78025 standard; protein; 208 AA. 01-JAN-2004 (first entry) ADC78025;

Novel human secreted and transmembrane protein PRO10196.

Human, secreted and transmembrane protein, PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping; gene therapy

Ното варіепв.

US2003096972-A1.

22-MAY-2003.

29-AUG-2002; 2002US-00232234.

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Goddard A, Godowski PJ; shan JF, Watanabe CK, Wood WI; Gerritsen ME, Goddard 1 Smith V, Stephan JF, Baker KP, Desnoyers L, Grimaldi JC, Gurney AL, KP,

WPI; 2003-765529/72. N-PSDB; ADC78024 Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as molecular weight markers, for treating arthritis and tumor.

Claim 11; Fig 78; 308pp; English.

The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cealls. PRO357, PRO1299, PRO1210 or PRO4405 polypeptide are useful for stimulating the proliferation of differentiation of chondrocyte cells. PRO357, PRO925, PRO1315, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF) alpha from human blood. PRO982, PRO3157, PRO1306, PRO1419, PRO214, PRO1214, PRO1314, PRO986, PRO1080, PRO1418, PRO1314, PRO986, PRO1080, PRO1314, PRO1314, PRO1366, PRO10186, PRO1192, PRO1244, PRO1319, PRO1314, PRO1316, PRO1319, PRO1317, PRO1318, PRO1319, P transmembrane PRO polypeptide.

Sequence 208 AA;

Gaps .. Length 208; 0; Indels Score 89; DB 7; I Pred. No. 9.2e-05; Mismatches 0 100.0%; 100.0%; Query Match
Best Local Similarity 100.
Matches 15; Conservative

ó,

1 HLPGNKSPHRDPAPR 15 g ð

ADD06260 standard; protein; 208 AA. RESULT 35 ADD06260

01-JAN-2004 (first entry) ADD06260;

Novel human secreted and transmembrane protein PRO10196.

release; human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release. (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;

therapy gene

Homo sapiens.

US2003073816-A1.

17-APR-2003.

26-AUG-2002; 2002US-00227873.

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The invertion describes an isolated FVO Secreted and transmembrane)

polypeptide (I). PRO982, PRO1166, PRO1187 or ERO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO1259, PRO1250 or DRO4465 polypeptide are useful for stimulating the proliferation of of gene expression in for stimulating the proliferation of defendation of chondrocyte cells. PRO351, PRO357, PRO1355, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TME)-alpha from human blood. PRO924, PRO1357, PRO1305, PRO1411, PRO1411, PRO1411, PRO1414, PRO1414, PRO1414, PRO1414, PRO1414, PRO1414, PRO1347, PRO1364, PRO1364, PRO1364, PRO1367, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PRO1365, PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polymucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PROSS7, PRO2S9, PRO1S7 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and
                                                                                                                                                                                                                                                                                                                                                                                New PRO polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                         Gerritsen ME, Goddard A, Godowski ÞJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention describes an isolated PRO (secreted and transmembrane)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; SEQ ID NO 78; 314pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane PRO polypeptide
                            01-JUN-2001; 2001WO-US017800.
                                                           2001WO-US021066.
                                                                                 2002US-00119480
                                                                                                                                                                                                         Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                                                                                                                                             (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                              WPI; 2003-644807/61.
                                                                                                                                                                                                                                                                                                                           N-PSDB, ADD06259
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                                                                                     09-APR-2002;
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100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05; 0; Mismatches 1 HLPGNKSPHRDPAPR 15 15; Conservative Local Similarity Query Match Best Loca Matches

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Gaps

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Indels

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ADC77779 standard; protein; 208 AA. HLPGNKSPHRDPAPR 158 ADC77779; RESULT 36 ADC77779 ID ADC7 XX AC ADC7 XX DT 01-J à 셤

01-JAN-2004 (first entry)

Novel human secreted and transmembrane protein PRO10196.

release; Human, secreted and transmembrane protein, PRO, cytostatic, vulnerary, antiarthritic, pericyte cell proliferation, pericyte cell differentiation, chondrocyte cell proliferation, tumour; chondrocyte cell differentiation, tumour necrosis factor alpha (TNR)-alpha release, dermal fibroblast cell proliferation, dermal fibroblast cell differentiation inhibitor; tumour; lung colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; gene therapy.

Homo sapiens

US2003088066-A1.

08-MAY-2003.

13-AUG-2002; 2002US-00219466

01-JUN-2001; 2001WO-US017800

29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

GETH) GENENTECH INC.

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Desnoyers L, Baker KP, De Grimaldi JC,

WPI; 2003-657980/62. N-PSDB; ADC77778

useful in gene therapy, or for preparing a medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody, One hundred and twenty two nucleic acids encoding PRO polypeptides, e.g. cancer.

Claim 11; Fig 78; 314pp; English.

The Inventor describes an isolated FRO 1807 Elected and Lambshen describes an isolated FRO 1807 FRO 18 in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polymucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic and mapping or gene therapy. (II) is useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, The invention describes an isolated PRO (secreted and transmembrane)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes an isolated PRO (secreted and transmembrane) polypeptide (1): PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO321, PRO135, PRO1155, PRO1155, PRO1160 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TMF) alpha from human blood. PRO982, PRO159, PRO106, PRO140, PRO247, PRO337, PRO526, PRO139, PRO181, PRO1069, PRO1078, PRO1134, PRO626, PRO1069, PRO1078, PRO1134, PRO126, PRO1180, PRO1126, PRO1195, PRO1179, PRO1137, PRO1369, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1376, PRO1409, PRO4333, PRO3543, PRO3544, PRO4322,
This is the amino acid sequence of a human secreted and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO), for use in recombinantly producing a PRO polypeptide, as a hybridization probe, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, secreted and transmembrane protein, PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; chondrocyte cell proliferation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
                                                                                                                                   Gaps
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                                                                                        Length 208;
                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human secreted and transmembrane protein PRO10196.
                                                                                          Score 89; DB 7; I
Pred. No. 9.2e-05;
                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                             ADD50742 standard; protein; 208 AA.
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                  transmembrane PRO polypeptide.
                                                                                          100.0%;
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09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                              144 HLPGNKSPHRDPAPR 158
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                                                                                             Query Match
Best Local Similarity 100.0
Matches 15; Conservative
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                                                                                                                                                                   1 HLPGNKSPHRDPAPR
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Grimaldi JC, Gurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-829361/77.
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sport injuries).
                                                      Sequence 208 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                   ADD50742;
                                                                                                                                                                                                                                                                        RESULT 37
                                                                                                                                                                                                                                                                                             ADD50742
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ER09940, PRO6079, PRO9036 or PRO10096 polypeptide are useful for stimulating the proliferation of normal human dermal fibroblasts cells. PRO6131, PRO2132, PRO41408, PRO6132, PRO4180, PRO6408, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, PRO6132, 
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Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    release;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        secreted and transmembrane protein; PRO; cytostatic; vulnerary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chodicocyte cell differentiation; chodicocyte cell differentiation; tumour necrosis factor alpha (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung dermal fibroblast chumour; prostate tumour; rectal tumour; prostate tumour; rectal tumour; lisue typing; chromosome mapping; gene mapping;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05; live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human secreted and transmembrane protein PRO10196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD50988 standard; protein; 208 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transmembrane PRO polypeptide.
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29-JUN-2001; 2001MO-US021066.
09-APR-2002; 2002US-00119480.
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Best Local Similarity 100.
Matches 15; Conservative
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N-PSDB; ADD50987.
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The invention describes an isolated rwo (secrete and transmembrane)

The invention describes an isolated rwo (secrete and transmembrane)

polypeptide (1). PRO982, PR01167 or PR01329 polypeptide are

useful for stimulating the proliferation of or gene expression in

Cor stimulating the proliferation or differentiation of chondrocyte

cells. PR0231, PR0357, PR0125, PR01155, PR01306 or PR01419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TMP)-

alpha from human blood. PR0982, PR0317, PR0125, PR01306, PR01419, PR0214,

CR0447, PR0337, PR0256, PR0363, PR0531, PR0183, PR0340, PR0141, PR01309,

CR01025, PR01134, PR0136, PR01185, PR01192, PR01241, PR01313,

CR010286, PR01319, PR01367, PR01309, PR01273, PR01279, PR01340, PR01338,

CR01343, PR01347, PR01387, PR01409, PR01414, PR01340, PR01322,

CR0343, PR05434, PR01801, PR01801, PR01917, PR01917, PR01861 for

CR1mulating the proliferation of normal human dermal fibroblast cells.

CR05723, PR05725, PR07154, or PR04281, PR07488, PR04302, PR04408,

CR05723, PR05725, PR07154, Or PR04281, PR07174, PR05778, PR04408,

CR05723, PR05725, PR07154, Or PR04281, PR07174, PR05778, PR04408,

CR05723, PR05725, PR07154, Or PR04281, PR07174, PR05778, PR04408,

CR05725, PR07154, Or PR04281, PR07174, PR05778, PR04408,

CR05725, PR07154, Or PR07425 polypeptide are useful for

checkindes such as PR06004, PR04981, PR07174, PR05778, PR04408,

CR05725, PR07154, Or PR07425 pr04681, PR07174, PR05778, PR04408,

CR05725, PR07154, Or PR07425 pr04681, PR07174, PR05778, PR04408,

CR05725, PR07164 proliferation of normal human dermal fibroblast cells.

CR05725, PR07154, Or PR07425 pr04681, PR07778, PR05778, PR04408,

CR05725, PR07154, Or PR07425 pr04681, PR0778, PR05778, PR04408,

CR05725, PR07154, Or PR07425 pr04681, PR0778, PR05778, PR04408,

CR05725, PR07754, PR074581, PR07754, PR05778, PR04408,

CR05725, PR07754, PR074581, PR07754, PR05778, PR04408,

CR05725, PR07754, PR07754, PR07754, PR07754, PR07754, PR07754, PR07754, PR07754, PR07754, PR07754, PR07754, PR07754, 
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polypeptide (PRO), for use in recombinantly producing a PRO polypeptide, as a hybridization probe, and in gene therapy.
                                                                                                                                                                                                                        invention describes an isolated PRO (secreted and transmembrane)
                                                                                                                                                  Claim 11; Fig 78; 309pp; English.
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Sequence 208 AA;

Gaps °, 100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05; Live 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0
Matches 15; Conservative

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RESULT 39 ADD50469

ADD50469 standard; protein; 208 AA.

15-JAN-2004 (first entry)

ADD50469;

Human PRO polypeptide #39.

Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-lalphs; TNP-alphs; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.

Homo sapiens.

US2003096971-A1

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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polypuble encoding them.

Cr The PRO polypeptides and polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours e.g. lung tumour, colon tumour, breast tumour, corposate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TNF) alpha from human constituting the proliferation of differentiation of condrover cells, for stimulating the proliferation of condrover cells, for stimulating the proliferation of congene capturession in pericyte cells or for stimulating the proliferation of consmal human dermal fibroblasts. The PRO nucleic acids are useful as commal human dermal fibroblasts. The PRO nucleic acids are useful as comparating probes, in chromosome and gene mapping, in generating cartisense RNA and DNA, in preparing PRO polypeptides by recombinant technology, in generating transgenic animals or knock-out animals which the development and screening of therapeutically useful craspenses and in generating probes. The PRO polypeptides, or anti-PRO markers and in generating probes. The PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving the resonance condition which is responsive to the PRO polypeptides are useful as disorders (e.g. arthritis, sports injuries), involving inducing the resonance represents a human PRO polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                      Novel isolated PRO polypeptide useful for tissue typing, as molecular weight markers in protein electrophoresis, for treating arthritis, tumor.
                                                                                                                                                                                                                                                            Wood WI;
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                                                                                                                                                                                                                                  Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, W
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Fig 78; 308pp; English.
                                                                                        01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                             29-AUG-2002; 2002US-00232229.
                                                                                                                                                                                                                                    Desnoyers L,
                                                                                                                                                                                      (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                            Grimaldi JC,
  22-MAY-2003
                                                                                                                                                                                                                                  Baker KP,
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.; 0 100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05; Live 0; Mismatches 0; Indels 15; Conservative Best Local Similarity Matches 15; Conserv ò

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ADD50223 standard; protein; 208 AA. 15-JAN-2004 (first entry) ADD50223;

RESULT 40

ADD50223

Human PRO polypeptide #39.

Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-alpha; TWF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.

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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polypucleotides encoding them.
The PRO polypeptides and polybucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, colon tumour, breast tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TMF) -alpha from human constitution the release of tumour necrosis factor (TMF) -alpha from human constitution the proliferation of or gene capacity to stimulating the proliferation of or gene capacity in perioryte cells or for stimulating the proliferation of conditions probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant technology, in generating transgenic animals or knock-out animals which reagents, in gene therapy, in chromosome identification, as chromosome markers and in generating probes. The PRO polypeptides, or anti-PRO antibodies, such as perioyte-associated tumours and bone and/or cartilage condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as perioyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the rectilished cultur markers for protein electrophoresis, and in tissue typing. This equence represents a human PRO polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                      Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated PRO polypeptides useful as molecular weight markers in
protein electrophoresis, and useful for tissue typing, for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Fig 78; 308pp; English.
                                                                                                                                                                    26-JUL-2000; 2000US-0220893P.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                             29-AUG-2002; 2002US-0023227.
                                                                                                                                                                                                                                                                                                                      Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arthritis, tumor.
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                                          US2003096970-A1.
    Homo sapiens.
                                                                                   22-MAY-2003
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Query Match
100.0%; Score 89; DB 7; Length 208;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 1 HLEGNKSPHRDPAPR 15

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1 HLPGNKSPHRDPAPR 15 |||||||||||||| 144 HLPGNKSPHRDPAPR 158 Search completed: March 2, 2004, 16:04:51 Job time : 9 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March 2, 2004, 15:51:17; Search time 1.4375 Seconds (without alignments) 543.341 Million cell updates/sec Run on:

US-10-060-765-8 89 1 HLPGNKSPHRDPAPR 15 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched: 141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

w		Description	Q9nsal homo sapien		_	porcine	Q14055 homo sapien	P38346 saccharomyc	Q91xr9 mus musculu		_	Ξ.	•								9								brach	homo	mus m	homo sa	bovine	344 bovine 1	P06486 herpes simp
SUMMARIES		1		COA1 PAVP9	COA1 PAVPK	COA1 PAVPN	CA29 HUMAN	YB90 YEAST	GX42 MOUSE	GX42 RAT	ELA3 HUMAN	CSF1 MOUSE	PYRG MYCLE	THO2 HUMAN	KASB STRCO	HID DROME	AMH2 HUMAN	ADP1_YEAST	MEI3 HUMAN	BAG4 MOUSE	ETS6 DROME	IBMP CAMVS	IBMP CAMVW	IBMP CAMVD	IBMP CAMVJ	AMH2 RAT	FXJ2_MOUSE		AXN2 BRARE	K852 HUMAN		NBEA HUMAN	GAG_BLVAU		US10_HSV11
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á	Query	Match	100.0	51.7	51.7	51.7	50.6	50.0	49.4	49.4	49.4	49.4	49.4	49.4	48.3	48.3	48.3	48.3	47.2	47.2	47.2	47.2	47.2	47.2			47.2		•	•	٠	47.2	9	46.6	46.1
		Score	68	46	46	46	45	44.5	44	44	44	44	44	44	43	43	43	43	42	42	42	42	42	42	42	42	42	42	42	42	42	42	ή.	41.5	44
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Q94425 ciona intes P22547 cauliflower P03558 cauliflower Q02954 cauliflower Q00957 cauliflower Q8ka45 buchnera ap Q9p0k8 homo sapien Q13444 homo sapien Q1344 homo sapien	049859 glycine max P30365 medicago tr P16329 pisum sativ
SYI CIOIN IBMP CAMV4 IBMP CAMVC IBMP CAMVB IBMP CAMVN FLIF BUCAP FAZZ HUMAN AD15 HUMAN RLPA_PSEAE	C824_SOYBN NO12_MEDTR NO75_PEA
413 620 620 620 620 630 630 630 630 630 630 630 630 630 63	525 103 112
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	45.5 44.9 44.9
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ALIGNMENTS

729 AA

STANDARD;

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MEDLINE=89319168; PubMed=2750278;

MEDLINE=89319168; PubMed=2750278;

MEDLINE=89319168; PubMed=2750278;

Sakurai M., Nishimori T., Ushimi C., Nakajima H.;

Sakurai M., Nishimori T., Ushimi C., Nakajima H.;

"Nucleotide sequence of capsid protein gene of porcine parvovirus.";

Virus Res. 13:79-86(1989)

Virus Res. 13:79-86(1989)

VII NONCAPRID PROTEIN NS-1.

-1- SUBUNIT: MATURA VIRON CONTAINS THREE CAPSID PROTEINS DESIGNATED CO. VP1, VP2, AND VP3 AND A NONCAPSID PROTEIN NS-1.

-1- MISCELLANBOUS: VP3 MIGHT BE A POSTTRANSLATIONAL CLEAVAGE PRODUCT OF VP2 IN SEVERAL AUTONOMOUS PARVOVIRUSES.

-1- SIMILARITY: Belongs to the parvoviruses coat protein family.

PIR; A60006; A60006.

R HSSP; PR30129; 4DPV.

InterPro; IPR001403; Parvo_coat.

R InterPro; IPR008975; Viral_cap_coat.

R Pfam; PF00740; Parvo_coat.

R Pfam; PF00740; Parvo_coat.
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                                                                                                                                                                                                                           Length 209;
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Pred. No. 26;
                                                                                                                                                                                              2230v ...,
100.0%; Score 89; DB 1; Lengtn zv.
                                                                                                                                 POTENTIAL.
FIBROBLAST GROWTH FACTOR-21.
MISSING (IN REF. 2).
7 27925C52A0023823 CRC64;
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01-FEB-1994 (Rel. 28, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Coat protein VPI (Contains: Coat protein VP2]
Porcine parvovirus (strain 90HS) (PPV)
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InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
PR10TS; PR00262; IL1HBGF.
ProDom; PD000831; IL1_HBGF; 1.
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
Growth factor; Signal.
SIGNAL.
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23 23 M
209 AA; 22300 MW;
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729 AA;
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les 15; Conserv
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P33484;
                                                                                                                                                      CHAIN
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                                                                                                                                                                                                                                                                                                                                                           MEDIJINE-96183900; PubMed=8642680;
Bergeron J., Hebert B., Tijssen P.;
"Genome organization of the Kresse strain of porcine parvovirus:
identification of the allotropic determinant and comparison with
those of NADL-2 and field isolates.";
J. Virol. 70:2508-2515(1996).
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-!- MISCELLANBOUS: VP3 MIGHT BE A POSTTRANSLATIONAL CLEAVAGE PRODUCT OF VP2 IN SEVERAL AUTONOMOUS PARVOVIRUSES.
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    !- SIMILARITY: Belongs to the parvoviruses coat protein family.

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P18546; P22964; O89816;
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 41, Last amnotation update)
28-FEB-2003 (Rel. 41, Last amnotation update)
coat protein VPI [Contains: Coat protein VP2].
Porcine parvovirus (serrain NADL-2) (PPV).
Viruses; sBDNA viruses; Parvoviridae; Parvovirins.
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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Coat protein VP1 (Contains: Coat protein VP2)
Porcine parvovirus (strain Kresse) (PPV).
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2; Mismatches
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InterPro; IPR01403; Parvo_coat.
InterPro; IPR0040375; Viral_cap_coat.
Pfam; PF00740; Parvo_coat; 1.
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61.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U44978; AAC40231.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coat protein; Glycoprotein.
CHAIN 1 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 PGNKSPHRDPAPR 15
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      573
604
651
729 AA;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         NCBI_TaxID=73487;
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RESULT 3 COAL_PAVPK

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MEDLINE=90085785; PubMed=2596019;

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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce) or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                           Ranz A.I., Manclus J.J., Diaz-Aroca E., Casal J.I.;
"Porcine parvovirus: DNA sequence and genome organization.";
J. Gen. Virol. 70:2541-2553 (1989).
J. Gen. Wirol. TO:2541-2553 (1989).
                                                                                                                                                                                                                                                                   VP1, VP2, AND VP3 AND A NONCAPSID PROTEIN NS-1.
-!- MISCELLANEOUS: VP3 MIGHT BE A POSTTRANSLATIONAL CLEAVAGE PRODUCT OF VP2 IN SEVERAL AUTONOMOUS PARVOVIRUSES.
        Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W., "Nucleotide sequence analysis of the capsid genes and the right-hand terminal palindrome of porcine parvovirus, strain NADL-2."; Virology 173:368-377(1989).
                                                                                                         Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W.; "The complete nucleotide sequence of an infectious clone of porcine parvovirus, strain NADL-2."; Virology 178:611-616(1990).
                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the parvoviruses coat protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COAT PROTEIN VP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001403; Parvo coat.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF00740; Parvo_coat; 1.
                                                                                                MEDLINE=91021005; PubMed=2219713;
                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=90010964; PubMed=2794971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80946 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M32787; AAA46918.1; --
EMBL; M38367; AAA46519.1; --
EMBL; M38367; AAA46921.1; --
EMBL; D00623; BAA00502.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M32787; AAA46917.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; Glycoprotein
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PIR; B33743; VCPVNA.
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715 7
729 AA;
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                                                                                    FROM N.A.
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G -> GKGSFKGVVAYILQIIFLYITG (IN REF. 3).
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                        (POTENTIAL)
                                                 (POTENTIAL)
                                                           (POTENTIAL)
                                                                         (POTENTIAL)
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0
                                                                                  (POTENTIAL)
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                                                                                                                                                                                                                                   EF816E246C80DB42 CRC64;
                                                                                                                                (IN REF. 3).
                                                                                                                                 YKY -> TI (IN REF. 3)
Y -> T (IN REF. 3).
G -> A (IN REF. 3).
T -> S (IN REF. 3).
V -> S (IN REF. 3).
E -> A (IN REF. 3).
R -> A (IN REF. 3).
R -> K (IN REF. 3).
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2; Mismatches
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 N-LINKED
N-LINKED
N-LINKED
N-LINKED
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N-LINKED
N-LINKED
                                                                                                 N-LINKED
                                                                                                             GLY-RICH
                                                                                                                                                                                                                                                                         61.5%;
                                                                                                                                                                                                                                                                      Local Similarity 61.5
nes 8; Conservative
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Science 285:409-412(1999).
                                                                                                                                                                                                       TIŜSUE=Foreskin;
MEDLINE=98370844; PubMed=9707347;
Pihlajamaa T., Vuoristo M.M., Annunen S., Peraelae M., Prockop D.J.,
Ala-Kokko L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Annunen S., Paassilta P., Lohiniva J., Peraelae M., Pihlajamaa T., Karppinen J., Tervonen O., Kroeger H., Laehde S., Vanharanta H., Ryhanen L., Goering H.H.H., Ott J., Prockop D.J., Ala-Kokko L.; "An allele of COL9A2 associated with intervertebral disc disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: Heterotrimer of an alpha 1(IX), an alpha 2(IX) and an
                                                                                                                                                                                                                                              "Human COL9A1 and COL9A2 genes. Two genes of 90 and 15 kb code for similar polypeptides of the same collagen molecule.";
Matrix Biol. 17:237-241(1998).
                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                          Peraelae M., Hanninen M., Hastbacka J., Elima K., Vuorio E., "Molecular cloning of the human alpha 2(IX) collagen cDNA and assignment of the human COL9A2 gene to chromosome 1."; FEBS Lett. 319:177-180(1993).
                                                                                                                                                                                                                                                                                                             Donnelly S.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                            (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 43, Last annotation update)
                                                        689 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT IDD TRP-326, AND VARIANT ARG-326.
MEDLINE=99340300; PubMed=10411504;
                                                                                                          Collagen alpha 2(IX) chain precursor.
                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                         TISSUE=Cartilage;
MEDLINE=93202262; PubMed=8454052;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 50-668 FROM N.A.
117 PGSKPPGKRPAPR 129
                                                      STANDARD;
                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the eye.
                                                                            28-FBB-2003 (
28-FBB-2003 (
15-MAR-2004 (
                                                        CA29 HUMAN
                                                                  014055
                                             CA29_HUMAN
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EMBL; AF019406; AAC33512.1; -.

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Gaps

Η,

Score 44.5; DB 1; Length 545; Pred. No. 31; 1; Mismatches 3; Indels 1

50.0%;

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EMBL; Z36139; CAA85233.1; -.
PIR; S46151; S46151.
GermCnline; 138813; -.
SGD; S0000474; YER270C.
HYPOCHETICAL protein:
SEQUENCE 545 AA; 61301 MW; 5655D51206EF728B CRC64;
                                                                                                                                                                                                                                    10; Conservative
                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            GX42_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q -> W (in IDD; requires 2 nucleotide substitutions).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Pungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Hypothetical 61.3 kDa protein in MRPL37-RIF1 intergenic region.
YBR270C OR YBR1738.
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ProDom; PD000007; Clg_helix; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                            Collagen; Signal; Glycoprotein; Proteoglycan; Disease mutation;
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INTERCHAIN (POTENTIAL).
O-LINKED (GLYCOSAMINOGLYCAN) (BY
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Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
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EB6106E02F6FA862 CRC64;
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TRIPLE-HELICAL REGION 2.
NON-HELICAL REGION 2.
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TRIPLE-HELICAL REGION 4.
NONHELICAL REGION 4.
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/FTId=VAR 012659.
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                                                                                                                               MIM; 603912; -.
GO; GO:0005594; C:collagen type IX; TAS.
GO; GO:0001501; P:skeletal development; TAS.
InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
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     EMBL; AL050341; CAB81611.1; -.
EMBL; M95610; AAA80977.1; -.
Genew; HGNC:2218; COL9A2.
MIM; 120260; -.
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Best Local Similarity 53.0.
Ref. 7; Conservative
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689
163
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632
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                                                                                                                                                                                                                                                                                                                                                                                              244
274
274
1164
1181
1181
633
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663
174
1178
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                                                                                                                                                                                                                                                                                                                                                                         Polymorphism.
SIGNAL
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ID YB90 YEA
AC P38346;
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MEDLINE=22453509; PubMed=12566075;

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A MEDLINE=22453509; PubMed=12566075;

A Motta L., Ran Q., Rao L., Van Remmen H., Shibatani T., Belter J.G.,

A Motta L., Richardson A., Prolla T.A.;

The selenoprotein GPX4 is essential for mouse development and

The selenoprotein GPX4 is essential for mouse development and

The Radic. Biol. Med. 34:496-502(2003).

The Radic. Biol. Med. 34:496-502(2003).

The Radic. Biol. Med. 34:496-502(2003).

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The Radic. Biol. Med. 34:496-502(2003).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21242617; PubMed-11344089;
Pfeifer H., Conrad M., Roethlein D., Kyriakopoulos A., Brielmeier M.,
Bornkamm G.W., Behne D.;
"Identification of a specific sperm nuclei selencenzyme necessary for
proteamine thiol cross-linking during sperm maturation.";
FASEB J. 15:1236-1238(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Mitochondrial;
lsoId=070325-1; Sequence=External;
-!- TISSUE SPECIFICITY: Repressed exclusively in sperm.
-!- SIMILARITY: Belongs to the glutathione peroxidase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q91XE9; Q8K4U8;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
Phospholipid hydroperoxide glutathione peroxidase, nuclear (EC 1.11.1.12) (GPX-4).
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STRAIN=129/SVJ; TISSUB=Liver;
Imai H. Nakagawa Y.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                     253 AA.
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1 HLPGNKSPHRDPAPR 15
                                                                                                        53 HLKTSKSPH-DAAPR 66
                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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ACT SITE
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Matches
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                GO; GO:0005739; C:mitochondrion; IDA.
GO; GO:0005635; C:muclear membrane; IDA.
GO; GO:0004602; P:glutathione_peroxidase activity; IDA.
GO; GO:0004602; P:establishment and/or maintenance of chromat. . .; IDA.
GO; GO:0007283; P:spermatogenesis; IDA.
InterPro; IPR000889; Glut_peroxidase.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2019 (Rel. 42, Last annotation update)
10-OCT-2019 (Agaroperoxide glutathione peroxidase, nuclear (EC 1.11.1.12) (GFX-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.4%; Score 44; DB 1; Length 253; 53.8%; Pred. No. 17; tive 2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nuclear process, Alternative splicing.
ACT SITE 129 129 BY SIMILARITY.
SECUS 129 129 BY SIMILARITY.
SECUS 253 AA; 29204 MW; C55E36875B830053 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-250 FROM N.A., AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Developmental protein; Selenium; Selenocysteine;
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                                                                                                                                                                                                                GO:0005829; C:cytosol; IDA.
                                                                                                                                                  EMBL; AF274027; AAK74112.1; -. EMBL; AB030643; BAC06509.1; -.
                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00255; GSHPx; 1.
PRINTS: PR01011; GLUTPROXDASE.
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Matches 7; Conserv
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Q91XR8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ537598; CAD61278.1; -.
EMBL; AF774028; AAK74113.1; -.
EMBL; AF774028; AAK74113.1; -.
GO; GO:00005524; C:nucleus; ISS.
GO; GO:0006325; F:establishment and/or maintenance of chromat...; ISS.
GO; GO:0007283; P:spermatcgenesis; ISS.
InterPro; IPR000889; Glut peroxidase.
Pfam; PF00255; GSHPx; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription elongation factor, elongin A3.";
J. Biol. Chem. 277:26444-26451(2002)
-:- FUNCTION: SIII, also knows elongin, is a general transcription elongation factor that increases the RNA polymerase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
RNA polymerase II transcription factor SIII subunit A3 (Elongin A3)
(EloA3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcription elongation past template-encoded arresting sites.
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101 101 S -> A (IN REF. 2).
253 AA; 29304 MW; FSAECICF187AD7BB CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., FUNCTION, AND SUBUNIT.
MEDLINE=22113023; PubMed=11994304;
Yamazari K., Gvo L., Sugahara K., Zhang C., Enzan H., Nakabeppu
Kitajima S., Aso T.;
"Identification and biochemical characterization of a novel
-!- COFACTOR: Selenocysteine. The active-site selenocysteine is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the glutathione peroxidase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO1011; GLUTPROXDASE.
PROSITE; PS00466; GLUTATHIONE PEROXID 1; 1.
PROSITE; PS00765; GLUTATHIONE_PEROXID 2; 1.
Oxidoreductaes; Peroxidase;
Developmental protein; Selenium; Selenocysteine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.4%; Score 44; DB 1; 53.8%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   546 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                           IsoId=Q91XR8-1; Sequence=Displayed;
                                                                                                                                                                                                              lsoId=P36970-1; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nuclear protein; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                        encoded by the opal codon, UGA.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 PGNKSPHRDPAPR 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                      Name=Mitochondrial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                     Name=Nuclear;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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us-10-060-765-8.rsp

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Biochim. Biophys. Acta 1174:143-152(1993)
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                    -!- SUBUNIT: Heterotrimer of an A (A1, A2 or A3), B and C subunit.
-!- SUBCELDULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Widely expressed.
-!- DOMAIN: The elongin BC complex binding domain is also known as BC-box with the consensus [APST]-L-x(3)-C-x(3)-[AILV].
-!- SIMILARITY: Contains 1 TFS2-N domain.
  Subunit A3 is transcriptionally active but its transcription activity is not enhanced by binding to the dimeric complex of the SIII regulatory subunits B and C (elongin BC complex). SUBUNIT: Heterotrimer of an A (A1, A2 or A3), B and C subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "CDNA cloning and expression of murine macrophage colony-stimulating factor from 1929 cells.";
Proc. Natl. Acad. Sci. U.S.A. 85:6706-6710(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borycki A.G., Lenormund J., Guillier M., Leibovitch S.A.; "Isolation and characterization of a cDNA clone encoding for rat CSF-1 gene. Post-transcriptional repression occurs in myogenic differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Macrophage colony stimulating factor-1 precursor (CSF-1) (MCSF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-88320507; PubMed=2457916;
Ladner M.B., Martin G.A., Noble J.A., Wittman V.P., Warren M.K.,
McGrogan M., Stanley E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Delamarter J.F., Hession C., Semon D., Gough N.M., Rothenbuhler
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVATION DOMAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 1; Length 546;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTING WITH ELONGIN BC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59760 MW; E98AE3DD548C5492 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequence of a cDNA encoding murine CSF-1 (Macrophage-CSF).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                552 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Macrophage-CSF).";
Nucleic Acids Res. 15:2389-2390(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=93363632; Pubmed=8357831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87174763; PubMed=3494232;
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                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB076840; BAC01113.1; -. InterPro; IPR003617; TFS2_N.
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162 PADSGPHRDPPTR 174
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es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003617; TFS
SMART; SM00509; TFS2N; 1
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CSF1_MOUSE

CSF1_M

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DT 01-FEB

DT 01-FEB

DT 01-FEB

CSF1 0

CS MARMEN

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MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=2288257; PubMed=12477932;

MEDLINE=288287; MEDLINE F.S., MEDLINE G.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MEDLINE F., John M., Moore T., Max S.I., Wang J., Hong L.,

Browneten M.J., Usdin T.B., Parmer A.A., Rubin G.M., Hong L.,

Brownetein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.B., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Michards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Milalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Milalon D.K., Murny D.M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffaxd G.G.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffaxd G.G.,

Mitterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

"Thuman and mouse cDNA sequences.",

"The Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-100 FROM N.A.
MEDIATURE-8714722; PubMed=3493488;
REJAVASA; PubMed=3493488;
Shively J.E., Lusis A.J.;
Shively J.E., Lusis A.J.;
"Cloning and tissue-specific expression of mouse macrophage colony-stimulating factor mRNA.";
Proc. Natl. Acad. Sci. U.S.A. 84:1157-1161(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and characterization of the murine promoter for the colony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ď
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino-terminal amino acid sequence of murine colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dobbins D.E., Sood R., Hashiramoto A., Hansen C.T., Wilder R.L.,
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MEDLINE=91340149; PubMed=1874443;
Harrington M.A., Edenberg H.J., Saxman S.M., Pedigo L.M., Daub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE OF 33-57.
MEDLINE=65242705; PubMed=3925458;
Ben-Arram C.M., Shively J.E., Shadduck R.K., Waheed A.,
Rajavashisth T.B., Lusis A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 294:1114-1120(2002)
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Gene 102:165-170(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Broxmeyer H.E.;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note-No experimental confirmation available;
Note-No experimental confirmation available;
Note-No experimental confirmation available;
Note-No experimental The predominant soluble form is a chondroitin sulfate-confaining proteoglycan.
-!- DISEASE: A defect in CSF1 is the cause of osteopetrosis.
Osteopetrotic mice (op/op) are severely deficient in mature macrophages and osteoclasts, display failed tooth eruption, and have a restricted capacity for bone remodelling.
-!- CAUTION: Ref. 3 sequence was originally thought to originate from rat, but was later shown (Ref. 8 and Ref. 9) to be derived from
MEDLINE=90259093; PubMed=2188141;
Yoshida H., Hayashi S.I., Kunisada T., Ogawa M., Nishikawa S.,
Yoshida H., Hayashi S.I., Kunisada T., Ogawa M., Nishikawa S.,
Yoshida H., Shultz L.D., Nishikawa S.-I.;
"The murine mutation osteoperrosis is in the coding region of the
macrophage colony stimulating factor gene.";
Nature 345.442-444(1990).
-!-FUNCTION: Granulocyte/macrophage colony-stimulating factors are
cytokines that act in hematopoiesis by controlling the production,
differentiation, and function of 2 related white cell populations
of the blood, the granulocytes and the monocytes-macrophage inneage. It plays a
role in immunological defenses, bone metabolism, lipoproteins
                                                                                                                                                                                                                                                                                                                                                                    clearance, fertility and pregnancy.
-!- SUBGNIT: Homodimer or heterodimer; disulfide-linked.
-!- SUBGENIUAR LOCATION: Extracellular. The precursors may exist as integral membrane proteins (By similarity).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MACROPHAGE COLONY STIMULATING FACTOR-1.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
Missing (in isoform 2).
/FIId-VSP_001189.
S -> P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A31401, A31401.
MGD; MGI:1339753; Ceff.
InterPro; IPR008001; MGSF-1.
Cytokine; Growth factor; Glycoprotein; Proteoglycan; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
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INTERCHAIN (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=2;
IsoId=P07141-2; Sequence=VSP_001189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P07141-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Alternative splicing.
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EMBL; M21952; AAA37481.1; -...
EMBL; M21149; AAA37482.1; -...
EMBL; M84361; AAA03032.1; -...
EMBL; MC025593; AAB25593.1; -...
EMBL; M15692; AAA37480.1; -...
EMBL; M15692; AAA19866.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         552
492
515
515
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171
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33
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516
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1172
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21128732; PubMed=11234002;

Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Srom D., Chillingworth T., Connor R.,
Davier R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).

--- FUNCTION: Catalyzes the ATP-dependent amination of UTP to CTP with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    either L-glutamine or ammonia as the source of nitrogen (By similarity).

-!-CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate + CTP.
-!-ENZYME REGULATION: Allosterically activated by GTP, when glutamine is the substrate. Inhibited by CTP (By similarity).
-!-PATHWAY: Pyrimidine biosynthesis; conversion of UMP to CTP; third (last) step.
-!- SUBUNT: Homotetramer (By similarity).
-!- SUBUNT: Homotetramer (By similarity).
-!- SIMILARITY: Belongs to the CTP synthase family.
-!- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase) (CTP synthetase).
PYRG OR ML1363 OR MLC1351.09C.
Mycobacterium leprae.
                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinomycetales; Corymebacteridae; Actinomycetales; Corymebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                     49.4%; Score 44; DB 1; Length 552; 58.3%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Smith D.R., Robison K.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
3 3 MISSING (IN REF. 5).

6 6 A -> R (IN REF. 5).

7 8 AG -> PR (IN REF. 5).

246 246 P -> A (IN REF. 1).

552 AA; 60648 MW; 3886D72D70B770AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   590 AA.
                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U00021; AAA50916.1; -.
EMBL; Z95117; CAB08284.1; -.
EMBL; AL583921; CAC31744.1; -.
PIR; S72961; S72961.
Leproma; Mil363; -; HAMAP; MF_01227; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                             | : |||: |||
202 PASASPHQPPAP 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                        3 PGNKSPHRDPAP 14
                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYRG MYCLE
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   CONFLICT
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CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P53529;
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Name=2;
Isoid=Q8NI27-2; Sequence=VSP_008587, VSP_008588;
          IsoId=Q8NI27-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                               Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KASB STRCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: The THO/TREX complex is recruited to transcribed genes and travels with the RNA polymerase during elongation. It may physically link proteins that function in transcription and in RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Part of the heteromultimeric THO/TREX complex containing THOC1, THOC2, THOC3, THOC4 and NFX1/UAP56.
SUBCELLULAR LOCATION: Nuclear (Probable).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Placenta;
Isogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Isogal T., Ota T., Hayashi K., Shiratori A., Sudo H.,
Nishikawa T., Nagai K., Zhugano S., Shiratori A., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishili S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninoniya K., Iwayanagi T.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Straesser K., Masuda S., Mason P., Pfannstiel J., Oppizzi M.,
Rodriguez-Navarro S., Rondon A.G., Aguilera A., Struhl K., Reed R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ottenwaelder B., Obermaler B., Deutschenbaur S., Mewes H.-W., Weil Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          furt E., t a conserved complex coupling transcription with messenger
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, AND INTERACTION WITH THE
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                          . 9
           Interpro; IPR004468; PyrG synth.
Pfam; PF00117; GATase; 1.
TIGRFMs; PS00422; GATASE TYPE; 1.
PYTHIA; PS00442; GATASE TYPE I; 1.
Pyrimidine biosynthesis; Ligase; Glutamine amidotransferase; Complete proteome.
                                                                                                                                                                Score 44; DB 1; Length 590; Pred. No. 40;
                                                                                                                                                                                         3; Indels
                                                                                           GLUTANINE AMIDOTRANSFERASE.
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GALOGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1151-1478 FROM N.A. (ISOFORM 2).
TISSUE-Salivary gland;
                                                                                   DOMAIN.
                                                                                                                                                                                                                                                                                                 PRT; 1478 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 444-1162 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                         2; Mismatches
                                                                                   AMINATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22010388; PubMed=11979277;
                                                                                                                                                                                                                                       567 HLPNSSNQHRDGVERSFPAP 586
                                                                                                                                                                                                                  1 HLPGNKSPHRD-----PAP 14
                                                                                                                                                                                                                                                                                                 THO2 HUMAN STANDARD; PR. QBN127; Q9H816; 10-OCT-2003 (Rel. 42, Last seque 10-OCT-2003 (Rel. 42, Last seque 10-OCT-2003 (Rel. 42, Last annot THO complex subunit 2 (Tho2).
                                                                                                                                              64081 MW;
 InterPro; IPR000991; GATase_1
                                                                                                                                                                     49.48;
                                                                                                                                                                                45.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 417:304-308(2002).
                                                                                                                                                                              Local Similarity 45.0
                                                                                   312
590
393
524
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                             590 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA export."
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TREX COMPLES
                                                                                               DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                      Query Match
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                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                           RESULT THOS HUN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
DSLI -> VSIA (in isoform 2).
/FILG-VSP 008587.
Missing (in isoform 2).
/FILG-VSP 008588.
F -> S (IN REF. 2).
E -> G (IN REF. 3).
E -> K (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Last annotation update)
Actinorhodin polyketide putative beta-ketoacyl synthase 2 (EC 2.3.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=A312) / M145;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Nucleotide sequence and deduced functions of a set of cotransc:
genes of Streptomyces coelicolor A3(2) including the polyketide
synthase for the antibiotic actinorhodin.";
J. Biol. Chem. 267:19278-19290(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 1; Length 1478; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=A3(2) / M145;
MEDLINE=92406871; PubMed=1527048;
Fernandez-Moreno M.A., Martinez E., Boto L., Hopwood D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                     Transport; mRNA transport; mRNA processing; mRNA splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169580 MW; FEICBCE28C560BCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein; RNA-binding; Alternative splicing
Note=No experimental confirmation available;
-:- SIMILARITY: Belongs to the THOC2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            407 A.A.
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01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYS-RICH
                                                                                                                                                                                                                                                                                       EMBL; AF441770; AAM28436.1; -.
EMBL; AK023659; BAB14630.1; ALT_INIT.
EMBL; BX648654; CAE46196.1; -.
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1066 IPENEFHHKDPPPR 1079
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                                                                                                                                                                                                                                                                                                                                                               HGNC:19073; THOC2
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1161
1241
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Best Local Similarity
7; Conserva
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Sabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Hopwood D.A.;
                                                                                                                                                                       Nature 417:141-147(2002).
-!- MISCELLANEOUS: This putative ketoacyl synthase lacks the active

    -!- SIMILARITY: Belongs to the beta-ketoacyl-ACP synthases family.

                                                                                                                          "Complete genome sequence of the model actinomycete Streptomyces coelicolor {\rm A3}\,(2) ",
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MEDLINE=95347579; PubMed=7622034;
Grether M.E., Abrams J.M., Agapite J., White K., Steller H.;
"The head involution defective gene of Drosophila melanogaster functions in programmed cell death.";
Genes Dev. 9:1694-1708(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.3%; Score 43; DB 1; Length 407; 46.7%; Pred. No. 38; cive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00109; ketoacyl-synt; l.
Pfam, PF02801; ketoacyl-synt_C; l.
Antibiotic biosynthesis; Transferase; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         407 AA; 42549 MW; 59FC75A5A0D94632 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HID DROME STANDARD, PRT; 410 AA. 024106; Q9VVD1; 01-NOV-1997 (Rel. 35, Created) 116-OCT-2001 (Rel. 40, Last sequence update) 110-OCT-2003 (Rel. 42, Last annotation update) Head involution defective protein (Wrinkled protein).
                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AL939122; CAC44201.1; -.
PIR; S25841; S25841.
HSSP; P73283; 1E5M.
InterPro; IPR000794; Ketoacyl_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Berkeley; MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X63449; CAA45044.1; -.
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hes 7; Conservative
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RA Bellew R.W., Basu A. An H.-D., ANDEWES-FIRINGCON C., Batolay B.M., Basul A. Basuladle J., Bayraktaroglu L., Beasley E.M., Basus A. Basuladle J., Bayraktaroglu L., Beasley E.M., Basus A. Basuladle J., Bayraktaroglu L., Beasley E.M., Basus A. Berman B.P., Bhandari D., Bolshakov S., Banckova D., Botchan M.R., Bouck J., Barckstein P., Botchier P., Botchier P., Botchier P., Botchier P., Botchier P., Botchier P., Botchier P., Botchier P., Botchier P., Botchier P., Battler B., Cawley S., Dalkov B., Dalkov D. B., Davies P., Dalkov B., Delack A., Goup L.S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., R.A. Botchier A., Demes M., Dugan-Rocha S., Pleischmann W., R.A. Botchier C., Gabrielian A.E., Garg N.S., Gelbart M.M. Glasser K., Glode K., Gong F., Gorrell J.H., Gu Z., Gun P., Harris M., Harvey D.A., Harway D.A., Harmandez J.R., Houck J., Houthout M.K., Havey D.A., Harmandez J.R., Houck J., J. Harnandez J.R., Houck J., J. J. H., J. Harnandez J.R., Houck J., J. J. J. H., Li Z., Liang Y., Lin X., J. Jalli M., Kalush F., Karpen G.H., Kazi, T.J., Harnandez J.R., Ketchum K.A., Jalush F., Karpen G.H., Kazi, M. M., M., M., Martei B., McIntosh T.C., McLeod M.P., McPherson D., Lai Z., Liang Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., M. M., Mulbinan N.V., Mosskern D.R., Palla N., Mulbinan N.V., Mosskern D.R., Palla N., Mulbinan S., Pollard J., Puri V., Reses M.G., R. A., Shue K., Mang Z., Pallar Kander K., Ramington K., Saunders R.D.C., Scheeler F., Shen H., Spier E., Schaer Kianos I., Simpson M., Strong R., Sinth T., Spier E., Stranking A.C., Stapleton M., Strong R., Sun E., Shen H., Spier E.W., Weissenbach J., Worley K., Wang Z.-Y., Wassarman D.A., Weinseck G.W., Weissenbach J., Wang Z., Zaveri J.S., Zaveri J.S., Zhan M., Zhan G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pattern of programmed cell death in the embryo, particularly in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: LIMITED AT THE N-TERMINAL REGION, TO GRIM AND RPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0006917; P:induction of apoptosis; IGI.
GO; GO:0002165; P:larval/pupal development (sensu Insecta); IMP.
GO; GO:0012501; P:programmed cell death; IMP.
Apoptosis; Developmental protein; Polymorphism.
DOMAIN 237 240 POLY-SER.
DOMAIN 332 340 POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE: Expression corresponds approximately
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S -> L (IN ALLELE A206).
P -> S (IN REF. 1).
63EBF913149E27E1 CRC64;
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EMBL, AR003521, AAK49270.1; --
Flymase; FSEM000397; W.
GO, GO:0008258; P:head involution; IMP.
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351 3
410 AA;
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CONFLICT
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Gaps

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4; Indels

0; Mismatches

7; Conservative 4 GNKSPHRDPAP 14

Matches

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Score 43; DB 1; Length 410; Pred. No. 38;

48.3%;

Query Match Best Local Similarity receptor subfamily.

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MEDLINE=21434063; PubMed=11549681;

MEDLINE=21434063; PubMed=11549681;

MEDLINE=21434063; PubMed=11549681;

MEDLINE=21434063; PubMed=11549681;

MEDLINE=21434063; PubMed=11549681;

MEDLINE=21434063; PubMed=11549681;

MEDLINE=21434063; PubMed=1.6., Belville C., Dutertre M., Ling L.,

Imbeaud S., Hughes I.A., Picard J.-Y., Josso N., di Clemente N.;

Thucosomal recessive segregation of a truncating mutation of a truncating mutation of a truncating mutation.

The action of a truncating mutation of a truncating mutation of anti-Mullerian bergets with its dominant of the register for anti-Mullerian hormone.

I. CIIn. Endocrinol. Metab. 86:4390-4397(2001).

I. CIIn. Endocrinol. Metab. 86:4390-4397(2001).

I. CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

I. CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

I. SUBCELIULAR LOCATION: Type I membrane protein.

I. DISEASE: Defects in AMHR2 are the cause of persistent Mullerian duct syndrome type II (PMDS-2) [MM:261550]; a form of male gestor product syndrome type II (PMDS-2) [MM:261550]; a form of male duct regression in otherwise normal males.

I. SIMILARITY: Belongs to the Ser/Thr family of protein kinases. TGPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
MEDLITHS=96028015; PubMed=7488027;
WREDLITHS=96028015; PubMed=7488027;
Visser J.A., McLuskey A., van Beers T., Weghuis D.O., van Kessel A.G.,
Grootegoed J.A., Themmen A.P.N.;
"Structure and chromosomal localization of the human anti-mullerian
hormone type II receptor gene.";
Biochem. Biophys. Res. Commun. 215:1029-1036(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Masiakos P.T., Maciaughiln D.T., Maheswaran S., Teixeira J., Fuller A.F. Jr., Shah P.C., Kehas D.J., Kenneally M.K., Dombkowski D.M., Ha T.U., Preffer F.L., Domahoe P.K.; "Human ovarian cencer, cell lines, and primary ascites cells express the human mullerian inhibiting substance (MIS) type II receptor, bind, and are responsive to MIS."; Clin. Cancer Res. 5:3488-3499(1999).
                                                                                                                               AMH2 HUMAN STANDARD; PRT; 573 AA.

Q16571, Q13762;

16-0CT-2001 (Rel. 40, Last sequence update)

10-0CT-2003 (Rel. 42, Last annotation update)

Auti-Mullerian hormone type II receptor precursor (BC 2.7.1.37) (AMH type II receptor) (MIS type II receptor)

AMHR2 OR AMHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND CYS-504.

MEDLINE=97056287; PubMed=8872466;
Imbeaud S., Belville C., Messika-Zeitoun L., Rey R., di Clemente N., Josso N., Picard J.-Y.;

Josso N., Picard J.-Y.;

"A 27 base-pair deletion of the anti-Mullerian type II receptor gene is the most common cause of the persistent Mullerian duct syndrome.", Hum. Mol. Genet. 5:1269-1277 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS PMDS-2 CYS-54; VAL-142; GLN-282; GLY-426; ALA-458; HIS-491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cate R.L., Picard J.-Y.;
"Insensityity to anti-mullerian hormone due to a mutation in the human anti-mullerian hormone receptor.";
Nat. Genet. 11:382-388(1995).
                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE=96083884; PubMed=7493017; Imbeaud S., Faure E., Lamarre I., Mattei M.-G., di Clemente N. Tizard R., Carre-Eusebe D., Belville C., Tragethon L., Tonkin Nelson J., McAuliffe M., Bidart J.-M., Lababidi A., Josso N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Testis;
MEDLINE=20055680; PubMed=10589763;
  24 GNSSPHNHPLP 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                       AMH2_HUMAN

AUG2_H

AUG12_H

AUG12_H

AUG12_H

DT 16-OCT

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EXTRACELLULAR (POTENTIAL).
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L -> V (IN REF. 2; CAA62593).
1347C10C2942FDBA CRC64;
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ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

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N-LINKED (GLCNAC. . .) (1

R -> C (in PMDS-2).
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V -> A (in PMDS-2).

/FTId=VAR_015530.

D -> H (in PMDS-2).

/FTId=VAR_015531.

R -> C (in PMDS-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VAR 015525.

G -> V (in PWDS-2).

H -> Q (in PWDS-2).

/FTId=VAR 015526.

/FTId=VAR 015527.

R -> Q (in PWDS-2).

/FTId=VAR 015528.

D -> G (in PWDS-2).

/FTId=VAR 015529.
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EMBL; AF172932; AAD48497.1; -.
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                                                                                                                                                                                                                                                                                                         CAA62593.1; CAA62593.1; CAA62593.1; CAA62593.1;
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CAA62593.1;
CAA62593.1;
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Genew; HGNC:465; AMHR2.
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573 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disease mutation.
SIGNAL 1
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X91159;
X91160;
X91161;
X91163;
X91164;
X91166;
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EMBL;
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EMBL;
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EMBL;
EMBL;
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EMBL;
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Best Local Similarity 63.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                      307 IPGYKSPSKOP 317
                                                                                                                                                                                                                                                                             2 LPGNKSPHRDP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                         1049 AA;
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50
1114
1165
221
815
935
940
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                  CARBOHYD
CARBOHYD
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    CARBOHYD
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MEDILINE=92227849; PubMed=1626432;

Skala J., Purnelle B., Goffeau A.;

Skala J., Purnelle B., Goffeau A.;

"The complete sequence of a 10.8 kb segment distal of SUF2 on the right arm of chromosome III from Saccharomyces cerevisiae reveals seven open reading frames including the RVS161, ADP1 and PGK genes.";

Yeast 8:409-417(1932).

-! - SUBCELIULAR LOCATION: Integral membrane protein (Potential).

-! - SUBCELIULAR Belongs to the ABC transporter family. MDR subfamily.
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=92160395; PubMed=1789009; 
Purnalle B., SRaia J., Goffeau A.; 
"The product of the YCR105 gene located on the chromosome III from Saccharomyces cerevisiae presents homologies to ATP-dependent
                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
PROBABLE ATP-DEPENDENT PERMEASE
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PROSITE; PS50893; ABC_TRANSPORTER 2; 1.
ATP-binding; Transmembrane; Glycoprotein; Transport; Signal.
                        3; Indels
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PIR; 919421; S19421.
PERCONTINE; 138916; -
SGD; S0000604; ADP1.
GO; GO: 0005793; C: endoplasmic reticulum; IDA.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC_transporter.
                                                                                                                                                                                                                                        01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
    61.5%; Pred. No. 55;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                    Probable ATP-dependent permease precursor.
ADP1 OR YCR011C OR YCR105.
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ProDom; PD000006; ABC transporter; 1.
SMART; SM00382; AAA; 1.
                                                              3 PGNKSPHRDPAPR 15
                                                                                     85 PGCESLHCDPSPR 97
                        8; Conservative
                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (east 7:867-872(1991)
    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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P25371;
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                        Matches
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(POTENTIAL)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97202105; PubMed=9049632; Steelman S., Moskow J.J., Muzynski K., North C., Druck T., Montgomery J.C., Huebner K., Daar I.O., Buchberg A.M.; "Identification of a conserved family of Meisl-related homeobox
                                                                                                                                                                                                                                                                                                                              .
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15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Homeobox protein Meis3 (Meis1-related protein 2) (Fragment).
MEIS3 OR MRG2.
                                                                                                                                                                                                                                                                Score 43; DB 1; Length 1049;
Pred. No. 1e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 7:142-156(1997).
--- SINCELLULAR LOCATION: Nuclear (Probable).
--- SINLIARITY: Belongs to the TALE/MEIS homeobox family.
--- SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                   MW; ABC9CE54BCFDF6A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blum H., Bauersachs S., Mewes H.-W., Weil B., Wiemann S. Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                (GLCNAC. . .)
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EMBL; U68385; AAB19195.1; -
HSSP; P40424; 1B72.

TRANSFAC; T0312; -
Genew; HGNC:7002; MEIS3.

GO; GO:0005634; C:nucleus; ISS.

GO; GO:0008283; P:cell proliferation; ISS.

InterPro; IPR001356; Homeobox.

Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                               GLCNAC
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PROSITE; PS50071; HOMEOBOX_2; 1.
DNA-binding; Nuclear protein; Homeobox..
NON_TER
     N-LINKED
N-LINKED
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SMART; SM00389; HOX; 1.
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                                                                                                                                                                                                                                                                              48.3%;
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Computed From N. N. State Embryonic stem cells;

KARAN=CSTSBL661, TISSUE=Embryonic stem cells;

KARAN=CSTSBL661, TISSUE=Embryonic stem cells;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S.,

Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Rofirian L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

By Gustincich S., Hill D., Hofmann M., Mume D.A., Kamiya M., Lee N.H.,

Nordone P., Rang B., Ringwald M., Rodriguez I., Sakamcto N.,

Nordone P., Rang B., Ringwald M., Rodriguez I., Sakamcto N.,

Basaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Wanshawa Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havashisaki Y.,

Havashisaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                      ;
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STRAIN=BALB/c; TISSUE=Testis;
MEDLINE=21907217; PubMed=11909948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miki K., Eddy E.M.;
"Tumor necrosis factor receptor 1 is an ATPase regulated by silencer
of death domain.";
Mol. Cell. Biol. 22:2536-2543(2002).
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                      ö
                    ASP/GLU-RICH (ACIDIC).
HOMEOBOX (TALE-TYPE).
KM -> RP (IN REF. 2).
M -> I (IN REF. 2).
D -> V (IN REF. 2).
R -> P (IN REF. 2).
R -> P (IN REF. 2).
VAPPG -> E (IN REF. 2).
VAPPG -> PEFAPA (IN REF. 2).
WASHALEG -> DEFGTRKE (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.2%; Score 42; DB 1; Length 382; 53.8%; Pred. No. 50; 5; Indels tive 1; Mismatches 5; Indels
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                     A2C11BE8061FB718 CRC64;
SER/THR-RICH.
                                                                                                                                                                                                                                                                           41821 MW;
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Mus musculus (Mouse).
                                                                                                                                                                                                                                                                           382 AA;
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                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 7; Conserv
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  217
259
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DOMAIN
DNA BIND
CONFLICT
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CONFLICT
SEQUENCE
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Matches
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F., Diatchenko I., Marusina K., Farmer A.A., Rubin G.M., Hong L., Bratchenko I., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H., Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Touchman J.W., Green B.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Humar and Mouse C.M. Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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L->P: ABOLISHES INTERACTION WITH HSP70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A->P: ABOLISHES INTERACTION WITH HSP70 AND TNFRSF1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Inhibits the chaperone activity of HSP70/HSC70 by promoting substrate release. Prevents constitutive TNPRSF1A signaling (By similarity).
-!- SUBUNT: Binds to the ATPase domain of HSP70/HSC chaperones. B to the death domain of TNFRSF12 (By similarity). Binds to the approach prevents Dinding of adapter molecules such as TRADD or TRAF2.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 0
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Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
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Last annotation update)
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EMBL; BC037239; AAH37239.1; ALT_INIT.
EMBL; BC058518; AAH58518.1; --
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01-APR-1993 (Rel. 25, Created)
10-OCT-2001 (Rel. 40, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF332863; AAL99586.1; -. EMBL; AK010765; BAB27167.1; -.
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Pfam; PF02179; BAG; 1.
SMART; SM00264; BAG; 1.
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hes 7; Conservative
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298
387
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387
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Franck A., Guilley H., Jonard G., Richards K., Hirth L., "Nucleotide sequence of cauliflower mosaic virus DNA."; Cell 21:285-294(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cauliflower mosaic virus (strain Strasbourg) (CaMV).
Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) Inclusion body matrix protein (Viroplasmin).
                  BMBL; AE003589; AAF51484.1; --
BMBL; M80475; AAA28452.1; ALT_FRAME.
HSSP; Q01543; IFLI.
FlyBase; FBGN0005660; Et821C.
InterPro; IPR00418; Ets.
InterPro; IPR002341; HSF ETS.
InterPro; IPR002341; HSF ETS.
                                                                                                                                                                                                                                                                                         PROSITE; PS00345; ETS DOMAIN 1; 1.
PROSITE; PS00346; ETS DOMAIN 2; 1.
PROSITE; PS50061; ETS DOMAIN 3; 1.
DNA binding; Nuclear Protein.
DNA BIND 255 335
ETS-DX
SEQÜENCE 475 AA; 51802 MW; 0D38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=81001865; PubMed=7407912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                           Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM PNT; 1.
PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
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Best Local Similarity 53.0.
7, Conservative
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                                                                                                                                                                                                                                                       RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Randlineary C.B., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E. I. P.W., Hoskins R.A., Galle R.F., Gotorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Ffeiffer B.D., R. Bardon R.C., Raders F. H.C., Blazej R.G., Champe M., Ffeiffer B.D., R.A. Barland J. B.C., Baxter E.G., Helt G., Wahbon C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D., R. Ballew R.M., Basu A., Baxendal J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Barman B.P., Bhandari D., Bolshakov S., Abrilor P., Botcher P., Carler P., R.A. Burtis R.C., Busam D.A., Paller H., Cadieu E., Center A., Chadra I., R.A. Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P., R. Burtis R.C., Busam D.A., Baller R., Canton E., Dowles R., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P. Bodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P., Bodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P., Bodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Busam D.A., Bathan T.J., Hernardez J.R., Houck J., R.A. Hostin D., Houston K.A., Hainan T.J., Wei M.-H., Ibegwam C., Jalli M., Kalush F., Karpen G.H., Kez J., Kennison J.A., Ketchum K.A., Jalli M., Kalush F., Karpen G.H., Kez J., Kennison J.A., Ketchum K.A., Jalli M., Kalush F., Karpen G.H., Kez J., Kennison J.A., Ketchum K.A., Jalli M., Murbhy B., Murphy L., Murshy D., Lai Z., Mount S.M., Molshina M.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Molshina M.V., Moharry C., Morris J., Moshrefi A., Spier E., Spradling A.C., Stapleton M., Stung K., Sung K., Shan H., Shue B.C., Siden-Kamos I., Simpson M., Stung S., Shap G., Shap G., Shan C., Shan H., Wang C., Jahan G., Shan C., Shan H., Wang C., Shan W., Woolseeler F., Wang S., Wholes B.C., Shan S., Wholes B.C., Shan J., Wang S., Whole S., Shap G., Shan W., Woolse G., Whole S., Shan S., Shan S., Sha
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Chen T., Bunting M., Karim F.D., Thummel C.S.;
"Isolation and characterization of five Drosophila genes that encode
an ets-related DNA binding domain.";
Dev. Biol. 151:176-191(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 235-352 FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL
DNA-binding protein D-ETS-6.
ETS2LO R ETS-6 OR CG2914.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Diptera; Dipterygota; Diptera; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                    WEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Canton-S; TISSUE=Larva;
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                          STRAIN-Berkeley;
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.; 0

Gaps

.; 0

47.2%; Score 42; DB 1; Length 475; 53.8%; Pred. No. 63; tive 2; Mismatches 4; Indels

119 PAVSSPHQAPSPR 131

3 PGNKSPHRDPAPR 15

520 AA.

STANDARD;

0D382C41C03B1502 CRC64;

ETS-DOMAIN

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                                                                                                                               CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
-i- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON POLYCISTRONIC MRNA'S DERIVED FROM CALLIFLOWER MOSAIC VIRUS.
-i- SUBCELLULAR LOCATION: CYtoplasmic inclusion bodies.
-i- MISCELLANEOUS: THE INILUZION BODIES ARE THE SITE OF VIRAL DNA SYNTHESIS, VIRION ASSEMBLY AND ACCUMULATION IN THE INPECTED CE.
-i- SIMILARITY: Belongs to the caulimoviruses viroplasmin family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002609; Caulimo_VI.
InterPro; IPR009027; L9 N like.
Pfam; PF01693; Caulimo_VI; I.
Trans-acting factor; Translation regulation.
SEQUENCE 520 AA; 57992 MW; DD41D89DD2D5E8EI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 1;
Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 69;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.2%;
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Best Local Similarity 58.3
Matches 7; Conservative
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-i - SUBCELLULAR LOCATION: Nuclear. -i - TISSUE SPECIFICITY: EMBRYONIC VENTRAL NERVOUS SYSTEM AND 1 FAIR NEURONS IN EACH THORACIC SEGMENT.

-!- DEVELOPMENTAL STACE: Expressed throughout development. -!- SIMILARITY: Belongs to the ETS family. -!- CAUTION: Ref.2 sequence differs from that shown due to a

frameshift in position 242.

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cauliflower mosaic virus.";
                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A04160;
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P13218;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93383405; PubMed-8372449; White-enantel W.M., Anderson E.J., Schoelz J.E.; ilflower mosaic virus "Identification of domains within gene VI of cauliflower mosaic virus that influence systemic infection of Nicotiana bigelovii in a light-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virology 196:789-798 (1993).

-!- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON POLYCISTRONIC MENA'S DERIVED FROM CAULIFLOWER MOSAIC VIRUS.
-!- SUBCELLULAR LOCATION: Cytoplasmic inclusion bodies.
-!- MISCELLANBOOR: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA SYNTHESIS, VIRION ASSEMBLY AND ACCUMULATION IN THE INFECTED CEST.
-!- SIMILARITY: Belongs to the caulimoviruses viroplasmin family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; Retroid viruses; Caulimoviridae; Caulimovirus. NCBI __TaxID=10645;
                                                                                                                                                                                                                                                                                                                  Cauliflower mosaic virus (strain W260) (CaMV).
Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01693; Caulimo \overline{\rm V17} 1. Translation regulation. Recerting factor; Translation regulation . SEQUENCE 520 AA; 57976 WW; 4BR110D55BBB9647 CRC64;
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15-JUL-1999 (Rel. 38, Last annotation update)
Inclusion body matrix protein (Viroplasmin).
                                                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Inclusion body matrix protein (Viroplasmin).
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                                                                                                                                                               520 AA.
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MEDLINE=83106468; PubMed=7152260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L09053; AAA46360.1; -.
InterPro; IPR002609; Caulimo VI.
InterPro; IPR009027; L9 N like.
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Les 7; Conservative
                                                   228 GTKKPSSDPAPK 239
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           GNKSPHRDPAPR 15
                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=31558;
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P03557;
                                                                                                                                                                 CAMVW
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Matches
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                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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Gene 19:239-249(1982).
--- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON POLYCISTRONIC MRNA'S DERLYDE FROM CAULIFLOWER MOSAIC VIRUS.
---- SUBCELLULAR LOCATION: Cytoplasmic inclusion bodies.
---- MISCELLAMBOUS: THE INCLUSION BODIES ARE THE SITE OF VIRLE DNA SYNTHESIS, VIRLON ASSEMBLY AND ACCUMILATION IN THE INFECTED CELL.
---- SIMILARITY: Belongs to the caulimoviruses viroplasmin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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-!- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cauliflower mosaic virus (strain S-Japan) (CaMV). Viruses, Retroid viruses, Caulimoviridae, Caulimovirus.NCBI_TaxID=10646,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002609, Caulimo VI.
InterPro; IPR009027, L9 N like.
Pfam, PF01693, Caulimo VI, II.
Trans-acting factor; Translation regulation.
SEQUENCE 522 AA, 58285 NW, F87CB62C1F30DD57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
115-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42; DB
Pred. No. 69;
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InterPro; IPR0005609; Caulimo VI.
InterPro; IPR009027; L9 N like.
Pfam; PF01693; Caulimo VI; 1.
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58.3%;
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nes 7; Conserv
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InterPro; PR000472; Activin receptor.
InterPro; IPR000472; Prot kinase.
InterPro; IPR000471; Prot kinase.
InterPro; IPR000471; Ser_thr_pkin_AS.
Pfam; PP01064; Activin recp; 1.
Pfam; PP01069; pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; FALSE_NEG.
PROSITE; PS00107; PROTEIN KINASE_ATP; FALSE_NEG.
PROSITE; PS00101; PROTEIN KINASE_DOM; 1.
Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding; Transmembrane; Glycoprotein; Signal.
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Best Local Similarity
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CONFLICT
SEQUENCE
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KM FEDLINE=20040636; PubMed=10570158;

KMEDLINE=20040636; PubMed=10570158;

Transcriptional regulation of the rat mullerian inhibiting substance "Transcriptional regulation of the rat mullerian inhibiting substance "Transcriptional receptor in rodent Leydig cells.";

Proc. Natl. Acad. Sci. U.S.A. 96:13831-13838(1999).

- - FUNCTION: Receptor for anti-Mullerian hormone.

- - CATALYTIC ACTIVITY: ATP + a protein.

- - SUBCELDIAR LOCATION: Type I membrane protein.

- - SUBCELDIAR LOCATION: Type I membrane protein.

- - BUVELOPMENTAL STAGE: Expressed in the mesenchymal cells and 16 and in tubular and follicular structures of the fetal gonads.

- - SIMILARITY: Belongs to the Ser/Thr family of protein kinases. TGFB receptor subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baarends W.M., Van Helmond N.J.L., Post M., Van der Schoot P.J.C.M., Hoogerbrugge J.W., de Winter J.P., Uilenbroek J.T.J., Karels B., Wilming L.G., Meijers J.H.C., Themmem A.P.N., Grootegoed A.J.; "A novel member of the transmembrane serine/threonine kinase receptor family is specifically expressed in the gonads and in mesenchymal cells adjacent to the mullerian duct.";
                                                                                                                                                                                                                                                                                                                                                                              AMH2 RAT STANDARD; PRT; 557 AA.

Q62893; Q63045; Q9R0A7;
16-0CT-2001 (Rel. 40, Created)
15-WAR-2004 (Rel. 40, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Anti-Wullerian hormone type II receptor precursor (EC 2.7.1.37) (AMH type II receptor) (MIS type II receptor) (MIS type II receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96107132; PubMed=8536608;
Teixeira J., He W.W., Shah P.C., Morikawa N., Lee M.M., Catlin B.A., Hudson P.L., Wing J., Maclaughlin D.T., Donahoe P.K.;
"Developmental expression of a candidate mullerian inhibiting substance type II receptor.";
Endocrinology 137:160-165(1996).
                                                                                                                                             Gaps
                                                                                                                                             .
0
                                                                                   47.2%; Score 42; DB 1; Length 522; 58.3%; Pred. No. 69;
                                                                                                                                             Indels
  Trans-acting factor; Translation regulation.
SEQUENCE 522 AA; 58410 MW; 8EB136BB17ED408A CRC64;
                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94163972; PubMed=8119126;
                                                                                                             Local Similarity 58.3%;
nes 7; Conservative
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                                                                                                                                                                                                                                                        228 GTKKPSSDPAPK 239
                                                                                                                                                                                                    4 GNKSPHRDPAPR 15
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
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                                                                                         Query Match
                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                         RESULT 24
                                                                                                                                                                                                                                                                                                                                                                      AMH2_RAT
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Gaps

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4; Indels

1; Mismatches

8; Conservative

Score 42; DB 1; Length 557; Pred. No. 74;

REDEE9COC32EBDD5 CRC64;

59748 MW; 47.2%; 61.5%;

557 AA;

(IN REF. 2)

ANTI-MULLERIAN HORMONE TYPE II RECEPTOR.

EXTRACELLULAR (POTENTIAL)

POTENTIAL. CYTOPLASMIC (POTENTIAL).

ATP (BY SIMILARITY) ATP (BY SIMILARITY)

145 166 201 207 228 331 66 119

PROTEIN KINASE.

BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

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STRAIN-FVB/N; TISSUE-Salivary gland;

STRAIN-FVB/N; TISSUE-Salivary gland;

STRAIN-FVB/N; TISSUE-Salivary gland;

STRAIN-E22388257; PubMed=12477932;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Riausner R.D., Collins F.S., Margner L., Shemmen C.M., Schuler G.D., A Lischnil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hableh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Ubdin T.B., Toshhyuki S., Carninci P., Parage C., Raha S.A., Ioquellano N.A., Perters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20480369; PubMed=11025217; Granadino B., Arias-de-la-Fuente C., Perez-Sanchez C., Parraga M., Lopez-Fernandez L.A., del Mazo J., Rey-Campos J.; "Fhx (Foxj2) expression is activated during spermatogenesis and very
                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                      16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
Forkhead box protein J2 (Fork head homologous X).
FOXLO OR FHX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 early in embryonic development.";
Mech. Dev. 97:157-160(2000).
3 PGNKSPHRDPAPR 15
                                            85 PGCESLHCDPVPR 97
                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                               (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                               FXJ2 MOUSE
Q9ES18;
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EMBL; X71916; CAA50731.1; -. EMBL; AF092445; AAC64138.1; -. EMBL; U42427; AAC52343.1; -.

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protein homolog implicated in neuronal membrane traffic.";
J. Neurosci. 20:8551-8565(2000).
-!- FUNCTION: Binds to type II regulatory subunits of protein kinase A
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Blutrerfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-: FUNCTION: Transcriptional activator. Able to bind to two different
type of DNA binding sites.
-: SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                     HSSP; Q63487; .......
TRANSEAC; T04170; ....
MUD; MGI:1926805; Foxj2.
Interpro; IPR001766; TF Fork_head.
Pfan; PF00260; FoxfRHEAD;
PRODOM; PF000623; FORKHEAD;
PRODOM; PF000425; TF Fork_head; 1.
PROSTE; PS00653; FORK_HEAD_1; FALSE_NEG.
PROSTE; PS00653; FORK_HEAD_2; 1.
PROSTE; PS00639; FORK_HEAD_2; 1.
PROSTE; PS50039; FORK_HEAD_2; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
TRANSCAID; PS0039; FORK_HEAD_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 1; Length 565;
Pred. No. 75;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-GLN.
9178AFF3F9227AD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang X., Herberg F.W., Laue M.M., Wullner C., Hu B.,
Petrasch-Parwez E., Kilimann M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                        -!- SIMILARITY: Contains 1 fork-head domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      793 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-SER.
POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20556611; PubMed=11102458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurobeachin protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last seqn
10-0CT-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 314 PC
565 AA; 61569 MW;
                                                                                                                                                                                                                                                                                                                   EMBL; AF253052; AAG30406.1; -. EMBL; BC040395; AAH40395.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nilarity 50.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HLPGNKSPHRDPAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                 HSSP; Q63245; 2HFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBL_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oppo<u>D</u>5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NBEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
and anchors/targets them to the membrane. May anchor the kinase cycoskeletal and/or organelle-associated proteins (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                SUBUNIT: Interacts with RII subunit of PKA (By similarity) SUBCELLUIAR LOCATION: Cytoplasmic and membrane-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   793 AA; 87803 MW; 19F5AC6C49A7F2A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the neurobeachin family.
                                                                                                                                                                                                                                                                                                            -!- TISSUE SPECIFICITY: Forebrain and cerebellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.2%; Score 42; DB 1; I
58.3%; Pred. No. 1.1e+02;
tive 3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Axin 2 (Axis inhibition protein 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50197; BEACH; PARTIAL.
PROSITE; PS50197; WEAEALS 1, PARTIAL.
PROSITE; PS50082; WD REPEATS 2; PARTIAL.
PROSITE; PS50082; WD_REPEATS_REGION; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               812 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (By similarity).
-!- SIMILARITY: Contains 1 RGS domain.
-!- SIMILARITY: Contains 1 DIX domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20171051; PubMed=10704853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Y18277; CAC18801.1;
InterPro; IPR00409; Baige BEACH.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::||| || :||
621 NVPGNLSPIKDP 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 58...
hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HLPGNKSPHRDP 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7955;
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P SEQUENCE FROM NA.

P SEQUENCE FROM NA.

YEQUINGE FROM NA.

MEDLINE=20057165; Pubmed=10591208; Bruskiewich R., Beare D.M.,
Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Babege A.K.,
Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
Brid C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
A Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Gilbert J.G.R., Goward M.E., Grandam D.V., Griffiths M.N.D., Hall C.,
A Hall R.E., Hall-Tamlyn G., Hearthcott R.W., Ho S., Holmes S.,
A Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE—99156230; PubMed=10046485;
Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XII.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 5:355-364(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                GSK3B BINDING SITE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·,
                                                                                                                                                                                 PRINTS; PRO130; MCSPROTEIN.
ProDom; PD003639; DIX; 1.
ProDom; PD001580; Regl Gprotein; 1.
SMART; SM00315; RGS; 1.
PROSITE; PS50841; DIX; 1.
PROSITE; PS50132; RGS; 1.
Developmental protein; Mrt signaling pathway; Phosphorylation.
DowAIN
84 203 RGS.
                                                                                                                                                                                                                                                                                                                                               BETA-CATENIN BINDING SITE (BY SIMILARITY).
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.2%; Score 42; DB 1; Length 812; 46.7%; Pred. No. 1.1e+02; Live 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       46E5ADA6DE2240CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K852_HUMAN STANDARD; PRT; 970 AA. Q9Y6X9; Q9Y6X9; (28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
modified and this statement is not remove entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                    InterPro; IPR001158; DIX.
InterPro; IPR000342; Regl Gprotein.
                                                                                     HSSP; P49799; LAGR.
ZFIN; ZDB-GENE-000403-2; axin2.
                                                                                                                                                                                                                                                                                                                                                                                                     730 812 D
812 AA; 91496 MW;
                                                                    EMBL; AB032263; BAA92440.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 457 HSPRSRSPEQRPLPR 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HLPGNKSPHRDPAPR 15
                                                                                                                                                      Pfam; PF00778; DIX; 1.
Pfam; PF00615; RGS; 1.
                                                                                                                                                                                                                                                                                                                  203
415
467
                                                                                                                                                                                                                                                                                                                                                                                         419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rotein KIAA0852.
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                                                                                                                                                                                                                                                                                                                                                    415
                                                                                                                                                                                                                                                                                                                                    329
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                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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haird G.K., Langford C.F., Liversha M. Matthers L.H., MCCARD D.H.,

M. McCLAY L. Langford C.F., Liversha M. Matthers L.H., MCCARD D.H.,

M. McCLAY L.M., Farith R.M., Kansay H., Mills S. A., McTidono B.J.C.J.,

M. McCLAY L.M., Farith R.M., Ramsay H., Mills S. A., McTidono B.J.C.J.,

M. Scotch C.M., Farith R.M., Ramsay H. Ramsay Y. Kogers L., Ross M.T.,

M. Scotch C.M., Schrad H.K., Shuce C.D., Shallow S., Shindon H.L.,

M. McHilles S.H., Malls Willia William M.H.,

M. McHilles S., Mahadad T. Berliet D. M. Beck S., Scots J. Shindia N.,

McHilles S., McHille, W. Mills William W.H.,

McHilles S., McHarley S., Mills W. M. Molland M. M. Miller Y. Del N. D. T.,

M. McHilles S., Mahadad T. Berliet D. D. Beck S., Scots J. Shindia N.,

McHilles S., McHille, W. William W. William W.,

McDeman A., Fang P., Pu. V. Crabtree J., Dels Delsays S., Laid H. Lao M. B.,

McDeman A., Fang P., Pu. V. Whitaki Y. Andi N. William Y.,

McDeman A., Fang P., Pu. V. White D. M. Miller N. Wink P.,

Zhan W. Chang C., Chasee S., White V. Wallis E., Wangen T., Pack S.,

M. A. Mandad M. M. Du Z., Pulcon L., Goola D., Graves T., Hawkins J.,

M. Minch M. M. Du Z., Pulcon L., Goola D., Graves T., Hawkins J.,

M. McHille M., McMan D., Servasis G., Farther D., Wallis M., Waller C.E.,

M. McHille M., McMan D., Servasis G., Farther D., Wallis M., Waller C.E.,

M. McHille M., McMan D., Servasis E., Franseon I., Tapia I., Ender C.E.,

M. McHille M., McMan D., Servasis E., Franseon I., Tapia I., Ender C.E.,

M. McHille M., McMan D., Servasis E., Franseon I., Tapia I., Ender C.E.,

M. McHille M., McMan D., Servasis E., Franseon I., Tapia I., Ender C.E.,

M. McHille M., McMan D., Servasis E., Franseon I., Tapia I., Ender C.E.,

M. McHille M., McMan D., Servasis E., Franseon I., Tapia I., Scheet Z.E.,

M. McHille M., McMan D., Waller M., McGarman K., McM. M., McHille M., McMan D., Waller M., McHille M., McMan D., Waller M., McHille M., McMan D., Waller M., McHille M., McMan D., Waller M., McHille M., McMan D., Waller M., McHille M., McMan D., Waller M., McHi
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STRAIN=C57BL/60; ITSSUB=Cerebellum;

MEDLINE=2534683; PubMed=1246681;

A Wazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Ansapin A., Matsuda H., Batalov S., Beisel K.W.,

Baldarelli E., Dragami T.A., Fletcher C.F., Forrest A., Frazer K.S.,

Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis R.D.,

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Maglott D.R., Maltais L., Marchiomi L., McKenzie L., Miki H.,

Nagashima T., Numata K., Okido T., Pertea G., Pesole G.,

Nagashima T., Numata K., Okido T., Pertea G., Pesole G.,

Nagashima T., Numata K., Pontius J.U., Qi D., Ramachandran S.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dyomin V.G., Chaganti S.R., Dyomina K., Palanisamy N., Murty V.V.V.S., Dalla-Favera R., Chaganti R.S.K.;
"BCL8 is a novel, evolutionarily conserved human gene family encoding proteins with presumptive protein kinase A anchoring function."; Genomics 80:158-165(2002).
                                                                                                                                                                                                                                                                                                Gaps
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Petrasch-Parwez E., Kilimann M.W.;
Neurobeachin: a protein kinase A-anchoring, beige/Chediak-Higashi
protein homolog implicated in neuronal membrane traffic.";
J. Neurosci. 20:8551-8565 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
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                                                                                                                                                                                                                  970 AA; 110724 MW; 459161807B8B53F6 CRC64;
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COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
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            EMBL; AB020659; BAA74875.1; -.
EMBL; AC004542; AAC12554.1; ALT_SEQ.
EMBL; BC012257; AAH19257.1; -.
EMBL; AL133637; CAB63760.1; -.
EMBL; T43455; T43455.
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MEDLINE=22150869; PubMed=12160729;
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485
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Thernev V.T., McMurtrie E.B. Nguyen Q.A., Mishra V.S.,

RA Barbosa M.D.F.S., McIndoe R., Kingsmore S.F.;

RT Indentification of INST2, a brain-specific member of the Chediak-
RT Higashi syndrome gene family.";

Rubmitted (JUN-1998) to the EMBL/Genbank/DDBJ databases.

L. FUNCTION: Binds to type II regulatory submits of protein kinase A and anchors/targets them to the membrane. May anchor the kinase to and anchors/targets them to the membrane. May anchor the kinase to cytoskeletal and/or organalle-associated proteins. May have a role in membrane trafficking.

C. SUBUNIT: Interacts with RII subunit of PKA.

C. SUBCELLULA LOCATION: Cytoplasmic and membrane associated.

Associated with pleomorphic tubulovesicular endomembranes near the trans sides of Golgi stacks and throughout the cell bodies and cell processes. Concentrated at the postsynaptic plasma membrane

C. I-ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanbe Y., Watlanbe Y., Walls C., Wang Y., Wang Y., Wang I., Yang I., Yang I., Yang I., Yang I., Yang I., Yang I., Yang I., Yang I., Yang I., Yang I., Yang I., Yang I., Komo H., Nakamura M., Sakazune N., Sato K., Hirozane-Kishikawa T., Komo H., Nakamura M., Sakazune N., Sato K., Rawai J., Aizawa K., Arakwa T., Fludua S., Hara A., Hashizune W., Incani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yashino M., Waterston R., Lander B.S., Rogers J., Yashilayais Of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q9EPN1-2; Sequence=VSP_050540;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=4;
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G0:0005829; C:cytosol; IDA.
G0:0012505; C:endowembrane system; IDA.
G0:0005802; C:colgi trans face; IDA.
G0:0005806; C:plasma membrane; IDA.
G0:0045211; C:postsynaptic membrane; NAS.
G0:0045211; C:postein kinase Anchoring a
G0:0019901; F:protein kinase binding; IDA.
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SEQUENCE FROM N.A. (ISOFORM 2)

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MEDLINE=22150869; PubMed=12160729;
MCDLINE=22150869; PubMed=12160729;
Dyomin V.G., Chaganti S.R., Dyomina K., Palanisamy N., Murty V.V.V.S.,
Dalla-Favera R., Chaganti R.S.K.;
"BCL8 is a novel, evolutionarily conserved human gene family encoding
proteins with presumptive protein kinase A anchoring function.";
denomics 80:158-165(2002).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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QBNRPS; QSHCM8; QSNSUI; QSNW98; Q9Y6JI;
10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last amnotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
Neurobeachin protein (Lysosomal trafficking regulator 2) (BCL8B
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Pred. No. 4.3e+02;
3; Mismatches 2; Indels
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/FTId=VSP 050540.
                                                                                                                                                                                                                                                                                       Membrane, Alternative splicing
GO; GO:0006892; P:post-Golgi transport; NAS.
InterPro; IPR008993; ARM.
InterPro; IPR000409; Beige_BRACH.
InterPro; IPR001680; WD40.
Pfam; PF002138; Beach; 1.
Pfam; PF00400; WD40; 5.
ProDom; PD007848; Beige_BEACH; 1.
                                                                                                                                                            PROSITE; PS50197; BEACH; 1.
PROSITE; PS50197; BEACH; 1.
PROSITE; PS00678; WD REPEATS 1; FALSE NEG.
PROSITE; PS50082; WD REPEATS 2; FALSE NEG.
PROSITE; PS50294; WD REPEATS REGION; 1.
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1513 NVPGNLSPIKDP 1524
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REPEAT 1316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X.TAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 2150-2563.
MEDLINE=22220051; PubMed=12234919;
Jog1 G., Shen Y., Gebauer D., Li J., Wiegmann K., Kashkar H.,
Kroenke M., Tong L.;
Kroenke M., Tong L.;
Crystal structure of the BEACH domain reveals an unusual fold and
extensive association with a novel PH domain.";
EMBO J. 21:4785-4795 (2002).
-!- FUNCTION: Binds to type II regulatory subunits of protein kinase A
and anchors/targets them to the membrane. May anchor the kinase to
cytoskeletal and/or organelle-associated proteins (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note-No experimental confirmation available;
IISSUE SPECIFICITY: Predominant in many brain structures. Also expressed at medium levels in spleen, thymus, prostate, testis and covary. Low level expression is seen in heart, kidney, pancreas, skeletal muscle and intestine.
DOMAIN: RII-alpha binding site, predicted to form an amphipathic helix, could participate in protein-protein interactions with a complementary surface on the R-subunit dimer (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1919-2946 FROM N.A. (ISOFORM 1).
MEDLINE=20450683; PubMed=10997877;
Nagaee T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
Prediction of the coding sequences of unidentified human genes.
XVIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:273-281(2000).
                                          Duesterhoeft A., Lauber J., Mewes H.-W., Gassenhuber J., Wiemann S.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

similarity).
SIMILARITY: Belongs to the neurobeachin family.
SIMILARITY: Contains 1 BEACH downin.
SIMILARITY: Contains 5 WD repeats.
CAUTION: Ref.3 sequence differs from that shown due to a stop codon in position 762.
CAUTION: Ref.5 sequence differs from that shown due to a frameshift in position 2900.

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                                                                                                                                                                                                                                                            Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Sushikkawa T., Magai K., Sugiano S., Takabashi-Pujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Makanatau A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 2428-2946 FROM N.A. (ISOFORM 1).
TChernev V.T., McMurtrie E.B., Nguyen Q.A., Mishra V.S.,
Barbosa M.D.F.S., McIndoe R., Kingsmore S.F.;
"Identification of LYST2, a brain-specific member of the Chediak-Higashi syndrome gene family.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q8NFP9-2; Sequence=VSP_050538, VSP_050539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity/.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q8NFP9-1; Sequence=Displayed;
                                                                                                                                                                             SEQUENCE OF 606-1118 FROM N.A.
                                                                                                                                                                                                                                TISSUE=Embryonic head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
TISSUE=Testis;
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342 3
367 3
392 AA;
                                                STRUCTURE BY NMR OF
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isolates.";
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ZN_FING
LIPID
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CHAIN
CHAIN
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GAG_BLVJ
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Coulston J., Naif H., Brandon R., Kumar S., Khan S., Daniel R.C.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
GAG polyprotein [Contains: Core protein P15 (Matrix protein); Core
GAG.
                                                                                                                                                                                                                                                                                                                                                   Pinerkro; irrocator;
Pfam; PF02138; Beach; 1.
Pfam; PF00408; WD40; 5.
ProDom; PD007848; Beige BEACH; 1.
PROSITE; PS500678; WD REPEATS 1; FALSE NEG.
PROSITE; PS50082; WD REPEATS 2; FALSE NEG.
PROSITE; PS50284; WD REPEATS 2; FALSE NEG.
PROSITE; PS50294; WD REPEATS Albernative splicing; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 1; Length 2946; Pred. No. 4.3e+02; 3; Mismatches 2; Indels
                                                                                                                                                                 GO, GO:0005829; C:cytosol; ISS.
GO; GO:0005829; C:cytosol; ISS.
GO; GO:0012505; C:endomembrane system; ISS.
GO; GO:0005802; C:Golgi trans face; ISS.
GO; GO:0005802; C:plasma membrane; ISS.
GO; GO:005079; P:protein kinase A anchoring activity; ISS.
GO; GO:00109901; P:protein kinase binding; ISS.
GO; GO:0006892; P:protein kinase binding; ISS.
InterPro; IPR00938; ARM.
InterPro; IPR0001680; MA40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Frid=vSP 050539.
S -> N (IN REF. 5).
S -> T (IN REF. 5).
MW; 6CDA70D61F1E255E CRC64;
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WD 3.
WD 4.
WD 5.
Missing (in isoform 2).
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                            R EMBL; AKO01059; CAR70903.1; -.
R EMBL; AKO01059; BAA91485.1; ALT_SEQ.
R EMBL; AB046764; BAB13370.1; -.
EMBL; AF072371; AAA41633.1; ALT_FRAME.
Genew; HGNC:7-SEP-02.
MIM; 604889: --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VSP
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WD 1.
BEACH.
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2946 AA; 327807
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Best Local Similarity 58.5-
The 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 HLPGNKSPHRDP 12
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P25058;
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REPEAT
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GAG BLVAU
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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CORE PROTEIN P24.

CORE PROTEIN P24. (GENOME-BINDING PROTEIN WITH REPEATED SEQUENCES).
                                                                           MEDITNE=9283625; PubMede8670827;
Matthews S., Miklhailov M., Burny A., Roy P.;
Matthews S., Miklhailov M., Burny A., Roy P.;
"The solution structure of the bovine leukaemia virus matrix protein and similarity with lentiviral matrix proteins.";

EMBO J. 15:3267-3274(1996).
-!- SIMILARITY: VERY STRONG, WITH THE BOVINE LEUKEMIA VIRUS GAG POLYPROTEIN FROM OTHER ISOLATES.
-!- SIMILARITY: Contains 2 CCHC-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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LOCYT-2003 (Rel. 42, Last annotation update)
GAG polyprotein [Contains: Core protein P15 (Matrix protein); Core protein P24, Core protein P12].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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Pfam; PF00228; GAG pl9; I.
Pfam; PF00607; GAG p24; 1.
Pfam; PF00099; zf-CCHC; 2.
PRINTS; PR00343; ZnF C2HC; 2.
PROSITE; PS50158; ZF CCHC; 1.
Core protein; Polyprotein; Phosphorylation; Repeat; Myristate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCHC-TYPE 1.
CCHC-TYPE 2.
N-myristoyl glycine (in host) (By
similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine leukemia virus (Japanese isolate BLV-1) (BLV).
Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42766 MW; A4D5F480D861B72C CRC64;
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InterPro; IPR003139; Gag_p19.
InterPro; IPR000721; Gag_p24.
InterPro; IPR0008916; Retrov capsid_C.
InterPro; IPR008919; Retrov capsid_N.
InterPro; IPR001878; Znf_CCHC.
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MEDLINE=85140159; PubMed=2983308;
Gen. Virol. 71:1737-1746(1990)
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Best Local Similarity 56.2.
Local 9; Conservative
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Zinc-finger; Lipoprotein.
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NCBI_TaxID=10299;
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Q94425;
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SEQUENCE
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CORE PROTEIN P24.

CORE PROTEIN P12 (GENOME-BINDING PROTEIN P12 (GENOME-BINDING PROTEIN CCHC-TYPE 1.

CCHC-TYPE 1.
                                                "Complete nucleotide sequence of the genome of bovine leukemia virus: its evolutionary relationship to other retroviruses."; Proc. Natl. Acad. Sci. U.S.A. 82:677-681(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-83210199; PubMed-6303852;
Copeland T.D., Morgan M.A., Oroszlan S.;
"Complete amino acid sequence of the nucleic acid-binding protein of
bovine leukemia virus.";
Sagata N., Yasunaga T., Tsuzuku-Kawamura J., Ohishi K., Ogawa Y.,
                                                                                                                                                                                                                                                                                       "Amino-terminal sequence of bovine leukemia virus major internal protein: homology with mammalian type C virus p30 structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 156:37-40(1983).
-!- SIMILARITY: VERY STRONG, WITH THE BOVINE LEUKEMIA VIRUS GAG POLYPROTEIN FROM OTHER ISOLATES.
-!- SIMILARITY: Contains 2 CCHC-type zinc fingers.
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SMART; SM00343; ZnF C2HC; 2.
PROSITE; PS50158; ZF CCHC; 1.
Core protein; Polyprotein; Phosphorylation; Repeat; Myristate;
Zinc-finger; Lipoprotein.
                                                                                                                                                                          SEQUENCE OF 110-164.
MEDLINE=79223918; PubMed=223166;
Oroszlan S., Copeland T.D., Henderson L.E., Stephenson J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 392;
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                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 76:2996-3000(1979)
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or send an email to license@isb-sib.ch).
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capsid_N.
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InterPro; IRR003199; Gag_D19.
InterPro; IRR008916; Regrov capsid C.
InterPro; IRR008916; Retrov capsid C.
InterPro; IRR008919; Retrov capsid N.
InterPro; IRR001878; Znf CCHC.
Ffan; PF00607; Gag_D19; I.
Pfan; PF00607; Gag_D24; I.
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Best Local Similarity
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ZN_FING
LIPID
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ID US10_H8
AC P06486
DT 01-JAN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=84169548; PubMed=6324121;
MEDLINE=84169548; PubMed=6324121;
Mixon F.J., McGecoh D.J.;
"A 3' co-terminal family of mRNAs from the herpes simplex virus type 1 short region: two overlapping reading frames encode unrelated polypeptide one of which has highly reiterated amino acid sequence.";
Nucleic Acids Res. 12:2473-2487(1984).
-- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-1 US10,
EHV-1 66, EHV-4 ORF3, AND VZV 64/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Probable isoleucyl-tRNA synthetase (EC 6.1.1.5) (Isoleucine--tRNA
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=85160822; PubMed=2984429;
McGeoch D.J., Dolan A., Donald S., Rixon F.J.;
Msequence determination and genetic content of the short unique region in the genome of herpes simplex virus type 1.";
J. Mol. Biol. 181:1-13(1985).
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Bird A.P., Clark V., Jones S.J.M., Leitgeb S., Lennard N.,
Tweedie S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
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12D01B0E7C920EA3 CRC64;
                                                                                                                        Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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Pred. No. 56;
01-JAN-1988 (Rel. 06, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Virion protein US10.
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                                                                                                                                                                                    Alphaherpesvirinae; Simplexvirus
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312 AA; 34055 MW;
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58.3%;
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Best Local Similarity 58.2
Tr Conservative
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Gaps

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Indels

46.1%; Score 41; DB 1; Length 520; 58.3%; Pred. No. 97;

Pred. No. 97; 1; Mismatches

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InterPro; IPR002609; Caulimo_VI.
InterPro; IPR009027; L9 N like.
Pfam; PF01693; Caulimo_VI; I.
Trans-acting factor; Translation regulation.
SEQUENCE 520 AA; 58140 MW; 6884E2952B6AA5D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   228 GTKRPSSDPAPK 239
                                                                                                                                                                                                                                                                       7; Conservative
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                                                                                                                                                                                                                                 Local Similarity
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IBMP_CAMVE
ID_IBMP_C
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          张珠珠 $3
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                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch):
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00133; tRNA-synt_1; 1.
PRINTS; PR00964; TRNASXNTHILE.
PROSITE; PS00176; AA_TRNA_LIGASE_I; PARTIAL.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                    -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON POLYCISTRONIC MRNA'S DERIVED FROM CAULIFLOWER MOSAIC VIRUS.
-i- SUBCELLULAR LOCATION: Cytoplasmic inclusion bodies.
-i- MISCELLANEOUS: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA SYNTHESIS, VIRION ASSEMBLY AND ACCUMULATION IN THE INFECTED CE -:- SIMILARITY: Belongs to the caulimoviruses viroplasmin family.
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MEDIJNE=92216136; PubMed=2134858;
MEDIJNE=92216136; PubMed=2134858;
Medific=92216136; PubMed=2134858;
Point mutations in calliflower mosaic virus gene VI confer host-specific symptom changes.";
Mol. Plant Microbe Interact. 3:341-345(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                         -i- CATALYTIC ACTIVITY: ATP + L-isoleucine + tRNA(Ile) = AMP + diphosphate + L-isoleucyl-tRNA(Ile).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.1%; Score 41; DB 1; Length 413; 70.0%; Pred. No. 76;
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      Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
NCBI_TaxID=10642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 301 ATP (BY SIMILARITY).
413 AA; 46895 MW; 69B098FD71C100CE CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPR002300; TRNA-8ynt la.
INTERPRO; IPR001412; TRNA-8ynt l.
INTERPRO; IPR002301; TRNA-8ynt ile.
INTERPRO; IPR009008; ValRS_ILeRS_edit.
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01-AUG-1991 (Rel. 19, Last sequ
15-JUL-1999 (Rel. 38, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z80904; CAB02584.1; -. PIR; T31663; T31663.
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                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-82014878; PubMed=6269062;
Gardner R.C., Howarth A.J., Hahn P., Brown-Luedi M., Shepherd R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                      Cauliflower mosaic virus (strain CM-1841) (CaMV). Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
NCBI_TaxID=10644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              520 AA; 57907 MW; F02E7885699B2F49 CRC64;
                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
Inclusion body matrix protein (Viroplasmin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor; Translation regulation.
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520 AA
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01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last Bequence update)
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1; Mismatches
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or send an email to license@isb-sib.ch)
PRT;
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Interpro; IPR009027; L9 N like.
Pfam; PF01693; Caulimo VI; 1.
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nes 7; Conservative
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STANDARD;
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modified and this statement is not removed.
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or send an email to license@isb-sib.ch).
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                                                                                                MEDLINE=93154593; PubMed=8428667;
Chenault K.D., Melcher U.K.;
"The complete nucleotide sequence of cauliflower mosaic virus isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: Cytoplasmic inclusion bodies.
-1- MISCELLAREOUS: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA SYNTHESIS, VIRION ASSEMBLY AND ACCUMILATION IN THE INFECTED CELL.
-1- SIMILARITY: Belongs to the caulimoviruses viroplasmin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Chenault K.D., Steffens D.L., Melcher U.K.;
"Nucleotide sequence of cauliflower mosaic virus isolate NY8153.";
                                                                                                                                                            nt Physiol. 100:542-545(1992).
FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON
POLYCISTRONIC MRNA'S DERIVED FROM CAULIFLOWER MOSALC VIRUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.1%; Score 41; DB 1; Length 520; ilarity 58.3%; Pred. No. 97; Conservative 1; Mismatches 4; Indels
                                   Cauliflower mosaic virus (strain BBC) (CaMV).
Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cauliflower mosaic virus (strain NY8153) (CaMV).
Viruses, Retroid viruses, Caulimoviridae, Caulimovirus.
NCBI_TaxID=31557;
                                                                                                                                                                                                                                                                                                                                                                                                                          Fram: Fries, Commandation regulation.
SEQUENCE 520 AA, 57969 MW; 08D7D5F0215DBEC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-FFB-1996 (Rel. 33, Last sequence update)
115-UTL-1999 (Rel. 38, Last annotation update)
115-UTL-1990 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
          Inclusion body matrix protein (Viroplasmin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   520 AA.
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InterPro; IPR002609; Caulimo VI.
InterPro; IPR009027; L9 N like.
Pfam; PF01693; Caulimo VI; 1.
                                                                                                                                                                                                                                                                                                                                                                  EMBL; M90542; AAA62376.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 GTKRPSSDPAPK 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                      Gene 123:255-257(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                      SEQUENCE FROM N.A.
                                                           NCBI_TaxID=31556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBMP CAMVN
Q00957;
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and for commercial
                                         (See http://www.isb-sib.ch/announce/
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A MEDLINE=22084549; PubMed=12089438;
Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
I. Science 296:2376.2379 (2002).
I. Science 296:2376.2379 (2002).
I. Science 296:2376.2379 (2002).
I. Science 296:2376.2379 (2002).
I. Science 296:2376.2379 (2002).
I. Science 296:2376.2379 (2002).
I. Science 206:2376.2379 (2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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Pred. No. 1e+02;
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    Usage by
                                                                                                                                                         EMBL, M90541; AAA46359.1; --
InterPro; IPR002609; Caulimo_VI.
InterPro; IPR0020027; L9. N. like.
Pfam; PF0163; Caulimo_VI. Trans-acting factor; Translation regulation.
SEQUENCE 520 AA; 57799 MW; 3459A028087CB41D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64260 MW; 57BB4D66475FE8F3 CRC64;
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-!- SIMILARITY: Belongs to the fliF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 41, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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                                              entities requires a license agreement (St or send an email to license@isb-sib.ch).
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InterPro; IPR000061; Flamring FLIF.
InterPro; IPR006183; YscJ FliF.
Pfam; PF01514; YscJ FliF; 1.
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TIGREAMS, TIGR00206; flif; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.1%;
58.3%;
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Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 58.3.
The Conservative
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28-FEB-2003 (Rel. 41, Last
Flagellar M-ring protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ansorge W., Wirkner U., Mewes H.-W., Weil B., Wiemann S.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Transcriptional activator. Able to bind to two different type of DNA binding sites. Isoform FOXJ2.L behaves as a more potent transactivator than FOXJ2.S.
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                       Perez-Sanchez C., Gomez-Ferreria M.A., de la Fuente C.A., Granadino B., Velasco G., Esteban A., Rey-Campos J.;
"FHX, a novel fork head factor with a dual DNA binding specificity.";
J. Biol. Chem. 275:12909-12916(2000).

[2]
WEDLINE-20425082; Pubméd-10966786;
Perez-Sanchez C., de la Fuente C.A., Gomez-Ferreria M.A.,
Granadino B., Rey-Campos J.;
Ferra-Gino B., Rey-Campos J.;
"FHX. and FHX.S. two isoforms of the human fork-head factor FHX (POXJ2) with differential activity.";
J. Mol. Biol. 301:795-806(2000).
                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prent=Alternative splicing, Named isoforms=2;
Name=FOXJ2.L; Synonyms=FHX.L;
IsoId=Q9P0K8-1; Sequence=Displayed;
                                                                                                                                         Q9PORE; Q96PS9; Q9NSNS; 16-CCT-2001 (Rel. 40, Treated) 116-CCT-2001 (Rel. 40, Last sequence update) 116-CCT-2003 (Rel. 42, Last annotation update) Forkhead box protein J2 (Fork head homologous X). FoxJ2 OR FHX. Homos spiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 458-574 FROM N.A. (ISOFORM FOXJ2.L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=FOXJ2.S; Synonyms=FHX.S;
IsoId=Q9P0K8-2; Sequence=V5P_001544;
-!- TISSUB SPECIFICITY: Widely expressed.
-!- SIMILARITY: Concains 1 fork-head domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF155132; AAF65927.1; -.
EMBL; AF155133; AAK49016.1; -.
EMBL; AL161978; CAB82315.1; -.
FIRSP; Q63245; ZHFH.
HSSP; Q63245; ZHFH.
TRANSFAC; T04109; -.
TRANSFAC; T04171; -.
INTERPRO; IPR001766; TF FORK head.
Pfam; PF00250; FORK head; 1.
PRINTS; RR00053; FORKHEAD.
PROSITE; PS00657; FORK HEAD_1; FALSE_NEG.
                                                                                                                            574 AA.
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM FOXJ2.L).
MEDLINE=20239944; PubMed=10777590;
                                                                                                                              STANDARD;
                                              102 HFSENNSPHRD 112
                  1 HLPGNKSPHRD 11
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0
                                                   FORK-HEAD.

POLY-SER.

POLY-GIN.

POLY-GIN.

POLY-GIN.

POLY-GIN.

POLY-FRO.

POLY-PRO.

VOSYGHPQAPHLYPGPSPMYPIPTQDSAGYNRPAHHMVPRP

SVPPPGANEEIPDDPDWDLIT -> GTAPSQLPWRWRLC
                                                                                                                                                                                                                                                         Gaps
PROSITE; PS00558; FORK HEAD 2; 1.

PROSITE; PS50039; FORK HEAD 3; 1.

Transcription regulation; DNA-binding; Nuclear protein; Activator;

Alternative splicing.

DNA BIND 66 143 FORK-HEAD.

DOMAIN 266 270 POLY-SER.
                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                           Score 41; DB 1; Length 574; Pred, No. 1.1e+02;
                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                  258120EDAE4B11EB CRC64;
                                                                                                                                                                          (in isoform FOXJ2.S). /FTId=VSP_001544.
                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                     Search completed: March 2, 2004, 16:05:27 Job time: 2.4375 secs
                                                                                                                                                                                                      574 AA; 62394 MW;
                                                                                                                                                                                                                               46.1%;
                                                                                                                                                                                                                                                                                                               479 HVPPQGGTHRPPAP 492
                                                                                                                                                                                                                                                                                    1 HLPGNKSPHRDPAP 14
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                                                       143
2298
2298
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3351
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nes 7; Conserva
                                                                                295
295
299
313
513
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DOMAIN
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM proteín - protein search, using sw model

March 2, 2004, 16:00:38; Search time 2.125 Seconds (without alignments) 678.999 Million cell updates/sec Run on:

US-10-060-765-8 89

1 HLPGNKSPHRDPAPR 15 Title: Perfect score: Scoring table: Sequence:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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proline-rich prote	gag-like process process	11 Politicaca proce	Tupl protein - Str	gag polyprotein -	gag polyprotein -	gag protein - bovi	related to suppres	hypothetical prote	hypothetical prote	hypothetical 13.2K	hypothetical prote	US10 protein - hum	isoleucine-tRNA li	hypothetical prote	hypothetical 58K p
T02436	T131/2	C86194	844956	FOLJGB	FOLJGA	S29356	T49868	H82597	T47161	S54309	A85076	OOBE07	T31663	D9CD60	JN0498
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818	1043	740	324	392	392	393	1174	111	117	118	282	312	413	520	520
47.2	47.2	46.0	46.6	46.6	46.6	46.6	46.6	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1
47	4.2	41.5	41.5	41.5	41.5	41.5	41.5	41	41	41	41	41	41	41	41

ALIGNMENTS

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C-terminal domain-binding protein rAl - rat C'species: Rattus norvegicus (Norway rat) C'species: Rattus norvegicus (Norway rat) C'species: 29-Oct-1999 #sequence_revision 5-Oct-1999 #sequence_revision 731421 R; Vijoshi, R.V.; Gentile, C.; Gebara, M.; Coxd R; Yuryev, A.; Patturajan, M.; Litingtung, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; Coxd A; Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts wit A; Reference number: Z21024; MUID:96293459; PMID:8692929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                            A;Accession: T31421
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1173 < YUR>
A;Cross-references: EMBL:U49056; NID:g1438531; PID:g1438532; PIDN:AACS2657.1
A;Experimental source: hippocampus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 52; DB 2; Length 1173;
Pred. No. 5.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                             58.4%;
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Best Local Similarity 66.7.
Best Local Similarity 7.14
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||: ||||:| | 224 PGDDSPHREPPP 235 g

hypothetical protein APE1416 - Aeropyrum pernix (strain K1)

Cispecies: Aeropyrum pernix
Cipate: 20-3049-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
Cipate: 20-3049-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
Cipacession: 372619
R.Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takalawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; P.
DNA Res. 6, 83-101, 1999
DNA Res. 6, 83-101, 1999
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy;
A; Reference number: A72450; MUID:99310339; PMID:10382966
A; Reference number: A72450; MUID:99310339; PMID:10382966
A; Reference number: A72450; MUID:99310339; PMID:10382966
A; Reference number: A72450; MUID:99310339; PMID:10382966
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A; Reference number: A72450; MUID:99310339; PMID:10382966
A; Reference number: A72450; MUID:10382966
A; Reference number: A72450; MUID

C;Genetics: A;Gene: APE1416

C; Superfamily: Aeropyrum pernix hypothetical protein APE1416

Gaps 5. 56.2%; Score 50; DB 2; Length 165; 68.8%; Pred. No. 1.5; 3; Indels tive 0; Mismatches 3; Indels Best Local Similarity 68.89 Matches 11; Conservative Query Match

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2 LPGNK--SPHRDPAPR 15

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Kiparkill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.I. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001

Nature 413, 523-527, 2001

A; Fittle: Genome sequence of Yersinia pestis, the causative agent of plague.

A; Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Keywords: coat protein. 91ycoprotein
F;151-729/Product: coat protein VP2 #status predicted <VP2>
F;172,198,282,330,433,471,573,604,651/Binding site: carbohydrate (Asn) (covalent) #stat
                                                                                      A,Accession: B33743
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-729 <VAS>
A,Cross-references: GB:M32787; NID:g332983; PIDN:AAA46917.1; PID:g332985
A,Cross-references: GB:M32787; NID:g332983; PIDN:AAA46917.1; PID:g332985
A;Bergeron, J.; Menezes, J.; Tijssen, P.
A,Title: Genomic organization and mapping of transcription and translation products of A,Reference number: A48472; MUID:94025614; PMID:8212598
Virology 173, 368-377, 1989
A,Title: Nucleotide sequence analysis of the capsid genes and the right-hand terminal
A,Reference number: A33743; MUID:90085785; PMID:2596019
                                                                                                                                                                                                                                                                                                                            A; Accession: D48472
A; Molecule type: DNA
A; Residues: 11-729 < BER>
A; Residues: 11-729 < BER>
A; Residues: 11-729 < BER>
A; Residues: 10-729 < BER>
A; Residues: 10-729 < BER>
A; Rote: sequence extracted from NCBL backbone (NCBIN:138789, NCBIP:138794)
C; Superfinents: 10/1
C; Superfinents: 10/1
C; Superfinents: 20-729 protein; glycoprotein
C; Reywords: coat protein; glycoprotein
F; 151-729 product: coat protein VP2 #status predicted < VP2>
F; 151-729 product: coat protein VP2 #status predicted < NF3>
F; 172, 198, 282, 330, 433, 471, 573, 604, 651 Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable carbohydrate kinase YPO1291 [imported] - Yersinia pestis (strain CO92)
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N;Contains: coat protein VP2
C;Species: porcine parvovirus
C;Species: porcine parvovirus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C;Accession: A60006
R;Sakurai, M;Nishimori, T;Ushimi, C.;Nakajima, H.
Virus Res. 13, 79-86, 1989
Virus Res. 13, 79-86, 1989
A;Htle: Nucleotide sequence of capsid protein gene of porcine parvovirus.
A;Reference number: A60006, MUD:89319168; PMID:2750278
A;Accession: A60006
A;Accession: A60006
A;Accession: A60006
A;Accession: A60006
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AG0157
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Similarity 61.5%; Pred. No. 29;
8; Conservative 2; Mismatches 3: Indelm
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Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: parvovirus coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.7%;
61.5%;
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117 PGSKPPGKRPAPR 129
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nes 8, Conservative
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Best Local S
Matches 8
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A;Title: Bvidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Title: Bvidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Rescassion: C72417
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-492 <ARN>
A;Cross-references: GB:AE001697; GB:AE000512; NID:g4980597; PIDN:AAD35210.1; PID:g498060
C;Genetics:
A;Gene: TW0116
C;Superfamily: xylulokinase
                                                                                                                                                                                            sugar kinase, FGGY family - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: C72417
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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N;Contains: coat protein VP2
C;Species: porcine parvovirus
C;Species: al-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C;Accession: B33743, D48472
R;Vasudevacharya, J.; Basak, S.; Srinivas, R.V.; Compans, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cispecies: porcine parvovirus
Cipace: 30-56p-1991 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1996
Cipacesion: B33302
R;Ranz, A.I.; Manclus, J.J.; Diaz-Aroca, E.; Casal, J.I.
J. Gen. Virol. 70, 2544-2553, 1989
A;Fills: Porcine parvovirus: DNA sequence and genome organization.
A;Reference number: A33302; MUID:90010964; PMID:2794971
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Pred. No. 9.5;
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(Superfamily: parvovirus coat protein
C;Keywords: coat protein
F;145-723/Product: coat protein VP2 #status predicted <VP2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
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VCPVPP

COCT protein VP1 - porcine parvovirus
N;Contains: coat protein VP2
                   53.9%;
ilarity 53.3%;
Conservative
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340 YLNGERTPHRDPFAR 354
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A,Residues: 1-723 <RAN>
A;Cross-references: BMBL:D00623
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 PGSKPPGKRPAPR 123
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Best Local Similarity
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nes 8; Conserv
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Cjaccession: T48849
RjBevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; A;Reference number: Z24492
A;Reference number: Z24492
A;Accession: T48349
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A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable purine nucleotide-binding protein YBR270c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR1738
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C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 20-Aug-1999
C;Accession: T05726
R;Hagen, G.; Guilfoyle, T.J.
A;Reference to the EMBL Data Library, July 1997
A;Reference number: Z15436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Saccharomyces cerevisiae
C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002
C;Accession: S46151
R;Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F. submitted to the Protein Sequence Database, August 1994
A;Reference number: S45940
                                         BIN2 protein - Arabidopsis thaliana
N;Alternate names: protein F12E4.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Keywords: ATP, P-loop, purine nucleotide binding; transmembrane protein E;259-26/Region: nucleotide-binding motif A (P-loop) F;321-337/Domain: transmembrane #status predicted <TWM>F;265/Binding site: ATP/GTP (Lys) #status predicted
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A;Cross-references: EMBL:AL162751
A;Experimental source: cultivar Columbia; BAC clone F12E4
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Pred. No. 36;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 5
A;Introne: 83/3; 112/3; 149/3; 220/3; 282/3; 1169/3
A;Note: F12E4.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 2;
Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
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8; Conservative
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Best Local Similarity
Matches 8; Conserv
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A, Map position: 2R
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Best Local
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GH1 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GDB:118810; OMIM:120260
A;Map position: 1p33-1p32.2
C;Complex: type IX collagen may be a heterotrimer of one alpha 1(IX) chain, one alpha 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ^{\text{the}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen cDNA and assignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Readudes: 1-26, QT', 22, S, 31-32, 'ILM', 35-561,'L', 563-578,'P',580-618 <PER2>
A; Cross-references: EMBL:195610; NID:g1054872
A; Cross-references: EMBL:195610; NID:g1054872
R; Diab, M.; Wu, J.J.; Eyre, D.R.
Bjochem J. 314, 327-332, 199
A; Title: Collagen type IX from human cartilage: a structural profile of intermolecular
A; Reference number: 864673; MUID:96195147; PMID:8660302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 123-133, P',135-137 <DIA>
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit
ed and subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Molecular cloning of the human alpha-2(IX) collagen cDNA and assignment of A; Reference number: $32436; WUID:93202262; PMID:8454052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                    A;Cross-references: GB:ALS90842; PIDN:CAC90122.1; PID:g15979342; GSPDB:GN00175 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           collagen alpha 2(IX) chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 15-Sep-2003
C;Accession: S32436; S34487; Š64673
C;Accession: S32436; S34487; Š64673
FEBS Lett. 319, 177-180, 1993;
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                                                                                                                                                                                                                             DB 2; Length 517;
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A, Cross-references: EMBL: M95610; NID: 91054872
B, Peraelae, M.; Haenninen, M.; Haestbacka, J.; Vuorio, E. submitted to the EMBL Data Library, March 1993
A, Description: Molecular cloning of the human alpha-2 (IX)
A, Reference number: $34487
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                                                                                                                                                                                                                                                           Pred. No. 29;
2; Mismatches
                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                50.6%; Score 45; 53.3%; Pred. No.
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                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                            A;Gene: YPO1291
C;Superfamily: xylulokinase
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Matches 7; Conserv
                                                                                                                                                                                                                                                           Local Similarity
                             A; Molecule type: DNA A; Residues: 1-517 < KUR>
preliminary
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: C72631
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aerop. A;Reference number: A72450; MUID: 99310339; PMID: 10382966
                                                                                                                                                                                                                   colony-stimulating factor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: 10-69p-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S35703
R;Borycki, A.G.; Lenormand, J.L.; Guillier, M.; Leibovitch, S.A.
Biochim Biophys. Act 1174, 143-152, 1993
A;Title: Isolation and characterization of a cDNA clone encoding for rat CSF-1 gene. A;Reference number: S35703; MUID:93363632; PMID:8357831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTP synthase (BC 6.3.4.2) pyrG - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: S72961
A,Status: preliminary
A,Molecule type: DNA
A,Residuss: 1-590 <SMI>
A,COSS-references: EMBL:U00021; NID:g467141; PIDN:AAA50916.1; PID:g467152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cross-references: EMBL:M84361, NID:g203640, PIDN:AAA03032.1, PID:g203641; Superfamily: macrophage colony-stimulating factor
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Pred. No. 44;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: 572961
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: Mycobacterium leprae cosmid L247.
A; Reference number: S72589
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45.0%; Pred. No. 4
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58.3%;
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                                                     202 PASASPHOPPAP 213
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nes 7; Conservative
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3 PGNKSPHRDPAP 14
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C,Superfamily: CTP synthase
C,Keywords: ligase
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Matches 9; Conserv
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A;Molecule type: mRNA
A;Residues: 1-552 <BOR>
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A;Status: preliminary
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Matches
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C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A31401; UN0294; A26575; A23166; A2883
C;Accession: A31401; UN0294; A26575; A23166; A2883
C;Accession: A31401; Moble, J2A; Witten, V.P.; Warren, M.K.; McGrogan, M.; St Proc. Natl. Acad. Sci. U.S.A. 85, 6706-6710, 1988
A;Title: cDNA cloning and expression of murine macrophage colony-stimulating factor from A;Reference number: A31401; MUID:88320507; PMID:2457916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: mRNA
A,Residues: 1-552 <LAD>
A,Cross-references: GB:M21952; GB:J03862; NID:g192804; PIDN:AAA37481.1; PID:g309199
A,Cross-references: GB:M21952; GB:J03862; NID:g192804; PIDN:AAA37481.1; PID:g309199
R;Harrington, M.A.; Edenberg, H.J.; Saxman, S.; Pedigo, L.M.; Daub, R.; Broxmeyer, H.E.
Gene 102, 165-170, 1991
A,Title: Cloning and characterization of the murine promoter for the colony-stimulating
A,Reference number: UN0294; MUID:91340149; PMID:1874443
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A)Accession: JN0294
A)Accession: JN0294
A)Accession: JN0294
A)Redecule type: DNA
A)Residues: 1-13 cHAR>
A)CROSS-references: GB:M81316; GB:M61708; NID:g192802; PIDN:AAA19866.1; PID:g192803
A)CROSS-references: GB:M81316; GB:M61708; NID:g192802; PIDN:AAA19866.1; PID:g192803
A)CROSS-references: GB:M81316; GB:M61708; NID:g192802; PIDN:AAA19866.1; PID:g192803
A)CROSS-Res: 15, 2389-2390, 1987
A)Title: Nucleotide sequence of a cDNA encoding murine CSF-1 (macrophage-CSF).
A)Reference number: A26575; MUID:87174763; PMID:3494232
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A; Residues: 1-5, K*, 7-245, A*, 247-552 CDEL>
A; Residues: 1-5, K*, 7-245, A*, 247-552 CDEL>
R: Ben-Avram, C.M*; Shively, J.E.; Shadduck, R.K.; Waheed, A.; Rajavashisth, T.; Lusis, Proc. Natl. Acad. Sci. U.S.A. 82, 4486-4489, 1985
A; Reference number: A23166; MUID: 85242709; PMID: 3925458
A; Accession: A23166
A; Molecule type: protein
A; Residues: 33-39, CC', 42-57 cBEN>
R; Rajavashisth, T.B.; Eng, R.; Shadduck, R.K.; Waheed, A.; Ben-Avram, C.M.; Shively, J.I.
R; Rajavashisth, T. B.; Eng, R. 84, 1157-1161, 1987
A; Thle: Cloning and tissue-specific expression of mouse macrophage colony-stimulating A; Reference number: A25883; MUID: 87147232; PMID: 3493488
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                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-339 <HBG>
A;Residues: 1-339 <HBG>
A;Cross-references: EMBL:AF016633; NID:g2388688; PIDN:AAB70005.1; PID:g2388689
A;Experimental source: cultivar Wayne
C;Genetics:
A;Gene: GHI
C;Superfamily: auxin-induced protein aux28
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A,Remidues: 1-2,4-5, RRN, 9-100 «RAJ>
A,Cross-references: GB:M15692; NID:g192800; PIDN:AAA37480.1; PID:g192801
C,Superfamily: macrophage colony-stimulating factor
C,Reywords: cytokine; glycoprotein; growth factor; macrophage
F;132.70main: signal sequence #status predicted «SIG»
F;33-552/Product: macrophage colony-stimulating factor #status predicted F;131-552/Product: macrophage colony-stimulating factor #status predicted F;154,172/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                    Length 339,
                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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N,Alternate names: colony-stimulating factor 1; M-CSF
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Pred. No. 27;
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Best Local Similarity 63.6
Matches 7; Conservative
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Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A31401
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              A; Accession: T05726
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A Map position: 12q13-12q13
A introns: 16/3, 77/3; 141/3; 167/3; 207/2; 284/2; 322/3; 380/2; 429/3; 475/2
A; Introns: 16/3; 77/3; 141/3; 167/3; 207/2; 284/2; 322/3; 380/2; 429/3; 475/2
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc C; Keywords: ATP; hormone receptor; transmembrane protein
F;11-57/Pomain: signal sequence #status predicted <SIG>F;11-57/Pomain: anti-muellerian hormone type II receptor #status predicted <MAT>F;17-141/Domain: extracellular hormone binding #status predicted <ELB>F;142-167/Domain: protein kinase homology <KIN>F;201-512/Domain: protein kinase homology <KIN>F
                                                                                         Rivisser, J.A.; McLuskey, A.; van Beers, T.; Weghuis, D.O.; van Kessel, A.G.; Grootegoed Blochem. Biophys. Res. Commun. 215, 1029-1036, 1995
Ajfille: Structure and chromosomal localization of the human anti-muellerian hormone tyte A;Reference number: JC4335; MUID:96028015; PMID:7488027
                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-573 «VIS.3 «VIS.4
A;Cross-references: GB:X91156; NID:g1107671; PIDN:CRA62593.1; PID:e198046; PID:g1107672
C;Comment: This is a receptor for anti-mullerian hormone (see PIR:WFHUM). It plays a cri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Map position: 1
A;Introns: 33/2; 130/1; 189/2; 238/1; 355/2; 388/3; 473/1; 540/2; 587/3; 670/1
C,Superfamily: Caenorhabditis elegans hypothetical protein F16D3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: Z78062; PIDN: CAB01499.1; GSPDB: GN00019; CBSP: F16D3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F16D3.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T21021
                      C;Species: Homo sapiens (man)
C;Date: 06-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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anti-mullerian hormone type II receptor precursor - human
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65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, August 1996 A;Reference number: Z19361 A;Accession: T21021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                              A;Gene: GDB:AMHR2
A;Cross-references: GDB:696210; OMIM:600956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: clone F16D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.3%;
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Best Local Similarity 61...
Local 8; Conservative
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206 RTPYRDPSPR 215
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A;Gene: CESP:F16D3.2
                                                                        C; Accession: JC4335
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T41551
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                         A, Residues: 1-105 <KAW>
A, Residues: 1-105 <KAW>
A; Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80505.1; PID:d1044291; PID:g510
A; Experimental source: strain K1
C; Genetics:
A, Gene: APE1506
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C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
F;21-400/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
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A;Title: Nucleotide sequence and deduced functions of a set of cotranscribed genes of A;Reference number: S25840; MUID:92406871; PMID:1527048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AL031035; PIDN:CAA19886.1; GSPDB:GN00070; SCOEDB:SC6A9.01cA;Experimental source: strain A3(2)
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C,Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C,Accession: T35432
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Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
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A;Reference number: Z21578
A;Accession: T35432
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-280 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable aldehyde dehydrogenase - Streptomyces coelicolor (fragment)
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48.3%; Score 43; DB 2; Length 407;
Best Local Similarity 46.7%; Pred. No. 46;
Matches 7; Conservative 2; Mismatches 6; Indels
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Pred. No. 31;
1; Mismatches 4; Indels
                                                                                                                                                                                     Score 43; DB 2; Length 105;
Pred. No. 11;
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                             3;
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                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                  h 48.3%;
Similarity 58.3%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 48.3%;
Similarity 61.5%;
B; Conservative
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HIPGRLLPQTDPSTR 73
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2 HNPGNATPDRFPA 14
                                                                                                                                                                                                                                                                                                  1 HLPGNKSPHRDP 12
                                                                                                                                                                                                                                                                                                                                                  56 HLPNNKASHKLP 67
                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
Matches 8; Conserv
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A; Status: preliminary
A; Molecule type: DNA
  A, Molecule type: DNA
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RESULT 17

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RESULT 18

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3-isopropylmalate dehydrogenase (EC 1.1.1.85) - Sphingomonas aromaticivorans plasmid phe 3-isopropylmalate dehydrogenase (EC 1.1.1.85) - Sphingomonas aromaticivorans c)Species: Sphingomonas aromaticivorans c)Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000 C;Accession: T31128 FxDemine, M.F.; Stillaell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; Sticenie, M.F.; Stillaell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; Submitted to the EMBL Data Library, July 1998 A;Beference number: 220992 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T31128 A;Accession: T311
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C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: OS-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T35379
R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, June 1999
A;Recession: T35379
A;Accession: T35379
A;Accession: T35379
A;Accession: T35379
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-278 AUR.
A;Residues: 1-278 AUR.
A;Crose-references: EMBL:AL079348; PIDN:CAB45478.1; GSPDB:GN00070; SCOEDB:SC66T3.22
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;1025-1041/Domain: transmembrane #status predicted <TM7>
F;50,114,165,221/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;429/Binding site: ATP (Lys) #status predicted
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Pred. No. 1.2e+02;
2; Mismatches 2; Indels
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Pred. No. 44;
0; Mismatches 5; Indels
A;Reference number: S25353; MUID:92327849; PMID:1626432 A;Contents: annotation
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63.6%;
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Best Local Similarity 61.5
Matches 8; Conservative
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Matches 7; Conservative
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A; Residues: 1-1049 <GOF>
A; Cross-references: EMBL:X59720; NID:g1907116; PIDN:CAA42328.1; PID:g1907154; GSPDB:GN0G
R; Purnelle, B.; Skala, J.; Goffeau, A.
R; Purnelle, B.; Skala, J.; Goffeau, A.
Fast 7, 867-872, 1991
A; Title: The product of the YCR105 gene located on the chromosome III from Saccharomyces A; Reference number: $40914; MUD:92160395; PMID:1789009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus musculus (house mouse)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2003
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2003
C;Date: 16-Feb-1994 #sequence_revision 18.Nov-1994 #text_change 15-Sep-2003
R;Li, K.; Ghristiano, A.M.; Copeland, N.G.; Gilbert, D.J.; Chu, M.L.; Jenkins, N.A.; Uit Genomics 16, 733-739, 1993
Genomics 16, 733-739, 1993
A;Title: CDNA cloning and chromosomal mapping of the mouse type VII collagen gene (Col7a A;Reference number: A45748; MUID:93315168; PMID:8325648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-1049 <PUR>
R;Skala, J.; Purnelle, B.; Goffeau, A.
R;skala, J.; Purnelle, B.; Goffeau, A.
A;Title: The complete sequence of a 10.8 kb segment distal of SUF2 on the right arm of K genes.
                                                                                                                                                                                                          A;Residues: 1-781 <WOO>
A;Cross-references: EMBL:AL023794; PIDN:CAA19355.1; GSPDB:GN00068; SPDB:SPCC70.05c
A;Experimental source: strain 972h-; cosmid c70
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ATP-dependent permease ADP1 precursor - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein YCR011c; protein YCR105
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 19-Jan-2001
C;Accession, A.; Purnelle, B.; Skala, J.
R;Goffeau, A.; Purnelle, B.; Skala, J.
A;Reference number: S19420
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A;Note: sequence extracted from NCBI backbone (NCBIN:135000, NCBIP:135001)
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A, Cross-references: GB: S63654; NID: 9386656; PIDN: AAB27492.1; PID: 9386657
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Pred. No. 1.1e+02;
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Pred. No. 90;
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                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A45748
collagen alpha 1(VII) chain - mouse (fragment)
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                       A; Reference number: Z22001
A; Accession: T41551
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Best Local Similarity
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A;Gene: SPDB:SPCC70.05c
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Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative 1
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Best Local Similarity 61.55
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                    228 GTKKPSSDPAPK 239
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                                                                                                                                                                                                                   Local Similarity 58.3
Les 7; Conservative
                                                                                                                                                                                                                                                                               4 GNKSPHRDPAPR 15
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A;Residues: 1-557 <BAA>
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            A;Cross-references: EMBL:AF079317; NID:g3378261; PID:g3378269; PIDN:AAD03852.1
C;Genetics:
A;Genome: plasmid pNL1
A;Note: orf047;
C;Superfamily: 3-isopropylmalate dehydrogenase
C;Keywords: oxidoreductase
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C;Species: cauliflower mosaic virus
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein 6 - cauliflower mosaic virus (strain Strasbourg)
C;Species: cauliflower mosaic virus
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 23-Jul-1999
C;Accession: A04162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein 6 - cauliflower mosaic virus (strain D/H)
C;Species: cauliflower mosaic virus
C;Date: 31-Oct-1980 #sequence_revision 05-Apr-1983 #text_change 30-Jun-1993
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R;Guilley, H.
submitted to the Nucleic Acid Sequence Database, October 1982
A;Reference number: A94613
A;Reference number: A94613
A;Anotecule type: DNA
A;Residues: 1-522 <GUI>
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A; Title: Nucleotide sequence of cauliflower mosaic virus DNA. A; Reference number: A90799; MUID:81001865; PMID:7407912
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R;Takahashi, H.; Shimamoto, K.; Suzuki, M.; Ehara, Y.
Nucleic Acids Res. 17, 7981, 1989
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84;
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58.3%; Pred. No. 85;
tive 1; Mismatches 4
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                                                                                                                                                         Score 42; DB
Pred. No. 57;
                                                                                                                                                                                                0; Mismatches
                                                                                                                                                         47.2%;
                                                                                                                                                                                                                                                                                 109 LPGIASPLRDKAP 121
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Best Local Similarity
7; Conserve
                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
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A, Residues: 1-355 < ROM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A04162
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A;Title: DNA sequence of gene VI of cauliflower mosaic virus Japanese strain S (CaMV S-i A;Reference number: S06092; MUID:90016879; PMID:2798138
A;Accession: S06092
A;Molecule type: DNA
A;Residues: 1-522 <TAK>
A;Cross-references: EMBL:X14911; NID:g58828; PIDN:CAA33037.1; PID:g58829
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X71916; NID:g453177; PIDN:CAA50731.1; PID:g453178
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C;Keywords: ATP
F;199-510/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mullerian-inhibiting substance type II receptor - mouse

G.Species: Mus musculus (house mouse)

G.Date: 14-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 04-Mar-2000

G.Accession: 4C5629

R.Mishina, Y.; Tizard, R.; Deng, J.M.; Pathak, B.G.; Copeland, N.G.; Jenkins, N.A.; Cate

R.Mishina, Y.; Tizard, Commun. 237, 741-746, 1997

A;Title: Sequence, genomic organization, and chromosomal location of the mouse Muelleria

A;Reference number: 4C5629; MUID:97445109; PMID:929437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 15
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
F;197-508/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: A novel member of the transmembrane serine/threonine kinase receptor family is A,Reference number: S41627; MUID:94163972; PMID:8119126
A,Accession: S41627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Baarends, W.M.; van Helmond, M.J.L.; Post, M.; van der Schoot, P.J.C.M.; Hoogerbrugge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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C,Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C,Accession: S41627
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A;Residues: 1-568 <MIS>
C;Comment: This receptor in involved in the mexual differeatiation.
                                                                                                                                                                                                                                                                                                                    Length 522;
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                                                                                                                                                                                                                                   A, Gene: VI
C, Superfamily: caulimovirus inclusion body matrix protein
                                                                                                                                                                                                                                                                                                                       Score 42; DB 2;
Pred. No. 85;
1; Mismatches
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Pred. No. 91;
1; Mismatches
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Pred. No. 92;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable anti-mullerian hormone receptor - rat
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Gaps

5,

Indels

Length 240;

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Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Roney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Status; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lmbI protein - Streptomyces lincolnensis
C;Species: Streptomyces lincolnensis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Oct-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Oct-1999
C,Accession: 869818; 844956
R;Peschke, U.; Schmidt, H.; Zhang, H.Z.; Piepersberg, W.
Mol. Microbiol. 16, 1137-1156, 1995
Mol. Microbiol. 16, 1137-1156, 1995
A;Fitle: Molecular characterization of the lincomycin-production gene cluster of Strept
A;Reference number: 869805; MUID:96020646; PMID:8677249
A;Accession: 869818
A;Accession: S69818
A;Accession: preliminary; nucleic acid sequence not shown; translation not shown
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A;Note: host sos sp. (cattle)
C;Date: 28-Aug-1985 #text_change 31-Mar-2000
C;Accession: A94063; A93812; A91311; A03942
R;Sagata, N.; Yasunaga, T.; Tsuzuku-Kawamura, J.; Ohishi, K.; Ogawa, Y.; Ikawa, Y.
Proc. Natl. Acad. Sci. US.A. 82, 677-681, 1985
A;Title: Complete nucleotide sequence of the genome of bovine leukemia virus: its evolt A;Reference number: A94063; MUID:85140159; PMID:2983308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA

A; Residues: 1-324 < PEL2>

A; Residues: 1-324 < PEL2>

A; Cross-references: EMBL:X79146; NID:9499194; PIDN:CRAS5755.1; PID:9581692

A; Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994

C; Genetics:
A; Gene: lmL

A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                  A,Molecule type: DNA
A,Residues: 1-240 <STO>
A,Cross-references: GB:AE005172; NID:g6850322; PIDN:AAF29399.1; GSPDB:GN00141
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A,Note: core protein p12 is a genome-binding protein with repeated sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:K02120; NID:g210767; PIDN:AAA42784.1; PID:g210768
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Nicontains: core protein p12; core protein p15; core protein p24
CiSpecies: bovine leukemia virus, BLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41.5; DB 2;
Pred. No. 45;
3; Mismatches 3;
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Best Local Similarity 45.0%;
Matches 9; Conservative
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89 PGDKAPPHRPPEP 101
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Matches 8; Conserv
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C86194

Dypochetical protein [imported] - Arabidopsis thaliana
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C86194
Kritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 22q12.1-qter
A;Introns: 18/2; 30/1; 53/1; 83/2; 135/1; 174/2; 221/2; 273/1; 308/2; 352/3; 377/3; 504/
A;Note: DJ430N08.2
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C; Date: 13.-Aug-1599 #sequence_revision 13.-Aug-1999 #text_change 17.-Nov-2000
C; Accession: T13172
R; Sheen, F; Levis, R.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 12510-12514, 1994
A; Titler Transposition of the LINE-like retrotransposon TART to Drosophila chromosome A; Reference number: Z17629; MUID:95107987; PMID:7809068
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                                                                                                                                                                                                                                                                                                                                  Ricordes, M.; Scheet, P. au Library, April 1998 submitted to the EMBL. Data Library, April 1998 A; Description: The Bequence of Homo sapiens PAC clone DJ430N08.
A;Reference number: Z14672
A;Accession: T02446
A;Actatus: preliminary; translated from GB/EMBL/DDBJ
A;Roteus: preliminary; translated from GB/EMBL/DDBJ
A;Roteus: Dreliminary;
A;Roteus: Dreliminary;
A;Cross-references: EMBL:AC004542; NID:G3041846; PIDN:AAC12954.1; PID:G3041848
C;Genetics:
                                                                                                                                                                                                                                             Species: Homo Bapiens (man)
Date: 05-Mar-1999 #sequence revision 05-Mar-1999 #text_change 05-Nov-1999
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A;Residues: 1-1043 <SHE>
A;Cross-references: EMBL:U14101; NID:g603662; PID:g603663; PIDN:AAC46493.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                        proline-rich protein DJ430N08.2 - human (fragment)
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A;Mobile element: transposon TART-B1
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50.0%;
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                                        97
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Matches 7; Conservative
          Local Similarity
nes 9; Conserv
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1;

Gaps

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Indels

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hypothetical protein XF2103 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: XyJella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: H82597
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenter Agonome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: H82597
R;Rice, N.R.; Stephens, R.M.; Burny, A.; Gilden, R.V.
Virology 142, 357-377, 1985
A;Title: The gag and pol genes of bovine leukemia virus: nucleotide sequence and analysi
A;Reference number: 829356; MUID:86045859; PMID:2997990
A;Accession: 229356
A;Status: preliminary
A;Molecule type: DNA
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R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, Briones, M.R.S.; Bloorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh J.D.; Junqueira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, B.E.; Laig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: T49868
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
A;Accession: T49868
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A;Molecule type: DNA
A;Residues: 1-111 <SIM>
A;Cross-references: GB:AE004026; GB:AE003849; NID:g9107228; PIDN:AAF84902.1; GSPDB:GN00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     related to suppressor protein SPT23 [imported] - Neurospora crassa
N;Alternate names: protein B24P11.240
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
                                                                                                                                                                                                                                 A;Residues: 1-393 <RIC>
A;Cross-references: EMBL:M10987; NID:g210784; PIDN:AAA42794.1; PID:g210785
C;Superfamily: mammalian retrovirus gag polyprotein II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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A;Experimental source: BAC clone B24P11; strain OR74A
                                                                                                                                                                                                                                                                                                                                                 Length 393;
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46.6%; Score 41.5; DB 2;
Best Local Similarity 37.5%; Pred. No. 2.3e+02;
Matches 9; Conservative 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                    ; Score 41.5; DE;
; Pred. No. 76;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 HTPGPKMPGPROPAPK 341
                                                                                                                                                                                                                                                                                                                                                          46.6%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 HLPGNKSP-HRDPAPR 15
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Best Local Similarity 56.2.
Best Accordance 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-1174 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: NCSP: B24P11.240
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         A;Note: the authors translated the codon TAT for residue 7 as Thr and TAC for residue 43 R;Oroszlan, S.; Copeland, T.D.; Henderson, L.E.; Stephenson, J.R.; Gilden, R.V. Proc. Natl. Acad. Sci. U.S.A. 76, 2996-3000, 1979
A;Title: Amino-terminal sequence of bovine leukemia virus major internal protein: Homolc A;Reference number: A3812; MUID:79223918; PMID:223166
A;Accession: A93812
                                                                                                                                                                                                              A,Molecule type: protein
A;Residues: 110-164 <ORO.
K;Copeland, T.D.; Morgan, M.A.; Oroszlan, S.
FEBS Lett. 156, 37-40, 1983
A;Title: Complete amino acid sequence of the nucleic acid-binding protein of bovine leuk
A;Reference number: A91311; MUID:83210199; PMID:6303852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Coulston, J.; Naif, H.; Brandon, R.; Kumar, S.; Khan, S.; Daniel, R.C.W.; Lavin, M.F. J. Gen. Virol. 71, 1737-1746, 1990
A;Title: Molecular cloning and sequencing of an Australian isolate of proviral bovine 18 A;Reference number: JQ0554; MUID:90362060; PMID:2167927
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C;Species: bovine leukemia virus, BLV
C;Date: 13-Jan.1995 #sequence_revision 13-Jan-1995 #text_change 26-Aug-1999
C;Accession: S29356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gag polyprotein - bovine leukemia virus (strain Australia)
N;Alternate names: core polyprotein
N;Contains: core protein p12; core protein p15; core protein p24
C;Species: bovine leukemia virus, BLV
C;Species: bovine leukemia virus, BLV
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 28-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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;Superfamily: mammalian retrovirus gag polyprotein II
;Reywords: core protein; duplication; phosphoprotein; polyprotein
;1-109/Product: core protein p15 #status predicted <P15>
;110-323/Product: core protein p24 #status predicted <P24>
;324-392/Product: core protein p12 #status experimental <P12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Keywords: core protein, duplication; polyprotein, tandem repeat E;1-109/Product: core protein p15 #status predicted <MAT> F;10-332/Product: core protein p15 #status predicted <MAC> F;324-392/Product: core protein p12 #status predicted <MAC> F;324-392/Product: core protein p12 #status predicted <MAO> F;342-362,367-387/Region: 21-residue repeats
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C; Superfamily: mammalian retrovirus gag polyprotein II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.6%; Score 41.5; D
llarity 56.2%; Pred. No. 75;
Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;342-362,367-387/Region: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 HTPGPKMPGPROPAPK 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTPGPKMPGPRQPAPK 340
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Best Local Similarity 56.2%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 324-392 <COP>
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nes 9; Conserv
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Matches
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Search completed: March 2, 2004, 16:08:07 Job time : 3.125 sec8
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Cypothetical 13.2K protein - fowl adenovirus 1

C;Species: Aviademovirus gall (fowl adenovirus 1, CELO)

C;Date: 08-Jul-1995 #sequence_revision 14-Feb-1997 #text_change 28-Jul-2000

C;Dates: 08-Jul-1995 #sequence_revision 14-Feb-1997 #text_change 28-Jul-2000

C;Accession: S54309

R;Hess, M.; Cuzange, A.; Chroboczeck, J.; Ruigrok, R.; Jacrot, B.

submitted to the EMBL Data Library, February 1995

A;Description: The sequence of the two fibers of an avian adenovirus (CELO) and organise

A;Reference number: S54125

A;Accession: S54109
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Cibate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
Cibate: 20-Apr-2000 #sequence_revision 20-Apr-2000
Cibacesion: T47161
Riansorge, W.; Wirkner, U.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24375
A;Accession: T47161
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: mRNA
A,Residues: 1-117 <AAA>
A,Cross-references: BMBL:AL161978
A,Experimental source: adult melanoma (MeWo cell line); clone DKFZp762A1712
C,Genetics:
A;Note: DKFZp762A1712.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Redidues: 1-118 <HES>
A; Cross-references: BMBL:X84724; NID:g780165; PIDN:CAA59209.1; PID:g780170
A; Cross-references: BMBL:X84724; NID:g780165; PIDN:CAA59209.1; PID:g780170
A; Change, M.; Cuzange, A.; Ruigrok, R.W.H.; Chroboczek, J.; Jacrot, B.
J. Mol. Biol. 252, 379-385, 1995
A; Title: The avian adenovirus penton: two fibres and one base.
A; Reference number: S59067; MUID:96025073; PMID:7563058
A; Contents: annotation
C; Superfamily: Aviadenovirus gall hypothetical 13.2K protein
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                                                                                                                                                                                                                                                                               Score 41; DB 2; Length 111; Pred. No. 25; Mismatches 4; Indels
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T47161
hypothetical protein DKFZp762A1712.1 - human (fragment)
                                                                                                                                                                                                                                                                                    46.18;
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72 HLPYWQRPHHDPS 84
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3 PGNKSPHRDPAPR 15

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Q63624 rattus norv
Q9yc35 aeropyrum p
Q9syc2 cucumis sat
Q9wxx1 thermocoga
Q9blt0 leishmania
Q7ux42 rhodopirell
Q7yx8 canis famil
Q9tz5 oryctolagus
Q87db2 xylella fas
Q7xy38 griffithsia
Q7x839 griffithsia
Q7x8289 yersinia pe
Q9sgg00 yersinia pe
Q9y2i5 homo sapien
Q86x52 homo sapien
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                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                    1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                 1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                     - protein search, using sw model
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Q9YC35
Q9YC35
Q9WXX1
Q9BLT0
Q7UX42
Q7YK8
Q9TRZ5
Q87DB2
Q9TRZ5
Q9TRZ5
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Q9U15
Q9Z35
Q9C15
Q8Z35
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
sp_unclassified:*
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sp_mammal:*
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Q8rve5 oryza sativ	Qarves	10	670	48.3	43	45
synech	070587	16	653	48.3	43	44
Q8cjq9 streptomyce	Q8CJQ9	16	511	48.3	43	43
	089154	16	481	48.3	43	42
	Q8VJI2	16	292	48.3	43	41
	Q9LDK8	10		48.3	43	40
С.	6HSN6Ö	4		48.3	43	39
08tv81 methanopyru	QBTV81	17		48.3	43	38
	Q8L479	10	193	48.3	43	37
	Q8BW77	11	184	48.3	43	36
	Q8BLG7	11	182	48.3	43	35
	Q8BW91	11	142	48.3	43	34
	Q9YBU3	17	105	48.3	43	3 6
Q94527 drosophila	094527	ß	971	4.64	4.4	3.0
Q9z1s8 mus musculu	09Z1SB	11	999	49.4	44	31
Q9r1x3 mus musculu	09R1X3	17	665	49.4	44	3.0
	Q9EQH1	11	999	49.4	44	29
D.	090252	Ŋ	613	49.4	44	28
Q8kz56 uncultured	08KZ56	N	520	49.4	44	27
Q83eh5 coxiella bu	Q83EH5	16	494	49.4	44	26
Q8gqm5 escherichia	OBGONS	~	487	49.4	44	25
052719 klebsiella	052719	7	487	49.4	44	24
Q8a0k9 bacteroides	QBA0K9	16	426	49.4	44	23
	022465	10	339	49.4	44	22
u	QBT2Z8	Ŋ	274	49.4	44	217
Q93jd6 streptomyce	93JD6	16	128	49.4	44	20
	Q8L4G8	10	625	50.0	44.5	19
L)	Q8T9L7	ហ	1687	50.6	45	18
Q9s814 arabidopsis	095814	50	1294	50.6	45	17

ALIGNMENTS

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Gaps
                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                      Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BCO184041, AAH18404.1; -. GO; GO:0008083; F:growth factor activity; IEA. InterPro: IRR0089896; Cytok IL1_like. InterPro: IRR0029896; Cytok IL1_like. Fight PRO02348; IL1_HBGF.
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PRINTS; PR00262; ILIHBGF.
PRODOM; PD000831; ILIHBGF; 1.
PRODOM; PD00442; FGF; 1.
SEQUENCE 209 AA; 22284 MW; 27925C43E5167823 CRC64;
                                                                            Last sequence update)
Last annotation update)
                               209 AA
                                            QN683;
01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last seqn
01-0CT-2003 (TrEMBLrel. 25, Last anno
Fibroblast growth factor 21.
                               PRT;
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Best Local Similarity 100.
Matches 15; Conservative
                                 PRELIMINARY;
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TISSUE=Lung;
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                                 Q8N683
RESULT 1
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1173 AA.

PRELIMINARY;

Q63624 ID Q63624

RESULT 2

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MEDLINE-9289316; Pubmd=10360571;
MEDLINE-99287316; Pubmd=10360571;
MEDLINE-99287316; Pubmd=10360571;
METLINE-99287316; Pubmd=10360571;
MATT D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.N., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.; "Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.";
Nature 399:322-329(1999).

ENBL, AB001667; AAD35210.1; -.
                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.

MEDLIFEZ-0267442; PubMed=10809445;

MEDLIFEZ-20567442; PubMed=10809445;

Pujii N., Kamada M., Yamasaki S., Takahashi H.;

Pujii N., Kamada M., Yamasaki S., Takahashi H.;

"Differential accumulation of Aux/IAA mRNA during seedling development

"Differential accumulation of Aux/IAA mRNA during seedling development
and gravity response in cucumber (Cucumis sativus L.).";

Plant Mol. Biol. 42:731-74(2000).

EMBL; AB026822; BAA858021-1;
                                                                                                                                                                                      Cucumis sativus (Cucumber).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.

NCBI_TaxID=3659;
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Pred. No. 16;
2; Mismatches 1; Indels
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GO; GO: 0006301; F: kinase activity; IEA.
GO; GO: 00064856; F: xylulokinase activity; IEA.
GO; GO: 00062465; P: carbohydrate metabolism; IEA.
GO; GO: 0005997; P: xylulose metabolism; IEA.
GO; GO: 0005997; P: xylulose metabolism; IEA.
InterPro; IPR004448; SASP.
InterPro; IPR004000; Xylulokinase.
Ffam; PF00370; FGGY; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02309; AUX IAA; I.
SEQUENCE 355 AA; 39030 MW; C471B7622522BD9 CRC64;
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                                                                               Last sequence update)
Last annotation update)
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GO; GO:0006445; P:regulation of translation; IEA.
InterPro; IPR00311; AUX IAA.
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PRT;
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78 LPGSESPERDP 88
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      Q9SSY2
Q9SSY2;
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A Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
A Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A.,
A Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
A Yamazaki J., Kushida N., Oguchi Y., Tanaka T., Kudoh Y.,
A Yamazaki J., Kushida N., Oguchi M., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
T. Complete genome sequence of an aerobic hyper-thermophilic
T. Tanarchaeou, Aeropyrum pernix Kl.";
DNA Res. 6.83-101(1999).
EMBL; AP000061; BAA80413.1; -.
EMBL; AP101(1999).
RR PR; G72619; G72619.
RR PR; G72619; G72619.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Desulfurococcaceae; Aeropyrum.
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein APR1416.
                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Matches 8; Conservative
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Best Local Similarity
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RESULT 4

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Q9SSY2

Query Match

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RESULT 3

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Gaps

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MEDLINE=22735913; PubMed=12835416;
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01-OCT-2003
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SEQUENCE
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NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zimmermann W., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
                                                                                                                                                                    Query Match
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A physical map of the Leishmania major Friedlin genome."; Genome Res. 8:135-145(1998).

EMBL; AL583933; CAC32260.1; -.

EMBL; AL583933; CAC32260.1; -.

EMBL; AL583933; CAC32260.1; -.

EMBL; AL583933; CAC32260.1; -.

EMBL; AL583933; CAC32260.1; -.

EMBL; AL583933; CAC3260.1; -.

EMBL; AL583933; CAC3260.1; -.

EMBL; AND AL5839 MN; C22D8283F006965E CRC64;
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                                                                                                                               492 AA; 54405 MW; 0F66A3AB451D88E1 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TTEMBLEE]. 17, Last sequence update) 01-0CT-2003 (TTEMBLEE]. 25, Last annotation update) Possible monocarboxylate transporter protein.
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                                                                                                                                                                                                                                                                                                                                                                                                             574 AA.
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                            TIGRFAMS; TIGR01312, XylB; 1.
PROSTITE; PRO033; FRGY KINASES_1; 1.
PROSTITE; PS00445; FGGY KINASES_2; 1.
PROSTITE; PS00304; SASP_1; 1.
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                                                                                                     Kinase, Complete proteome.
SEQUENCE 492 AA: 54405
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Best Local Similarity 57.1:
Matches 8; Conservative
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          Pfam; PF02782; FGGY_C; 1
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Q7UX42;
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MEDLINE=96181606; PubMed=8601571;
Sekiguchi M., Nakabeppu Y., Sakumi K., Tuzuki T.;
Sekiguchi M., Nakabeppu Y., Sakumi K., Tuzuki T.;
Sekiguchi M., Nakabeppu Y., Sakumi K., Tuzuki T.;
Suha-repair methyltransferase as a molecular device for preventing mutation and cancer.";
J. Cancer Res. Clin. Oncol. 122:199-206(1996).
HSSP; P06134; 15FE.
Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R.; "Complete genome sequence of the marine planctomycete Pirellula sp.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
0(6)-methylguanine-DNA methyltransferase (EC 2.1.1.63).
0xyctolagus cumicalus (Rabbit).
Cryctolagus cumicalus (Rabbit).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
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Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
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                                                                                                                                                                                                                                                                                                    DB 16; Length 601; 28;
                                                                                                                                                                                                                                                                                                                                                               4; Indels
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                                                                                                                                                  EMEL, BX24135; CAD72170.1; -. Acad. Sci. U.S.A. 100:8298-8303(2003).

EMEL, BX24135; CAD72170.1; -. Aminoacyl-tRNA synthetase; Ligase; Complete proteome. SEQUENCE 601 AA; 68668 MW; 0C6B526811FF4CD3 CRC64;
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01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
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Pred. No. 2.1e+02;
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Pred. No. 28;
0; Mismatches
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Local Similarity 57.1%;
les 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
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                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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STRAIN=cv. Nipponbare;
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Q7U8Z9
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MEDLINE=22421331; PubMed=12533478;
MEDLINE=22421331; PubMed=12533478;
Mydxi C.Y., Furlan L.K., Camargo L.B.A., da Silva A.C.R., Moon D.H.,
Mydxi C.Y., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tasi S.M.,
Goldman M.H.S., Goldman G.H., Lemos M.V., El-Dorry H., Tasi S.M.,
Carrer H., Carraro D.M., de Olivaira R.C., Nunes L.R., Siqueira W.J.,
Marino C.L., Gigiloti E., Abreu I.L., Alves L.M., od Amaral A.M.,
Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
A Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sana J.A.D.,
A Glosolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
Kitajima J.P.,
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GO; GO:0003908; F:methylated-DNA-[protein]-cysteine S-methylt. . .; IEA. GO; GO:0006281; P:DNA repair; IEA. InterPro; IPR008332; MethylG_Mtase. InterPro; IPR01497; Methyltransf_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xylella fastidiosa (strain Temeculal / ATCC 700964).
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
Xanthomonadaceae, Xylella.
NCBI_TaxID=183190,
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Pred. No. 14;
2; Mismatches 4; Indels
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InterPro; IPR010437; Prok lipprot S.
PROSITE; PS010013; PROKAR_IPOPROTEIN; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 111 AA; 13336 MW; 492CB96C4507E840 CRC64;
                                                                                   Pfam; PF01035; Methyltransf 1; 1.
Pfam; PF02870; Methyltransf 1; 1.
TIGREPAMS; TIGR0589; ogt; 1.
PROSITE; PR0374; MGMT; 1.
SEQUENCE 181 AA; 19397 MW; 12DF60974AA41A16 CRC64;
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01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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(TrEMBLrel. 25, Last sequence update)
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Pred. No. 16;
1; Mismatches
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Best Local Similarity 53.8
Matches 7; Conservative
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8; Conservative
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MEDLINE-2285697; PubMed=12917641;
Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain P., Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
Dufresne A., Partensky F., Webb E.A., Waterbury J.;
Nature 424:1037-1042 (2003).
PROBI, EX569690; CAR60975.1; -
SROUR SX569690; CAR60975.1; -
SROUR 3.26 AA, 35270 MW; EDC4DBDC51ER3526 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (OSJNBa0086P08.1 protein).
Oryza sativa (Rice).
Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Serine palmitoyltransferase (Fragment).
Griffithsia japonica.
Bukaryota; Rhodophyta; Florideophyceae; Ceramiales; Ceramiaceae; Griffithsia.
NCBI_TAXID=83288;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative glycosyltransferase family 4 protein (BC 2.4.1.-).
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Best Local Similarity 57.1%; Pred. No. 44;
Matches 8; Conservative 1; Mismatches 5; Indels
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Liu C., Lee Y., Lee H.,
Submitted (1907-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AFS42030, AAP80840.1; -.
                                                                                                                                                                                                                                                                                                                                                                          NON TER 178 178 SEQUENCE 178 AA; 20056 MW; 4264182D29A597FF CRC64;
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NCBI_TaxID=84588;
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114 HIPGPRTPHDQPS 126
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Matches 6; Conservative
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TIGRFAMB; TIGR01312; XylB; 1
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STRAINS=KIMS / Biovar Mediaevalis;
STRAINS=KIMS / Biovar Mediaevalis;
STRAINS=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
Perry R.D.;
"Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
EMBL; AJ41417; CAC90122.1.
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MEDLINE=21470413; PubMed=11586360;
MEDLINE=21470413; PubMed=11586360;
MEDLINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Banham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague.";
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Enterobacteriaceae; Yersinia.
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                                                                                                                                   Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0708G02.";
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Pred, No. 47;
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                                                                 Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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GO, GO:0016301, F:Kinase activity; IEA.
GO, GO:0004886; F:xylulokinase activity; IEA.
GO, GO:0005975; P:carbohydrate metabolism; IEA.
GO:0005997; P:xylulose metabolism; IEA.
InterPro; IPR000577; FGGY kin.
InterPro; IPR006000; Xylulokinase.
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Pfam; PF02782; FGGY C; 1.
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Matches 9; Conservative
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MEDLINE-99246063; PubMed=10231032;
Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
Miyajima O., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XIII.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 6:63-70(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE=11486534; PubMed=11514575; Kitagawa H., Uyama T., Sugahara K.; Kitagawa H., Uyama T., Sugahara K.; "Molecular Cloning and Expression of a Human Chondroitin Synthase."; J. Biol. Chem. 276:38721-38726 (2001). EMBL; AB03207; BAA76834.1; -. EMBL; AB071402; BAB64936.1; -.
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Homo sapiens (Human).

Busaryota: Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                           50.6%; Score 45; DB 16; Length 517; 53.3%; Pred. No. 71;
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                                                                                                                                                                                  Indels
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Pfam; PF05679; CHGN; 1.
Hypothetical protein.
SEQUENCE 802 AA; 91729 MW; 9115C204FAF298D7 CRC64;
PROSITE; PS00933; FGGY_KINASES_1; 1.
PROSITE; PS00445; FGGY_KINASES_2; 1.
Hypothetical protein; Kinase; Complete proteome.
SEQUENCE 517 AA; 54066 MW; C836FB87C12BB111 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (Trembirel. 12, Created)
01-NOV-1999 (Trembirel. 12, Last sequence update)
01-OCT-2003 (Trembirel. 25, Last annotation update)
Hypothetical protein KIAA0990 (Chondroitin synthase)
KIAA0990 OR CHSY.
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01-UNN-2003 (TrEMBLrel. 24, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
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2; Mismatches
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                                                                                                                                                                                                                                             1 HLPGNKSPHRDPAPR 15
                                                                                                       Query Match
Best Local Similarity 55...
Best Local Similarity
Formula 19 Conservative
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es 7; Conservative
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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939 HLPNNKSGYWDPS 951
 1 HLPGNKSPHRDPA 13
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nes 9; Conserv
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Matches
                                                           RESULT 18
QBT9L7
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                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicocyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W., Rudd S.,
Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1294 AA; 140955 MW; 1A806303B8BBB71B CRC64;
                                                                         Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBU databases.
                  Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC046247; AAH46247.1; -. SEQUENCE 802 AA; 91784 MW; SB4C02670332FA0E CRC64;
                                                                                                                                                                                                                          01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                          50.6%; Score 45; DB 4; I
63.6%; Pred. No. 1.1e+02;
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GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                     PRT; 1294 AA
                                                                                                3; Mismatches
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MEDLINE=99316073; Pubmed=10381874;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA REG. 4:215-230(1997).
EMBL; AF141203; AAD41077.1;
EMBL; AF141202; AAD41076.1;
EMBL; AL162751; CAB83384.1;
EMRL; AB349; T48349.
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PRINTS; PR00447; NATRESASSCMP.
ProDom; PD001861; Nramp; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                          Science 284:2148-2152(1999)
                                                                            Query Match 50.6
Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                             519 LPGSKSEHKEP 529
                                                                                                                        2 LPGNKSPHRDP 12
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE FROM N.A.
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            rissum=Brain;
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Gaps

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8; Conservative

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Int. J. Parasitol. 0:0-0(2002).

EMBL; AV059630; AAL27793.2; --
GO; GO:0005737; G:cytoplasm; IEA.
GO; GO:000524; F.ATP binding; IEA.
GO; GO:0016874; F.ATP binding; IEA.
GO; GO:0016874; F.Riges activity; IEA.
GO; GO:0016876; F.Riges activity; IEA.
GO; GO:0006807; P:nitrogen metabolism; IEA.
GO; GO:0019896; P:ryrimidine base biosynthesis; IEA.
                                                                       01-JUN-2003 (TrEMBLrel: 24, Last sequence update)
01-OCT-2003 (TrEMBLrel: 25, Last annotation update)
Carbamoyl phosphate synthetase II (EC 6.3.5.5).
Toxoplasma gondii.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fox B.A., Bzik D.J.; "Novel organization and sequences of glutamine-dependent carbamoyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1687;
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60.0%; Pred. No. 2.4e+02;
.ive 0; Mismatches 6; Indels
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PRT; 1687 AA.
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InterPro; IPRO05483; CPase_L_D2.
InterPro; IPRO05480; CPase_L_D2.
InterPro; IPRO05480; CPase_L_D3.
InterPro; IPRO05481; CPase_L_D3.
InterPro; IPRO05481; CPase_L_D3.
InterPro; IPRO0591; GATSE-I_N.
InterPro; IPRO0991; GATSE-I_N.
InterPro; IPRO0991; GATSE-I_D2; Pfam; PF02289; CPSase_L_D2; 2.
Pfam; PF02786; CPSase_L_D2; 2.
Pfam; PF02787; CPSASE_L_D3; 1.
PRINTS; PRO0099; CPSASE.
PRINTS; PRO0099; CPSASE.
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TIGREAMS; TIGRO1369; CPSASELI_LYG; 1.
PROSITE; PSO0866; CPSASE_1; 2.
PROSITE; PSO0867; CPSASE_2; 1.
PROSITE; PSO0442; GATASE_TYPE_1; 1.
                                                           01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2003 (TrEMBLrel. 24, Last sequen-o1-OCT-2003 (TrEMBLrel. 25, Last and
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21848414; PubMed=11859373;
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PRINTS; PR00099; CPSGATASE.
PRINTS; PR00096; GATASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Toxoplasma gondii.";
Nature 415:926-929(2002).
         PRELIMINARY;
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339 AA; 36477 MW;
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(TrEMBLrel. 05, L
(TrEMBLrel. 24, L
(Fragment).
                                                                                                                                          49.48;
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                                                                                                                     Query Match
Best Local Similarity 66...
8; Conservative
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194 DKSPHNDPLP 203
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CL Brener;
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01-JUN-2003 (
GH1 protein (
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01-JUN-2002
01-JUN-2002
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                                                                                                                       01-UNA-2002 (TrEMBLrel. 22, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
P067GG08.4 protein (OSJNBB0093M23.16 protein).
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryzeae; Oryzeae; Oryzeae; Oryzeae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CY. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
-clone:OSJNBb0093M23.";
Submitted (JUL-2001) to the BMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CV. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone:P0676G08.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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Gramen; QBL4G8; -.
GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPR004655; C4dc/mal_transpt.
Pfam; PP03595; C4dic_mal_tran; 1.
Pramenre 625 AA; 68596 MW; BOEBCA498ECC47DB CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRA-2003 (TrEMBLrel. 23, Last annotation update)
Putative secreted protein.
SCO5991 OR STBAC16H6.26 OR SCBAC16H6.26.
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                                                                                        PRELIMINARY;
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Best Local Similarity
Matches 9; Conserv
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
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                                                                                                                                                                                                                             Gaps
"Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
BMBL; A1939125; CAC44605.1; -.
Complete proteome.
SEQUENCE 128 AA; 12736 MW; CD0FC3CFAE94821E CRC64;
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Hagen G., Guilfoyl T.J.;
Submitted (ULL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF016633; AAB70005.1; -.
PIK; TOF526; TOF526.
TRANSTAC; TOF524; -.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0006445; P:regulation of translation; IEA.
InterPro; IFR003311; AUX IAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andersson B., Bontempi E.J.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC096945; AAL190893.1; -
SEQUENCE 274 AA; 28374 MW; 76635EA2BA24A09D CRC64;
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Bscherichia.
       MEDLINE-98304087; PubMed=9639934;
Henel H., Shakeri-Garakani A., Turgut S., Lengeler J.W.;
"Genes for D-arabinitol and ribitol catabolism from Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kane P.W., LaFayette P.R., Parrott W.A.;

Kane P.M., LaFayette P.R., Parrott W.A.;

"Cloning and characterization of the arabitol operon.";

"Cloning and characterization of the arabitol operon.";

"Cloning and characterization of the arabitol operon.";

"Explainted (MAY-2001) to the EMEL/GenBank/DDBJ databases.)

R GO; GO:001301; F:kinase activity; IEA.

R GO; GO:0004856; F:xylulokinase activity; IEA.

R GO; GO:0005975; P:xylulokinase activity; IEA.

R GO; GO:0005975; P:xyluloke metabolism; IEA.

R InterPro; IPR006000; Xylulokinase.

R Fram: PF00782; FGGY_C; 1.

R FIGRFAMS; TIGR01312; XylB; 1.

R PROSTIE; PS00933; FGGY_KINASES_1; 1.
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46.7%; Pred. No. 96;
tive 3; Mismatches 5; Indels
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Last annotation update)
                                                                                  pneumoniae.";
Microbiology 144:1631-1639(1998).

EMBL; ARO45245; AAC26499.1;
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0004856; F:xylulokinase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0005997; P:xylulose metabolism; IEA.
InterPro; IPR000577; FGGY kin.
InterPro; IPR006000; Xylulokinase.
FEan; PF00370; FGGY (2; 1.)
FFan; PF00370; FGGY (2; 1.)
FFan; PF00370; FGGY (2; 1.)
FFAN; PF00370; FGGY (1; 1.)
FFAN; PF00370; FGGY (2; 1.)
FFAN; PF00370; FGGY (1; 1.)
FFAN; FF00370; FGGY (1; 1.)
FFAN; FF00370; FGGY (1; 1.)
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FFAN; FF00370; FGGY (1; 1.)
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Best Local Similarity 46...
7; Conservative
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Escherichia coli.
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MEDINRE-2550868; PubMed=12663928;

X.M. J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,

Chiang H.C., Hooper L.V., Gordon J.I.;

"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";

Science 299:2074-2076(2003).

EMBL; AE016943; AA079117.1; -.

R GO; GO:0016020; C:membrane; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004009; F:ATP binding; Cassette (ABC) transporter acti. ..; IEA.

RO; GO:0006810; P:transport; IEA.

InterPro; IFR003493; ABC transporter.

R AIP-binding; Complete proteome.

SR AIP-binding; Complete proteome.

SR SEQUENCE 426 AA, 48748 MW; 635D2514FF7FEBF8 CRC64;
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MEDLINE=97464425; PubMed=9324246;
Heuel H., Turgut S., Schmid K., Lengeler J.W.;
Hauel H., Turgut S., Schmid K., Lengeler J.W.;
substrate recognition domains as revealed by active hybrids between the D-arabinitol and ribitol transporters from Klebsiella
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Enterobacteriaceae; Klebsiella
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
NCBI_TaxID=818;
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01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CTT-2003 (TrEMBLrel. 25, Last annotation update)
Putative ABC oligo/dipeptide transport, ATP-binding protein.
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                           DB 10; Length 339;
66;
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Pred. No. (
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                                49.48;
                                                    ilarity 63.6%;
Conservative
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Matches 8; Conservative
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                                                                                                                         2 LPGNKSPHRDP 12
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Best Local Similarity
Matches 7; Consera
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SEQUENCE
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MEDLINE=21822632; PubMed=11832943;
MEDLINE=21822632; PubMed=11832943;
Habela O., Suzuki M.T., Fraser C.M., DeLong E.F.,
Hamada T., Eisen J.A., Fraser C.M., DeLong E.F.,
"Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
"Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
"Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
"Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
GO, GO:0016593; P:oxidoreductase activity, acting on iron-sul. .; IEA.
GO, GO:0016593; P:chlocopyll biosynthesis; IEA.
GO, GO:0016685; P:photosynthesis, dark reaction; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                     STRAINE-NINE Wile phase I / RSA 493;
MEDLINE=22608657; PubMed=12704232;
Seahadri R., Paulusen I.T., Eisen JA., Read T.D., Nelson K.E., Seahadri R., Paulusen I.T., Eisen JA., Read T.D., Nelson K.E., DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J., Thouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A., Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F., "Complete genome sequence of the Q-fever pathogen, Coxiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                      Coxiella burnetii.
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.4%; Score 44; DB 16; Length 494; 46.7%; Pred. No. 97; arive 3; Mismatches 5; Indels
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 24, Last annotation update)
Light-independent protochlorophyllide reductase, B subunit.
BCHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54281 MW; D9A2C6C9F48C254E CRC64;
                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                      GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0004856; F:xylulokinase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR000577; FGGY kin.
InterPro; IPR006000; Xylulokinase.
Pfam; PF02702; FGGY 7:
Pfam; PF02702; FGGY 7: 1.
Pfam; PF02702; KGGY 7: 1.
                                                                                                                                                                                                                                                                                                   burnetii.";
Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uncultured proteobacterium.
Bacteria; Proteobacteria; environmental samples.
NCBI_TaxID=153809;
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                  494 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGREAMS; TIGRO1312; XylB; 1.
PROSITE; PS00933; FGGY_KINASES_1; 1.
PROSITE; PS00445; FGGY_KINASES_2; 1.
Kinase; Complete protecome.
                                           Created)
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                  PRT;
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337 YLSGERTPHNDPYAR 351
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                                       01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25, Xylulokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                  PRELIMINARY;
                                                                                                                                       Coxiellaceae; Coxiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         494 AA;
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               CBU0346; -.
                                                                                                 XYLB OR CBU0346.
                                                                                                                                                  NCBI_TaxID=777;
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                     083EH5
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Matches
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       Q83EH5
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"Identification of Gab2 as the major molecule responsible for EGF-
induced PI3-kinase activation and DNA synthesis in rat hepatocytes.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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I. SIMILARITY: CONTAINS 1 PH DOWAIN.
EMBL, AF230367; AG44268.2;
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InterPro; IPR001849; PH.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                          Length 520;
                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    investigating biology.";
Science 283:2012-2018(1998).
EMBL, AL132864; CAB63392.1; -.
WORTHER: V5314A.1; CE22431.
SEQUENCE 613 AA; 68897 MW; B55ABCA6062C338D CRC64;
InterPro; IPR000510; Oxred_nitrognsel.
InterPro; IPR00569; Protochl_reductB.
Pfam; PF00148; oxidored_noxidored_noxidored_TGR01278; DPOR_BchB; 1.
IIGREDAMS; TIGR01278; DPOR_BchB; 1.
SEQUENCE 520 AA; 57358 MW; CB71D34682586EEI CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                             49.4%; Score 44; DB 2; 61.5%; Pred. No. 1e+02;
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152 PGTQRPSRDPAVR 164
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                                                                                                                                                                       Best Local Similarity 61.5
Matches 8; Conservative
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Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y53H1A.1 protein.
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094527
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Gu H., Pratt J.C., Burakoff S.J., Neel B.G.;
"Cloning of p97/Gab2, the major SHP2-binding protein in hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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EMBL, AB01841TY: CONTAINS 1 PH DOMAIN.
                                                                                                                                                                                                                     Gaps
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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GQ; GQ:0005515; F:protein binding; IPI.
GQ; GQ:0016477; P:cell migration; IDA.
GQ; GQ:0007229; P:integrin-mediated signaling pathway; IDA.
InterPro; IPR001849; PH.
Pfam; PF00169; PH; 1.
PROSITE; PS50003; PH; 1.
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                                                                                                                                                   Score 44; DB 11; Length 665;
Pred. No. 1.3e+02;
2; Mismatches 2; Indels
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SMO0233; PH; 1.
2; PSSC0003; PH DOMAIN; 1.
2; PSSC0003; PH DOMAIN; 1.
73208 MW; E8955EE638174085 CRC64; 1-ength
                                            SMART; SM00233; PH; 1.
PROSITE; PS50003; PH DOMAIN; 1.
SEQUENCE 665 AA; 73328 MW; BEB170B69406063E CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
PH domain containing adaptor molecule p97/Gab2.
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Last annotation update)
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                49.4%;
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
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                                                                                                                                                                   Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                          610 PGSPSPHRKPS 620
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                  Pfam; PF00169; PH; 1.
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Best Local Similarity
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
Adamstides P.G., Scherer S.E., Holt P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Holt P.W., Hongkins R.A., Henderson S.N.,
Sutton G.G., Wortunn J.R., Yandell M.D., Champe M., Pfeiffer B.D.,
Brandon R.C., Rogers Y.-H.C., Plazej R.G., Champe M., Pfeiffer B.D.,
Abril J.F., Agbayani A., An H.-J., Andrews P.Famnkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews P.Famnkoch C., Baldwin D.,
Ballew R.M., Banos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Besson K.Y., Benos P.V., Berman B.P., Braderi D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Broketen P., Brottier P.,
Burtis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Burtis R.C., Daulew S., Dahlke C., Davenport L.B., Davies P.,
A Deablos B., Delcher A., Deng Z., Mays R.J., Dew I., Dietz S.M.,
A Dodson K.J., Evangelista C.C., Ferraz C., Ferriers S., Fleischmann W.,
A Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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cells, reveals a novel pathway for cytokine-induced gene activation.";
-!- SIMILARITY: CONTAINS 1 PH DOMAIN.
BMBL; AF104244; AAD05166.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     094527; Q9VHIO; Q9U6H5; 02, Created) 01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-CT-2003 (TrEMBLrel. 25, Last annotation update) 8e1/NF-kappa B homolog (Rel protein) (Transcription factor maternal isoform) (GH01881p).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 11; Length 666;
Pred. No. 1.3e+02;
                                                                                                                                                      MGD; MGI:1333864; Gab2.

GO; GO:005515; F:protein binding; IPI.

GO; GO:005515; F:protein binding; IPI.

GO; GO:0007229; F:integrin-mediated signaling pathway; IDA.

GO; GO:0007229; F:integrin-mediated signaling pathway; IDA.

InterPro; IPR001849; PH.

PFam; PF00169; PH; 1.

PRORTIE; PS50003; PH: DOMAIN; 1.

SEQUENCE 666 AA; 73295 MW; D3B6D568CFCBA3F7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (MAJOR ISOFORM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 63...
7; Conservative
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Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
Houstin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Rimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Nelson D.R., Nelson K.A., Nixon K., Pallard J., Puri V., Reese M.G.,
Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Siden-Kiamos I., Simpson M., Skrong R., Sun B.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Williams S.M., Woodage T., Weinsteck G.M., Weissenbach J.,
Ra Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhu S., Zhu X., Smith H.O.,
Rh Gibbs R.A., Myers E.W., Rubin G.M., Wenter J.C.;
Rh Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
R. Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0014018; Rel. GO; GO:0005634; C:nucleus; NAS. GO; GO:0005634; C:nucleus; NAS. GO; GO:0003704; F:specific RNA polymerase II transcription fa. . .; NAS. GO; GO:0006963; P:antibacterial polypeptide induction; IMP. GO; GO:0006967; P:antifungal polypeptide induction; IMP. GO; GO:0006955; P:immune response; IEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Y. C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRUBLIE; FSDV&21; ALLETALIVE SPLICING; Repeat.
ANK repeat; Alternative Splicing; Repeat.
VARSPLIC 1 112 Missing (in isoform Maternal).
/FTId=VSP_050089.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Maternal;

Isord=0945.7-2; Sequence=VSP_050089;

EMBL; U62005; AAB17264.1; --

EMBL; AF186073; AAF07931.1; --

EMBL; AF186073; AAF07932.1; --

EMBL; AE003681; AAF07933.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q94527-1; Sequence=Displayed;
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PROSITE; PS50297; ANK REP REGION; 1.
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InterPro; IPR002110; Ig-like.
InterPro; IPR000110; Ig-like.
InterPro; IPR000909; IPT IIG.
InterPro; IPR000909; IPT IIG.
InterPro; IPR000967; F53-like.
Pfam; PP00023; ank; 5.
Pfam; PP00554; RHD; 1.
Pfam; PP01833; IIG; 1.
PRINTS; PR00057; NPKBINSCPECT.
SMART; SM00429; ANK; 4.
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The RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:652-573 (2002).
EMBL, AK053193, BAC35307.1; -.
MON; MGT.2442914; E030030106Rik.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0006468; P:protein winase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IRR000719; Prot_kinase.
ProDom; PD000001; Prot_kinase; 1.
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                                                                                                                                                                                                                                                                     Ή.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                   Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi l Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Fumahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Pred. No. 28;
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                                                                                                                                     Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales; Desulfurococcaceae, Aeropyrum.
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OGT-2003 (TrEMBLrel. 25, Last annotation update)
Weakly similar to cyclin-dependent kinase 6 (Fragment).
B030030106RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; C72631; C72631.
Hypothetical protein; Complete proteome.
SEQUENCE 105 AA; 11568 MW; 5E33500281A43CC0 CRC64;
                         01-NOV-1999 (TrEWBLrel. 12, Created)
01-NOV-1999 (TrEWBLrel. 12, Last sequence update)
01-JUN-2003 (TrEWBLrel. 24, Last annotation update)
Hypothetical protein APE1506.
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58.3%; Pred. No. 20,
           105 AA
                                                                                                                                                                                                                                                                                                                                                                         crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
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STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=22354683; PubMed=12466851;
           PRT;
                                                                                                                                                                                                                                            MEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP000061; BAA80505.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 HLPNNKASHKLP 67
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             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxiD=10090;
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                             Aeropyrum pernix.
                                                                                                                                                                              NCBI_TaxID=56636;
                                                                                                                                                                                                                                STRAIN=K1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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             O9YBU3
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Matches
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O9YBU3
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Gaps

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2; Mismatches

7; Conservative

Matches

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Nature 420:563-573 (2002).
EMBL; AK054034; BAC35627.1; -.
MGD; MGI:1914869; Noblp.
                                                                                                                                                                                                                                             20995 MW;
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                                                                                                         InterPro; IPR002051; DUF133.
InterPro; IPR005056; PINC.
ProDom; PD013236; DUF133; 1.
SEQUENCE 184 AA; 20995 MW;
                                                                                                                                                                                                                                                                                                          48.3%;
                                                                                                                                                                                                                                                                                                                                       50.0%;
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129 HLPSKVNPFRSPGP 142
50,770 full-length cDNAs.";
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                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.0%
Tocal Similarity 50.0%
Tocal Similarity 50.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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01-OCT-2002
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XRAIN-C57BL/6J;

XRAIN-C57BL/6J;

XA The FARTOM Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team;

Analysis of the mouse transcriptome based on functional annotation of

"Analysis of the mouse transcriptome based on functional annotation of

"Analysis of the mouse transcriptome based on functional annotation of

"Go, 770 full-length cDNAs.";

In Nature 420:553-573 (2002).

REMBL, AKO45260; BAG12285-1;

RGD, GO:0005524; F:ATP binding; IEA.

GO; GO:0006469; P:protein kinase activity; IEA.

RO; GO:0006469; P:protein amino acid phosphorylation; IEA.

REMDL, PRODON; PROL_Kinase.

REMDL, PRODONO1; Prot_Kinase.

REMDL, PRODONO1; Prot_Kinase.

REMDL, PRODONO1; Prot_Kinase.

REMDL, PRODONO1; Prot_Kinase.

REMDL, PRODONO1; Prot_Kinase.

REMDL, PRODONO1; Prot_Kinase.

REMDL, PRODONO1; Prot_Kinase.

REMDL, PRODONO1; Prot_Kinase.

REMDL, PRODONO1; Prot_Kinase.

REMDL, PRODONO1; Prot_Kinase.
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STRAIN=C57BL/6J; IISSUE=Oviduct;
MEDLINE=22356681; PubMed=12466851;
The FANTOM Consortium.
the RANTOM Cenome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                   48.3%; Score 43; DB 11; Length 142; 63.6%; Pred. No. 38; 1; Mismatches 3; Indels tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Weakly similar to cyclin-dependent kinase 6 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20254 MW; 2CDCF1C442030048 CRC64;
                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23,
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                                                                                                                   Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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NOB1P OR 1700021109RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEGUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
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                                                                                                                       Gaps
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Gryza sativa (japonica cultivar-group).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
predicted serine protein kinase homologous to HPr protein kinase,
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Pred. No. 53;
1; Mismatches 3; Indels
                                                     Score 43; DB 11; Length 184;
Pred. No. 50;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
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193 AA; 20042 MW; A6F4D87037409BC0 CRC64;
705EEF164881F74E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 AA.
                                                                                                                                                                                                                                                                                                                                                                                                       193 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B1129G05.17 protein (B1151A10.8 protein). B1129G05.17 OR B1151A10.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 22, Created)
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1 HLPGNKSPHRDPAPR 15 |:| :| || || || 21 HIPTPGAPHSDPGAR 35

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Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.S.,
A. Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.S.,
A. Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
A. Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
A. Reichwald K., Rump A., Schillabel M., Schudy A., Zimmermann W.,
A. Reichwald K., Rump A., Schillabel M., Schudy A., Zimmermann W.,
A. Rosenthal A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
A. Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
A. Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Blocker H.,
A. Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
A. Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
A. Lehrach H., Reinhardt R., Yappo M.L.,
E. Bubl., Anis 302, CabBodel I.J.
E. Embl., Anis 302, CabBodel I.J.
E. Embl., Anis 302, CabBodel I.J.
E. Goloobson; F.copper ion binding; IEA.
GO; GO:0005108; Pelectron transporter activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                     Machanian 2017, Mazhevaya K.V., Makarova K.S., Polushin N.N., Sheazrev A.I., Mazhevaya K.V., Makarova K.S., Polushin N.N., Sheazrev J.I., Mazhevaya K.V., Belova G.I., Aravind L., Natcharle D.A., Rogorin I.B., Tatusov K.L., Wolf Y.I., Stetter K.O., Malykh A.G., Koonin E.V., Kozyavkin S.A., "The complete genome of hyperthermophile Methanopyrus kandleri AVI9 and monophyly of archaeal methanogens.";

Proc. Natl. Acad. Sci. U.S. A. 199:4644-4649(2002).

EMBL, AB010441; AAM02725.1; -.. 99:4644-4649(2002).

GO, GO:0005224; Fapre binding; IEA.

GO, GO:0006524; Fapre ein kinase activity; IEA.

GO, GO:0006109; Piregulation of carbohydrate metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.3%; Score 43; DB 4; Length 211; 46.7%; Pred. No. 58; 6; Indels varive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             48.3%; Score 43; DB 17; Length 208; 50.0%; Pred. No. 57; tive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 AA; 22808 MW; CACB55D0EB2DF1AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          208 AA; 23128 MW; 2C5007356A714665 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                              SEQUENCE FROM N.A.
STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000923; BlueCu 1.
PROSITE; PS00196; COPPER_BLUE; 1.
                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003755; Hpr kinase.
Pfam; PF02603; Hpr kinase; 1.
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141 IPGPHHPHHDPSMR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LPGNKSPHRDPAPR 15
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Best Local Similarity 50.0
Matches 7; Conservative
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Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                       NCBI_TaxID=2320;
          Methanopyrus
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NON TER
SEQUENCE
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Gaps

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                                                                                                    ESTS AU083004.

Oryza sativa (Rice).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
                                                                                                                                                                                                               SEGUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Sasaki T., Matsumotto T., Yamamotto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                     SEGUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.3%; Score 43; DB 10; Length 281; 66.7%; Pred. No. 78;
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                                                                                                                                                                                                                                                                                                                                                                                   clode:P0431F01.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001859; BAA94790.1;
EMBL; AP001856; BAA92982.1;
                                                                                                                                                                                                                                                                                           Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gramene, Q9LDK8; -.

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0006445; P:regulation of translation; IEA.
Interpro; IPRO3311; AUX IAA.
Pfam; PFC2309; AUX IAA, 1.
SEQUENCE 281 AA; 30298 WW; 895B293680354BA0 CRC64;
                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                           281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
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                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
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61 LPGSESPORRPA 72
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                           PRELIMINARY;
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Best Local Similarity
Matches 8; Conserv
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                             Q9LDK8
RESULT 40
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